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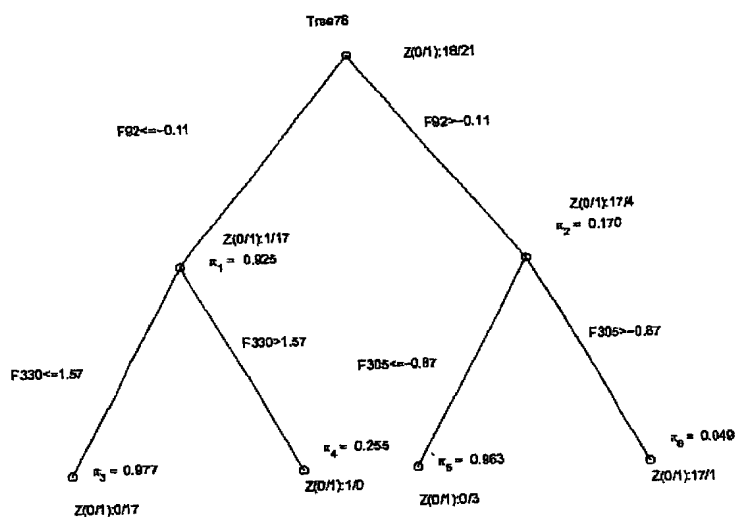
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(54) Title: BINARY PREDICTION TREE MODELING WITH MANY PREDICTORS AND ITS USES IN CLINICAL AND GENOMIC APPLICATIONS



(57) Abstract: The statistical analysis described and claimed is a predictive statistical tree model that overcomes several problems observed in prior statistical models and regression analyses, while ensuring greater accuracy and predictive capabilities. Although the claimed use of the predictive statistical tree model described herein is directed to the prediction of a disease in individuals, the claimed model can be used for a variety of applications including the prediction of disease states, susceptibility of disease states or any other biological state of interest, as well as other applicable non biological states of interest. This model first screens genes to reduce noise, applies kmeans correlation-based clustering targeting a large number of clusters, and then uses singular value decompositions (SVD) to extract the single dominant factor (principal component) from each cluster. This generates a statistically significant number of cluster-derived singular

factors, that we refer to as metagenes, that characterize multiple patterns of expression of the genes across samples. The strategy aims to extract multiple such patterns while reducing dimension and smoothing out genespecific noise through the aggregation within clusters. Formal predictive analysis then uses these metagenes in a Bayesian classification tree analysis. This generates multiple recursive partitions of the sample into subgroups (the "leaves" of the classification tree), and associates Bayesian predictive probabilities of outcomes with each subgroup. Overall predictions for an individual sample are then generated by averaging predictions, with appropriate weights, across many such tree models. The model includes the use of iterative out-of-sample, cross-validation predictions leaving each sample out of the data set one at a time, refitting the model from the remaining samples and using it to predict the hold-out case. This rigorously tests the predictive value of a model and mirrors the real-world prognostic context where prediction of new cases as they arise is the major goal.



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BINARY PREDICTION TREE MODELING WITH MANY PREDICTORS AND ITS USES IN CLINICAL AND GENOMIC APPLICATIONS

FIELD OF THE INVENTION

5 The field of this invention is the application of classification tree models incorporating Bayesian analysis to the statistical prediction of binary outcomes especially in clinical, genomic and medical applications.

BACKGROUND OF THE INVENTION

10 Bayesian analysis is an approach to statistical analysis that is based on the Bayes's law, which states that the posterior probability of a parameter p is proportional to the prior probability of parameter p multiplied by the likelihood of p derived from the data collected. This increasingly popular methodology represents an alternative to the traditional (or frequentist probability) approach: whereas the
15 latter attempts to establish confidence intervals around parameters, and/or falsify a-priori null-hypotheses, the Bayesian approach attempts to keep track of how a-priori expectations about some phenomenon of interest can be refined, and how observed data can be integrated with such a-priori beliefs, to arrive at updated posterior expectations about the phenomenon.

20 Bayesian analysis have been applied to numerous statistical models to predict outcomes of events based on available data. These include standard regression models, e.g. binary regression models, as well as to more complex models that are applicable to multi-variate and essentially non-linear data. Another such model is commonly known as the tree model which is essentially based on a
25 decision tree. Decision trees can be used in clarification, prediction and regression. A decision tree model is built starting with a root mode, and training data partitioned to what are essentially the "children" modes using a splitting rule. For instance, for clarification, training data contains sample vectors that have one or more measurement variables and one variable that determines that class of the sample.

30 Various splitting rules have been used; however, the success of the predictive ability varies considerably as data sets become larger. Furthermore, past attempts at determining the best splitting for each mode is often based on a "purity" function

calculated from the data, where the data is considered pure when it contains data samples only from one clan. Most frequently used purity functions are entropy, gini-index, and towing rule. The success of each of these tree models varies considerably and their applicability to complex biological and molecular data is often prone to difficulties. Thus, there is a med statistical model that can consistently deliver accurate results with high predictive capabilities. The present invention describes a statistical predictive tree model to which Bayesian analysis is applied incorporating several key innovations described herewith.

The statistical analysis enabled by the statistical models of the present invention enable a predictive analysis of complex multi-variable data to predict an outcome of a state. Such outcomes include, but are not limited to, biological outcomes, such as clinical and medical outcomes. In a preferred embodiment, such clinical and/or medical outcomes are the occurrence of a disease or a disease state based on the statistical analysis of clinical and/or genomic data. The present invention allows the integration of currently accepted risk factors with genomic data and carries the promise of focusing the practice of medicine on the individual patient – not merely to groups of patient populations. Such integration requires interpreting the complex, multivariate patterns in gene expression data, and evaluating their capacity to improve clinical predictions. The present invention enables this in a study of predicting nodal metastatic states and relapse for breast cancer patients.

The present invention identifies aggregate patterns of gene expression termed metagenes that associate with disease state indicators such as lymph node status and with recurrence, and that are capable of honestly predicting outcomes in individual patients with about 90% accuracy. The identified metagenes define distinct groups of genes, suggesting different biological processes underlying these two characteristics of breast cancer. This is important from both a regulatory, mechanistic and clinical perspective.

Multiple aggregate measures of gene expression profiles define valuable predictive associations with clinical indicators for the individual patient. These results indicate the potential for gene expression data to aid in achieving more accurate individualized prognosis. Importantly, this is evaluated in terms of precise numerical predictions, via ranges of probabilities of outcome, for the individual

patient. Such precise and statistically valid assessments of patient-specific risk will ultimately be of most value to clinical practitioners faced with treatment decisions.

Genomic information, in the form of gene expression signatures, has an established capacity to define clinically relevant risk factors in disease prognosis.

- 5 Recent studies have generated such signatures related to lymph node metastasis and disease recurrence in breast cancer (See West,M. *et al.* Predicting the clinical status of human breast cancer by using gene expression profiles. *Proc. Natl. Acad. Sci. USA* 98, 11462-11467 (2001); Spang,R. *et al.* Prediction and uncertainty in the analysis of gene expression profiles. *In Silico Biol.* 2, 0033 (2002); van'T Veer,L.J. *et al.* Gene expression profiling predicts clinical outcome of breast cancer. *Nature* 415, 530-536 (2002); van de Vijver,M.J. *et al.* A gene-expression signature as a predictor of survival in breast cancer. *N. Engl. J. Med.* 347, 1999-2009 (2002); Huang,E. *et al.* Gene expression predictors of breast cancer outcomes. *Lancet* in press, (2003)) as well as in other cancers (See Pomeroy,S.L. *et al.* Prediction of central nervous system embryonal tumour outcome based on gene expression. *Nature* 415, 436-442 (2002); Alizadeh,A.A. *et al.* Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. *Nature* 403, 503-511 (2000); Rosenwald,A. *et al.* The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma; Bhattacharjee,A. *et al.*
- 15 Classification of human lung carcinomas by mRNA expression profiling reveals distinct adenocarcinoma subclasses. *Proc. Natl. Acad. Sci. USA* 98, 13790-13795 (2001); Ramaswamy,S. *et al.* Multiclass cancer diagnosis using tumor gene expression signatures. *Proc. Nat'l. Acad. Sci.* 98, 15149-15154 (2001); Golub,T.R. *et al.* Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science* 286, 531-537 (1999); Shipp,M.A. *et al.* Diffuse large B-cell lymphoma outcome prediction by geneexpression profiling and supervised machine learning. *Nat. Med.* 8, 68-74 (2002); Yeoh,E.-J. *et al.* Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. *Cancer Cell* 1, 133-143 (2002)) and non-cancer disease contexts. The challenge addressed by the instant invention is the integration of such genomic information into prognostic models that can be applied in a clinical setting to improve the accuracy of treatment decisions as
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well as the development of new treatment and drug regiments for the treatment of disease.

Two issues are critical in achieving this goal. First, we need modeling approaches that focus on the generation of predictions for the individual patient rather than associating risks for large groups of patients are required. Second, we statistical models that can discover and evaluate interactions of multiple risk factors, and combine them to produce informed predictions are needed. Although gene expression profiles may prove to be more powerful indicators of tumor behavior, analysis should not force a choice of one form of data over the other; all forms of data should be accommodated and evaluated. As new technologies develop, new forms of genomic data will be capable of improving prediction of disease outcomes; analytic models must therefore be technology-independent and able to accommodate emerging forms of molecular and clinical data. This integrative view underlies the development of clinico-genomic models in the instant invention. Thus, it permits a more integrative approach to prognostic systems in support of personalized health planning.

SUMMARY OF THE INVENTION

This invention discusses the generation and exploration of classification tree models, with particular interest in problems involving many predictors. Problems involving multiple predictors arise in situations where the prediction of an outcome is dependent on the interaction of numerous factors (predictors), such as the prediction of clinical or physiological states using various forms of molecular data. One motivating application is molecular phenotyping using gene expression and other forms of molecular data as predictors of a clinical or physiological state.

The invention addresses the specific context of a binary response Z and many predictors x_i ; in which the data arises via case-control design, *i.e.*, the numbers of 0/1 values in the response data are fixed by design. This allows for the successful relation of large-scale gene expression data (the predictors) to binary outcomes, such as a risk group or disease state. The invention elaborates on a Bayesian analysis of this particular binary context, with several key innovations.

The analysis of this invention addresses and incorporates case-control design issues in the assessment of association between predictors and outcome with nodes of a tree. With categorical or continuous covariates, this is based on an underlying non-parametric model for the conditional distribution of predictor values given
5 outcomes, consistent with the case-control design. This uses sequences of Bayes' factor based tests of association to rank and select predictors that define significant "splits" of nodes, and that provides an approach to forward generation of trees that is generally conservative in generating trees that are effectively self-pruning. An innovative element of the invention is the implementation of a tree-spawning
10 method to generate multiple trees with the aim of finding classes of trees with high marginal likelihoods, and where the prediction is based on model averaging, *i.e.*, weighting predictions of trees by their implied posterior probabilities. The advantage of the Bayesian approach is that rather than identifying a single "best" tree, a score is attached to all possible trees and those trees which are very unlikely
15 are excluded. Posterior and predictive distributions are evaluated at each node and at the leaves of each tree, and feed into both the evaluation and interpretation tree by tree, and the averaging of predictions across trees for future cases to be predicted.

To demonstrate the utility and advantages of this tree classification model, several embodiments are provided. The first embodiment concerns the prediction of
20 levels of fat content (higher than average versus lower than average) of biscuits based on reflectance spectral measures of the raw dough. The second embodiment concern gene expression profiling using DNA microarray data as predictors of a clinical states in breast cancer. The clinical states include estrogen receptor ("ER") prediction, tumor recurrence, and lymph node metastases. The example of ER status
25 prediction demonstrates not only predictive value but also the utility of the tree modeling framework in aiding exploratory analysis that identify multiple, related aspects of gene expression patterns related to a binary outcome, with some interesting interpretation and insights. The embodiments also illustrate the use of metagene factors – multiple, aggregate measures of complex gene expression
30 patterns – in a predictive modeling context. The third embodiment relates to the prediction of atherosclerotic phenotype determinative genes. This embodiment is claimed by reference to pending U.S. Patent Application No. No. 10/291,885 filed

on November 12, 2002, titled "Atherosclerotic Phenotype Determinative Genes and Methods for Using the Same."

In the case of large numbers of candidate predictors, in particular, model sensitivity to changes in selected subsets of predictors are ameliorated through the generation of multiple trees, and relevant, data-weighted averaging over multiple trees in prediction. The development of formal, simulation-based analyses of such models provides ways of dealing with the issues of high collinearity among multiple subsets of predictors, and challenging computational issues.

The invention also describes a comprehensive modeling approach to combining genomic and clinical data for prediction of disease outcomes in individual patients. Statistical analysis, using predictive classification tree models, evaluates the contributions of multiple forms of data, both clinical and genomic; the latter makes use of metagenes, gene expression signatures derived from microarray analyses. In a breast cancer recurrence study, it is demonstrated that multiple metagenes are far more powerful in predicting outcomes than any single metagene. Furthermore, combining metagenes with clinical risk factors proves most accurate at the individual patient level. This framework for combining multiple forms of data provides a platform for development of models for personalized prognosis.

In one embodiment, the integration of clinical and genomic data has been applied to an initial case study of breast cancer recurrence. The models of the invention incorporate, evaluate and weigh multiple gene expression patterns, clinical factors and treatment regimens in combination, and produce very accurate predictions of recurrence for individual patients. Prediction accuracy assessment includes honestly representing and interpreting uncertainties in prediction -- a key emphasis in the modeling approach taught by the invention.

The complexity of the oncogenic process, and of gene-environment interactions that define unique aspects of the course of disease for the individual patient, argue against the view that a simple gene expression profile will accurately predict outcomes for individual patients. Recent examples of gene expression profiling to predict disease recurrence do well in defining broad groups of patients but fall far short of predicting outcomes for an individual. Consistent with this view,

that successive sub-categorization of patients according to combinations of both clinical and genomic risk factors highlights the predictive value of multiple genomic patterns in smaller patient subgroups. This combination of risk factors customized to the individual patient level provides accurate predictions of recurrence, and

5 identifies gene patterns and candidates that can now be studied to shed light on potential mechanisms and regulatory pathways. Furthermore, customization of the clinico-genomic integrative model at the individualized patient level, allows for the customization of treatment regimens and development of drug regimens with respect to class of drug, dosage, formulation, and administration with respect to the

10 individual patient.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1: An example prediction tree for cookie fat outcomes. The root node splits on predictor/factor 92, followed by two subsequent splits on additional predictors 330 and 305. The Π values are point estimates of the predictive probabilities of high

15 fat versus low fat at each of the nodes, with suffixes simply indexing nodes. The labels $Z(0=1)$ indicate the numbers of low fat (0) and high fat (1) samples within each node, and the $F\#$ symbols indicate the thresholds that define the predictor based splits within each node.

Figure 2: Two predictive factors in cookie dough analysis. All samples are

20 represented by index numbers 1 through 78. Training data are denoted by blue (low fat) and red (high fat), and validation data by cyan (low fat) and magenta (high fat). The two full lines (black) demarcate the thresholds on the two predictors in this example tree.

Figure 3: Scatter plot of cookie data on three factors in example tree. Samples are

25 denoted by blue (low fat) and red (high fat), with training data represented by filled circles and validation data by open circles.

Figure 4: Three ER related metagenes in 49 primary breast tumors. Samples are denoted by blue (ER negative) and red (ER positive), with training data represented by filled circles and validation data by open circles.

30 Figure 5: Three ER related metagenes in 49 primary breast tumors. All samples are represented by index number in 1-78. Training data are denoted by blue (ER

negative) and red (ER positive), and validation data by cyan (ER negative) and magenta (ER positive).

Figure 6: Honest predictions of ER status of breast tumors. Predictive probabilities are indicated, for each tumor, by the index number on the vertical probability scale, together with an approximate 90% uncertainty interval about the estimated probability. All probabilities are referenced to a notional initial probability (incidence rate) of 0.5 for comparison. Training data are denoted by blue (ER negative) and red (ER positive), and validation data by cyan (ER negative) and magenta (ER positive).

Figure 7: Cross-validation probability predictions of lymph node status. Samples (tumors) are plotted by index number, and the plotted numbers are marked on the vertical scale at the estimated predictive probabilities of high-risk (red) versus low-risk (blue). Approximate 90% uncertainty intervals about these estimated probabilities are indicated by vertical dashed lines.

Figure 8: Gene expression patterns from the major metagenes that predict lymph node status. Levels of metagenes for samples are plotted by sample index number and by color (color coding as in Figure 7).

Figure 9: Gene expression patterns from the major metagenes that predict lymph node status from current and earlier Duke breast cancer study. Levels of metagenes as in Figure 8, with current study samples now colored cyan (low-risk) and magenta (high-risk). External validation samples from the 2001 Duke breast cancer study appear as red (high-risk) and blue (low-risk).

Figure 10: Cross-validation probability predictions of 3-year recurrence. Samples (tumors) are plotted by index number, and the plotted numbers are marked on the vertical scale at the estimated predictive probabilities of 3 year recurrence (red) versus 3 year recurrence free survival (blue). Approximate 90% uncertainty intervals about these estimated probabilities are indicated by vertical dashed lines.

Figure 11: Cross-validation and external validation probability predictions of lymph node status. Samples (tumors) are plotted by index number, and the plotted numbers are marked on the vertical scale at the estimated predictive probabilities of high-risk versus low risk. Color coding is as in Figure9: predictions for the cases in the current study are the same in Figure7, but now color coded as magenta (high-risk) and cyan

(low risk), the cases from the Duke (PNAS 2001) study are correspondingly color coded red (high-risk) and blue (low-risk). Approximate 90% uncertainty intervals about these estimated probabilities are indicated by vertical dashed lines.

Figure 12. Kaplan Meier survival curve estimates based on high-low-risk

5 categorization of breast cancer patients on two key metagenes

A. Empirical survival estimates based on the clinical determination of lymph node involvement groupings, labeled LNpos (low-risk: 0-3 positive nodes; high-risk, at least 4 positive nodes).

10 B. Empirical survival estimates based on a partition into two groups via a threshold on the gene expression pattern of Mg440.

C. Empirical survival estimates showing evidence of interaction between clinical (lymph node status) and genomic (Mg440) factors.

D. Refined empirical survival estimates for two subgroups of the "low Mg440" group, defined by a partition on Mg408.

15 E. Refined empirical survival estimates for two subgroups of the "high Mg440" group, defined by a partition on Mg109.

Figure 13: Use of successive metagene analysis to improve predictions of breast cancer recurrence. Gene expression patterns shown as standard intensity images that relate to splits in the patient sample based on metagene factors. The top image shows the expression pattern of 35 genes of the 117 in Mg440 (the 35 most
20 correlated with Mg440, ordered vertically by correlation with Mg440) on the entire group of 158 patients. Samples are ordered (horizontally) by the value of Mg440, and the vertical black line indicates the threshold on Mg440 defining the optimal split in these trees (threshold of -0.23); this split of patients is that underlying the empirical survival curves in Figure 1B. The two subgroups of patients defined by
25 this initial split are then further split with two additional metagenes. The group with Mg440 value less than -0.23 (samples 1-61) is further split based on Mg408 and the Mg440 group with value greater than -0.23 (samples 62-158) is split on Mg109. The subsequent two images show the patterns of genes within each of Mg408 and
30 Mg109 for the corresponding two subgroups of patients, arranged similarly within each group and also indicating the second level splits in the tree model. These splits underlie the refined survival curve estimates in Figure 12D and 12E. It is evident

that, in this traditional format, genes defining these key metagenes clearly show analogue expression patterns that underlie the strong predictive discrimination.

Figure 14. Predictive genomic and clinico-genomic

- 5 A. Metagene tree models. Two of the highest probability trees in analysis of the metagene data alone, showing how metagenes combine to determine successive partitions of the patient sample with associated predictions. The boxes at each node of the tree identify the number of patients and the number under each box is the corresponding modelbased point estimate of the 4-year recurrence-free probability (given as a percentage) based on the tree model predictions for that group.
- 10 B. Clinico-genomic tree models. Two of the highest probability trees illustrating the contribution of lymph node status (lymph node positive count LNpos). Details are as described in panel A.

Figure 15: Predictor variables in top tree models.

- 15 A. Metagene tree models. The figure summarizes the level of the tree in which each variable appears and defines a node split. The numbers on the left simply index trees, and the probabilities in parentheses on the left indicate the relative weights of trees based on fit to the data. The probabilities associated with metagenes (in parentheses on horizontal axis)
- 20 are sums of the probabilities of trees in which each metagene occurs, and so define overall weights indicating the relative importance of each metagene to the overall model fit and consequent recurrence predictions. Note the appearance of metagenes predictive of ER status (Mg315 and 351) and lymph node metastasis (Mg328 and 408).
- 25 B. Clinico-genomic tree models. Predictor variables in top tree models using both clinical data and metagene data. Details are as in Panel A but now the analysis selects from clinical data as well as genomic. Note the appearance of metagenes predictive of lymph node metastasis (Mg408) and Her-2-nu/Erb-b2 status (Mg20). The former is key in the top trees that,
- 30 defined initially by Mg440, together dominate predictions.

Figure 16. Honest cross-validation predictions from clinico-genomic tree model.

A. Estimates and approximate 95% confidence intervals for 5-year survival probabilities for each patient. Each patient is honestly predicted in an out-of-sample cross validation based on a model completely regenerated from the data of the remaining patients. Each patient is located on the horizontal axis at the recorded recurrence or censoring time for that patient. Patients indicated in blue are the 5-year recurrence-free cases and those in red are patients that recurred within 5 years. The interval estimates for a few cases that stand out are wide, representing uncertainty due to disparities among predictions coming from individual tree models that are combined in the overall prediction.

B. Estimates and approximate 95% confidence intervals for 4-year survival probabilities for each patient, in the format of panel (A).

Figure 17. Predicted survival curves for selected patients. Predictive survival curves, and uncertainty estimates for four patients whose clinical and genomic parameters match four actual cases in the data set (cases indexed 15, 158, 98 and 148). Depending on sample sizes within subgroups defined by the tree model analysis, sampling variability, and patterns of “conflict” between the specific set of predictor parameters, the predicted survival curve estimates may have quite substantial associated uncertainties, as indicated by some of these cases. Others, as illustrated, are very much more surely predicted.

DETAILED DESCRIPTION OF THE INVENTION

I. Development of the Tree Clarification Model: Model Context and Methodology

Data $\{Z_i, x_i\}$ ($i = 1, \dots, n$) are available on a binary response variable Z and a p -dimensional covariate vector x : The 0/1 response totals are fixed by design. Each predictor variable x_j could be binary, discrete or continuous.

1. *Bayes' factor measures of association*

At the heart of a classification tree is the assessment of association between each predictor and the response in subsamples, and we first consider this at a general level in the full sample. For any chosen single predictor x ; a specified threshold $_$ on the levels of x organizes the data into the 2×2 table.

	$Z = 0$	$Z = 1$	
$x \leq \tau$	n_{00}	n_{01}	N_0
$x > \tau$	n_{10}	n_{11}	N_1
	M_0	M_1	

With column totals fixed by design, the categorized data is properly viewed as two Bernoulli sequences within the two columns, hence sampling densitie

$$p(n_{0z}, n_{1z} | M_z, \theta_{z,\tau}) = \theta_{z,\tau}^{n_{0z}} (1 - \theta_{z,\tau})^{n_{1z}}$$

for each column $z = 0, 1$. Here, of course, $\theta_{0,\tau} = Pr(x \leq \tau | Z = 0)$ and $\theta_{1,\tau} = Pr(x \leq \tau | Z = 1)$. A test of association of the thresholded predictor with the response will now be based on assessing the difference between these Bernoulli probabilities.

5 The natural Bayesian approach is via the Bayes' factor B_τ comparing the null hypothesis $\theta_{0,\tau} = \theta_{1,\tau}$ to the full alternative $\theta_{0,\tau} \neq \theta_{1,\tau}$. We adopt the standard conjugate beta prior model and require that the null hypothesis be nested within the alternative. Thus, assuming $\theta_{0,\tau} \neq \theta_{1,\tau}$, we take $\theta_{0,\tau}$ and $\theta_{1,\tau}$ to be independent with common prior $Bc(a_\tau, b_\tau)$ with mean $m_\tau = a_\tau / (a_\tau + b_\tau)$. On the null hypothesis $\theta_{0,\tau} = \theta_{1,\tau}$, the common value has the same beta prior. The resulting Bayes' factor in favour of the alternative over the null hypothesis is then simply

$$B_\tau = \frac{\beta(n_{00} + a_\tau, n_{10} + b_\tau) \beta(n_{01} + a_\tau, n_{11} + b_\tau)}{\beta(N_0 + a_\tau, N_1 + b_\tau) \beta(a_\tau, b_\tau)}.$$

As a Bayes' factor, this is calibrated to a likelihood ratio scale. In contrast to more traditional significance tests and also likelihood ratio approaches, the Bayes' factor will tend to provide more conservative assessments of significance, consistent with the general conservative properties of proper Bayesian tests of null hypotheses (See Sellke, T., Bayarri, M.J. and Berger, J.O., Calibration of p-values for testing precise null hypotheses, *The American Statistician*, 55, 62-71, (2001) and references therein).

15 In the context of comparing predictors, the Bayes' factor B_τ may be evaluated for all predictors and, for each predictor, for any specified range of thresholds. As the threshold varies for a given predictor taking a range of (discrete or continuous) values, the Bayes' factor maps out a function of τ and high values identify ranges of interest for thresholding that predictor. For a binary predictor, of course, the only relevant threshold to consider is $\tau = 0$.

20 2. Model consistency with respect to varying thresholds

A key question arises as to the consistency of this analysis as we vary the thresholds. By construction, each probability $\theta_{z,\tau}$ is a non-decreasing function of τ , a

constraint that must be formally represented in the model. The key point is that the beta prior specification must formally reflect this. To see how this is achieved, note first that $\theta_{z\tau}$ is in fact the cumulative distribution function of the predictor values χ ; conditional on $Z = z$; ($z = 0; 1$); evaluated at the point $\chi = \tau$. Hence the *sequence* of beta priors, $Be(a_\tau, b_\tau)$ as τ varies, represents a set of marginal prior distributions for the corresponding set of values of the cdfs. It is immediate that the natural embedding is in a non-parametric Dirichlet process model for the complete cdf. Thus the threshold-specific beta priors are consistent, and the resulting sets of Bayes' factors comparable as τ varies, under a Dirichlet process prior with the betas as margins. The required constraint is that the prior mean values m_τ are themselves values of a cumulative distribution function on the range of χ , one that defines the prior mean of each θ_τ as a function. Thus, we simply rewrite the beta parameters (a_τ, b_τ) as $a_\tau = \alpha m_\tau$ and $b_\tau = \alpha(1 - m_\tau)$ for a specified prior mean cdf m_τ , and where α is the prior precision (or "total mass") of the underlying Dirichlet process model. Note that this specialises to a Dirichlet distribution when χ is discrete on a finite set of values, including special cases of ordered categories (such as arise if χ is truncated to a predefined set of bins), and also the extreme case of binary χ when the Dirichlet is a simple beta distribution.

3. *Generating a tree*

The above development leads to a formal Bayes' factor measure of association that may be used in the generation of trees in a forward-selection process as implemented in traditional classification tree approaches. Consider a single tree and the data in a node that is a candidate for a binary split. Given the data in this node, construct a binary split based on a chosen (predictor, threshold) pair (χ, τ) by (a) finding the (predictor, threshold) combination that maximizes the Bayes' factor for a split, and (b) splitting if the resulting Bayes' factor is sufficiently large. By reference to a posterior probability scale with respect to a notional 50:50 prior, Bayes' factors of 2.2, 2.9, 3.7 and 5.3 correspond, approximately, to probabilities of .9, .95, .99 and .995, respectively. This guides the choice of threshold, which may be specified as a single value for each level of the tree. We have utilised Bayes' factor thresholds of around 3 in a range of analyses, as exemplified below. Higher thresholds limit the growth of trees by ensuring a more stringent test for splits.

The Bayes' factor measure will always generate less extreme values than corresponding generalized likelihood ratio tests (for example), and this can be especially marked when the sample sizes M_0 and M_1 are low. Thus the propensity to split nodes is always generally lower than with traditional testing methods, especially with lower samples sizes, and hence the approach tends to be more conservative in extending existing trees. Post-generation pruning is therefore generally much less of an issue, and can in fact generally be ignored.

The method then incorporates the following steps: Indexing the root node of any tree by zero, and consider the full data set of n observations, representing M_z outcomes with $Z = z$ in 0, 1. Labeling successive nodes sequentially: splitting the root node, the left branch terminates at node 1, the right branch at node 2; splitting node 1, the consequent left branch terminates at node 3, the right branch at node 4; splitting node 2, the consequent left branch terminates at node 5, and the right branch at node 6, and so forth. Any node in the tree is labelled numerically according to its "parent" node; that is, a node j splits into two children, namely the (left, right) children $(2j + 1; 2j + 2)$: At level m of the tree ($m = 0; 1; \dots$) the candidates nodes are, from left to right, as $2^m - 1; 2^m; \dots; 2^{m+1} - 2$.

Having generated a "current" tree, each of the existing terminal nodes are run through one at a time, and assessed as to whether or not to create a further split at that node, stopping based on the above Bayes' factor criterion. Unless samples are very large (thousands) typical trees will rarely extend to more than three or four levels.

4. Inference and prediction with a single tree

Assuming the method generates a tree with m levels, the tree has some number of terminal nodes up to the maximum possible of $L = 2^{m+1} - 2$. Inference and prediction involves computations for *branch probabilities* and the predictive probabilities for new cases that these underlie. This is detailed for a specific path down the tree, *i.e.*, a sequence of nodes from the root node to a specified terminal node.

First, the method considers a node j that is split based on a (predictor, threshold) pair labeled (χ_j, τ_j) , (note that we use the node index to label the chosen

predictor, for clarity). It then extends the notation of Section 2.1 to include the subscript j indexing this node. Then the data at this node involves M_{0j} cases with $Z = 0$ and M_{1j} cases with $Z = 1$. Based on the chosen (predictor, threshold) pair (χ_j, τ_j) these samples split into cases $n_{00j}, n_{01j}, n_{10j}, n_{11j}$ as in the table of Section 2.1, but
 5 now indexed by the node label j . The implied conditional probabilities $\theta_{z,\tau_j} = Pr(\chi_j \leq \tau_j | Z = z)$, for $z = 0, 1$ are the *branch probabilities* defined by such a split (note that these are also conditional on the tree and data subsample in this node, though the notation does not explicitly reflect this for clarity). These are uncertain parameters and, following the development of Section 2.1, have specified beta priors, now also
 10 indexed by parent node j , i.e., $Be(a_{\tau_j}, b_{\tau_j})$. Assuming the node is split, the two sample Bernoulli setup implies conditional posterior distributions for these branch probability parameters: they are independent with posterior beta distributions

$$\theta_{0,\tau_j} \sim Be(a_{\tau_j} + n_{00j}, b_{\tau_j} + n_{10j}) \text{ and } \theta_{1,\tau_j} \sim Be(a_{\tau_j} + n_{01j}, b_{\tau_j} + n_{11j}).$$

15

These distributions allow inference on branch probabilities, and feed into the predictive inference computations as follows.

Consider predicting the response Z^* of a new case based on the observed set of predictor values x^* . The specified tree defines a unique path from the root to the
 20 terminal node for this new case. To predict requires that we compute the posterior predictive probability for $Z^* = 1/0$. We do this by following x^* down the tree to the implied terminal node, and sequentially building up the relevant likelihood ratio defined by successive (predictor, threshold) pairs.

For example and specificity, suppose that the predictor profile of this new
 25 case is such that the implied path traverses nodes 0, 1, 4, 9, terminating at node 9. This path is based on a (predictor, threshold) pair (χ_0, τ_0) that defines the split of the root node, (χ_1, τ_1) that defines the split of node 1, and (χ_4, τ_4) that defines the split of node 4. The new case follows this path as a result of its predictor values, in sequence:

$(x_0^* \leq \tau_0)$, $(x_1^* > \tau_1)$ and $(x_4^* \leq \tau_4)$. The implied likelihood ratio for $Z^* = 1$ relative to $Z^* = 0$ is then the product of the ratio of branch probabilities to this terminal node, namely

$$\lambda^* = \frac{\theta_{1,\tau_0,0}}{\theta_{0,\tau_0,0}} \times \frac{(1 - \theta_{1,\tau_1,1})}{(1 - \theta_{0,\tau_1,1})} \times \frac{\theta_{1,\tau_0,0}}{\theta_{0,\tau_0,0}}.$$

Hence, for any specified prior probability $Pr(Z^* = 1)$, this single tree model implies that, as a function of the branch probabilities, the updated probability π^* is, on the odds scale, given by

$$\frac{\pi^*}{(1 - \pi^*)} = \lambda^* \frac{Pr(Z^* = 1)}{Pr(Z^* = 0)}.$$

Hence, for any specified prior probability π $Pr(Z^* = 1)$, this single tree model implies that, as a function the branch probabilities, the updated probability π^* is, on the odds scale, given by

$$\frac{\pi^*}{(1 - \pi^*)} = \lambda^* \frac{Pr(Z^* = 1)}{Pr(Z^* = 0)}$$

The case-control design provides no information about $Pr(Z^* = 1)$ so it is up to the user to specify this or examine a range of values; one useful summary is obtained by simply taking a 50:50 prior odds as benchmark, whereupon the posterior probability is

$$\pi^* = \lambda^* / (1 + \lambda^*).$$

Prediction follows by estimating π^* based on the sequence of conditionally independent posterior distributions for the branch probabilities that define it. For example, simply “plugging-in” the conditional posterior means of each θ . will lead to a plug-in estimate of λ^* and hence π^* . The full posterior for π^* is defined implicitly as it is a function of the θ .. Since the branch probabilities follow beta posteriors, it is trivial to draw Monte Carlo samples of the θ . and then simply compute the corresponding values of λ^* and hence π^* to generate a posterior sample for summarization. This way, we can evaluate simulation-based posterior means and uncertainty intervals for π^* that represent predictions of the binary outcome for the new case.

5. *Generating and weighting multiple trees*

In considering potential (predictor, threshold) candidates at any node, there may be a number with high Bayes' factors, so that multiple possible trees with difference splits at this node are suggested. With continuous predictor variables, small variations in an "interesting" threshold will generally lead to small changes in the Bayes' factor – moving the threshold so that a single observation moves from one side of the threshold to the other, for example. This relates naturally to the need to consider thresholds as parameters to be inferred; for a given predictor x , multiple candidate splits with various different threshold values τ reflects the inherent uncertainty about τ , and indicates the need to generate multiple trees to adequately represent that uncertainty. Hence, in such a situation, the tree generation can spawn multiple copies of the "current" tree, and then each will split the current node based on a different threshold for this predictor. Similarly, multiple trees may be spawned this way with the modification that they may involve different predictors.

In problems with many predictors, this naturally leads to the generation of many trees, often with small changes from one to the next, and the consequent need for careful development of tree-managing software to represent the multiple trees. In addition, there is then a need to develop inference and prediction in the context of multiple trees generated this way. The use of "forests of trees" has recently been urged by Breiman, L., *Statistical Modeling: The two cultures (with discussion)*, *Statistical Science*, 16 199-225 (2001), and our perspective endorses this. The rationale here is quite simple: node splits are based on specific choices of what we regard as parameters of the overall predictive tree model, the (predictor, threshold) pairs. Inference based on any single tree chooses specific values for these parameters, whereas statistical learning about relevant trees requires that we explore aspects of the posterior distribution for the parameters (together with the resulting branch probabilities).

Within the current framework, the forward generation process allows easily for the computation of the resulting relative likelihood values for trees, and hence to relevant weighting of trees in prediction. For a given tree, identify the subset of nodes that are split to create branches. The overall marginal likelihood function for the tree is then the product of component marginal likelihoods, one component from each of these split nodes. Continue with the notation of Section 2.1 but now, again,

indexed by any chosen node j : Conditional on splitting the node at the defined (predictor, threshold) pair (x_j, τ_j) , the marginal likelihood component is

$$m_j = \int_0^1 \int_0^1 \prod_{z=0,1} p(n_{0zj}, n_{1zj} | M_{zj}, \theta_{z,\tau_j,j}) p(\theta_{z,\tau_j,j}) d\theta_{z,\tau_j,j}$$

where $p(\theta_{z,\tau_j,j})$ is the $Be(a_{\tau,j}, b_{\tau,j})$ prior for each $z = 0, 1$. This clearly reduces to

$$m_j = \prod_{z=0,1} \frac{\beta(n_{0zj} + a_{\tau,j}, n_{1zj} + b_{\tau,j})}{\beta(a_{\tau,j}, b_{\tau,j})}.$$

The overall marginal likelihood value is the product of these terms over all nodes j that define branches in the tree. This provides the relative likelihood values for all trees within the set of trees generated. As a first reference analysis, we may simply normalise these values to provide relative posterior probabilities over trees based on an assumed uniform prior. This provides a reference weighting that can be used to both assess trees and as posterior probabilities with which to weight and average predictions for future cases.

II. Specialized Tree Models Incorporating Multiple Forms of Data: Statistical Tree Models for Survival Time Data With Respect to Breast Cancer Recurrence

The statistical models of the invention can be used for survival time data. In order to aim to evaluate and summarise the regression relationship between multiple, possibly many predictors and the survival time outcomes. In one embodiment, the statistical model can be used for survival time data for relapses/recurrence in breast cancer. The development of the invention uses standard tree model ideas, utilising a Bayesian approach to tree generation, construction, analysis and resulting inference and prediction, and applies the analysis to survival time data.

Survival distributions for outcomes

Survival times, such as breast cancer recurrence outcomes following primary surgery, are modelled as arising from conditional survival distributions of Weibull form. This is a flexible class of survival distributions, and in a tree model context it is assumed that each terminal node (or leaf) of any specific tree model is

characterized by a specific Weibull distribution particular to that node. If a survival time is denoted t , then we represent $t = y^a$ for some Weibull shape parameter and where y is an exponential random variable. The value of a is assessed by examining marginal likelihood functions and results discussed are all conditional on a value
5 selected to approximately maximise the marginal likelihood. Hence the model is applied in terms of exponential distributions on the transformed y scale, assuming a specified value of a that will be determined in this empirical Bayes' manner.

This results in data $\{y_i, X_i\}_{i=1}^n$ where y_i is the transformed survival time of individual i and X_i is a p -dimensional vector of covariates. Each predictor variable
10 (each element of X_i) could be categorical or continuous, and the survival times may be right-censored or observed; y_i represents the censored time in the latter case, under the assumption of non-informative censoring. Censoring in the breast cancer study is generally due to short-term but continuing follow-up.

Tree Models

15 A single tree model can be viewed as a recursive partition of a population into refined subgroups based on conjunctions of values of predictor variables. The model is constructed by defining such partitions of the sample data set, and here trees are based on splits of sets of patients according to whether a chosen predictor variable lies above or below a threshold. All predictor variables are considered as
20 candidates for node splits at each node of a tree, and a range of pre-specified threshold values is considered for each predictor. The pre-specified values are taken to span the range of predictor variables at a fairly coarse level. In the examples in breast cancer, metagene data are normalised to zero mean and unit standard deviation, and the grid of thresholds is the quintiles of the empirical distribution
25 across all metagenes, plus the median rounded to zero; categorical clinical predictors are considered for thresholding to categories defined by traditional clinical categories.

At any given node it is possible that any of several (predictor, threshold) pairs would yield a split – as described below – so the ability to generate multiple trees at
30 a node is key. With a continuous predictor a small change in threshold can lead to a

change in the resulting model which reflects the uncertainty in the choice of the threshold. The generation of multiple trees is then key in reflecting this uncertainty. So, copies of the “current” tree are made and the current node is split on the predictor but at a different threshold value for each copy. Multiple trees are
 5 generated similarly when the (predictor,threshold) pairs involve different predictors as well as different thresholds.

The reported analyses utilise a formal forward-search specification of trees. At a given node of a tree, all possible (predictor,threshold) pairs are considered and evaluated. Pairs that define significant splits are then ranked and the top several
 10 chosen; how many splits we consider is limited only by computation. In reported analyses here, we allow up to 10 root node splits and then up to 5 splits of all subsidiary nodes, and generate trees up to a maximum of 5 levels (the root node labeled level 1). Additional constraints to numbers of samples within each node can be considered, though the evaluation using a Bayes’ factor test generates a
 15 conservative strategy that limits both the proliferation of trees and the depth of any tree, essentially automatically “pruning” the tree.

Bayes’ Factor Testing

At any “current” node of a tree, (predictor, threshold) combinations are assessed to split the data at the node into two, more homogeneous subsets based on a
 20 standard Bayesian test. With data y_1, \dots, y_n in this node, and any given single predictor x with a specified threshold τ , the test assesses whether the data are more consistent with a single exponential distribution (with exponential parameter μ) than with two separate exponentials (parameters μ_0 and μ_1) defined by partitioning via x at threshold τ . The Bayesian setup assigns a gamma prior to each of μ, μ_0, μ_1 . The
 25 prior is $\text{Gamma}(a, a/m)$ with mean m . We specify m globally, and treat a as to be estimated, doing so by empirical Bayes’ (EB) and then simply utilising the EB estimate of a in the evaluation of the test.

The data summaries can be organised as

	r	s	
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$\chi \leq \tau$	r_0	s_0	n_0
$\chi \geq \tau$	r_1	s_1	n_1

- where r is the number of observed survival times, s the sum of all times (observed and censored), and the (r_i, s_i) represent the same summaries for the two subsamples. The test of association is based on assessing the Bayes' factor (integrated likelihood ratio) test statistic $B\tau$ (8) to compare the null hypothesis $H_0 : \mu_0 = \mu_1$, taking the common value μ , with the alternative $H_1 : \mu_0 \neq \mu_1$. The full model (likelihood and prior) defines H_0 as a null hypothesis properly nested within H_1 .

Under the conjugate gamma prior structure,

$$B = \frac{\Gamma(\alpha + r_0) \Gamma(\alpha + r_1)}{\Gamma(\alpha) \Gamma(\alpha + r)} \frac{\alpha^\alpha (\alpha + sm)^{\alpha+r}}{(\alpha + s_0 m)^{\alpha+r_0} (\alpha + s_1 m)^{\alpha+r_1}}$$

- The Bayes' factor is calibrated to the likelihood-ratio scale. However, it provides more conservative estimates of significance than both likelihood-based approaches and more traditional significance tests such as (See Selke, T., Bayarri, M., and Berger, J. (2001), Calibration of p -values for testing precise null hypotheses, *The American Statistician*, 55, 62-71). The Bayes' factor will naturally choose smaller models over more complex ones if the quality of fit is comparable and hence provide a control on the size of the trees generated. A useful way to interpret the Bayes' factor is to view $B/(1+B)$ as a reference posterior probability for the split based on a 50:50 prior. Thus, for example, reference probabilities of 0.9 and 0.95 correspond approximately to Bayes' factor values of 9 and 19, respectively. In comparing predictors the Bayes' factor can be evaluated for each predictor at a number of thresholds. This yields a range of values of B which indicate (predictor, threshold) values of interest, and allow us to rank them.

In generating multiple splits at each node of multiple trees a strategy of proliferating trees is adopted. The proliferating trees once constructed are properly

compared and evaluated via the likelihood function over trees. Adopting a lower threshold on Bayes' factors (we use $B = 9$ in reported analyses here) leads to more trees than for a higher value, but it is the overall fit of any given tree that is of ultimate interest – relative to other trees and based on its full structure and configuration of the resulting data into subgroups. We may find trees that have individual nodes split at a high level of significance, but that, overall, receive lower weight. Similarly, and more importantly in forward-selection procedures for generating trees, we will generally find trees in which one or more nodes are split at lower levels of significance, but for which the resulting full tree is in fact very much more highly weighted than others. Thus it is important to use a relatively low significance level and then, once multiple trees are generated, sort out which ones are in fact, overall, most significant by evaluating and ranking them according to the tree-model likelihood function (see below).

In most cases a split (*parent*) node will result in two *children* nodes. However some non-ordinal categorical predictors may have several categories. The decision to split on such a variable is then based on calculating the Bayes' factor values for all pairwise comparisons among variable levels: a split is made on all levels if the Bayes' factor in one of these comparisons is among the highest across all variables, and exceeds the specified Bayes' factor threshold. A split will result in children nodes which will subsequently define further nodes.

Given a *current* tree the splitting process continues until either the existing model cannot be improved, i.e., the Bayes' factor criterion is not met at any node, or until all of the remaining candidate split points have few observations. The root node of a tree (level 1) is labeled as node 1 and contains n observations. Nodes are labeled sequentially from left to right; for example, the leftmost branch from the root leads to node 2 while the rightmost branch leads to node $2 + k_1 - 1$, where k_1 is the number of children of the root node. These children form level 2 of the tree. The branches from node 2 lead to nodes $2+k_1, \dots, 2+k_2-1$ where k_2 is the number of children of node 2 (children located at level 3 of the tree), and so on. As the Bayes' factor criterion is relatively conservative, no post-generation tree pruning is necessary.

Inference in one Tree Model

Suppose a tree with m levels has been generated with a total of L terminal nodes or leaves. Look at (nonterminal) node j of the tree and suppose that it is split on the pair (χ_j, τ_j) where j is now the node index. We now need to modify the earlier notation to include the node index. So the number of individuals in node j is now n_j ; of these, r_j individuals have observed survival times and the sum of all survival and censored times is s_j . These data are divided at the node, by (χ_j, τ_j) , yielding n_{0j} cases with $\chi_j \leq \tau_j$ (of which r_{0j} cases are observed and with sum of all times s_{0j}), and n_{1j} cases with $\chi_j > \tau_j$ (of which r_{1j} cases are observed and with sum of all times s_{1j}).

Once the node is split, the two resulting exponential parameters have conditional posterior probabilities that are conjugate updates of the Gamma prior. Thus, with the common prior at the parent node $\text{Gamma}(a_j, a_j/m)$ (now indexing the shape parameter, estimated by empirical Bayes' within the node, by j too) posterior gamma distributions are generated as follows:

$$\mu_{0j} \sim \text{Gamma}(a_j + r_{0j}, a_j/m + s_{0j}) \text{ and } \mu_{1j} \sim \text{Gamma}(a_j + r_{1j}, a_j/m + s_{1j})$$

These distributions allow inferences, and feed into predictions, both at nodes in the body of the tree and of course at the terminal nodes (leaves) of the tree. There is "data sharing", via Bayesian analysis induced shrinkage, between branches at a node since we are utilising all data withing the node to help estimate, via empirical Bayes', the weight parameter a_j of the common prior. Thus, for example, in a case where r_{0j} is small but r_{1j} is larger, it may still be possible to split the node.

Prediction in one Tree Model

Consider now a future case to be predicted - an individual with predictor variables x . The tree defines a single, unique path from the root node to a terminal node (leaf). Prediction requires the evaluation of the posterior (to the training data) predictive distribution for the individual, and can be performed at any node of the tree through which the individual passes, including the root and terminal nodes. Thus, not only as a formal predictive distribution at the terminal node generated, but

partial information about how predictions are modified based on the succession of significant node splits on the relevant covariates as they are defined “down the tree are also generated.”

5 The details are given at the terminal node the individual resides in based on sequential passage down the tree defined by her predictor variables and the (predictor,threshold) pairs defining the tree. At this node, the model implies a conditional exponential survival time distribution and the corresponding posterior gamma distribution, say $\text{Gamma}(a^*, a^*/m^*)$, at the node. The implied (posterior) predictive distribution is then Pareto, implied by integrating the exponential mean
10 with respect to the gamma. This is most easily summarised in terms of the implied survival function, at any point $t > 0$, given by

$$S(t) = \Pr(y > t | x) = (1 + m^*t/a^*)^{-a^*}, \quad (t > 0).$$

It is trivial to directly compute point estimates of the predicted survival time for this individual, and quantiles of the distribution to feed into display and
15 interpretation of uncertainties in prediction.

Multiple Trees and Tree Likelihoods

The forward selection procedure can generate hundreds and thousands of trees that then need evaluating and weighting for follow-on inferences and prediction. The invention does this by computing relative likelihood values across
20 trees, which can then be normalised (or weighted by prior probabilities and then normalised) to produce relative posterior probabilities across the set of candidates.

For any single tree the overall marginal likelihood can be calculated, up to a constant, by identifying the terminal nodes (leaves) and computing marginal likelihood components within each and then taking the product. At any one terminal
25 node, suppose there are n cases with r having observed times and the rest censored, and that the sum of all times (censored and uncensored) is s . Then, under the $\text{Gamma}(a, a/m)$ prior at that node (with the estimated value of a having been inherited from the parent node, and m specified a priori), the marginal likelihood component is just the integral, with respect to this prior, of the product exponential

components (density values for cases with observed times, and survival function values for cases that are right-censored). This standard calculation results in

$$\frac{a^a m^r}{(a + sm)^{a+r}} \frac{\Gamma(a + r)}{\Gamma(a)}$$

Taking the product of such terms across all terminal nodes leads to the
 5 unnormalised overall marginal likelihood value for the tree. This value is relative to the overall marginal likelihood values of all of the trees generated, which can be normalized to provide relative posterior probabilities for the trees based on an assumed uniform (or other) prior. These probabilities are valuable for both tree assessment and as relative weights in calculating average predictions for future
 10 observations.

Prediction using Multiple Trees

Given a set of trees with normalised tree probabilities based on the above discussion, consider predicting the new case. Index the trees by k , so that we have trees $k = 1, \dots, K$, say, where K may be hundreds. The likelihood values convert to
 15 posterior tree probabilities p_1, \dots, p_K . We may choose to ignore very low probability trees in the calculation, so simply restricting to p_k values above a small threshold and then renormalising (this is of interest for primarily computational reasons since saving many, many unlikely trees has overhead).

In tree k , the individual with predictor variable x has conditional predictive
 20 distribution defined by the Pareto result in the unique terminal node where the individual resides; now index that distribution by k , so that, for example, the relevant Pareto survival function is $S_k(t)$. Considering all trees, the overall prediction is based on model averaging – theoretically correct and also generally understood to deliver more accurate and reliable predictions that will be generated from any one
 25 single, selected model (5; 7) – in this case, any single tree – especially in cases where multiple trees have appreciable probabilities. For example, the survival function can be computed as the simple mixture

$$S(t) + \sum_{k=1}^K P_k S_k(t), \quad (t > 0).$$

Uncertainty assessments about this “estimated” predictive survival function can be evaluated in a number of ways. Perhaps most direct and easily accessible, as well as most appropriate, is to generate point-wise uncertainty intervals, such as, say, 90% posterior credible intervals around $S(t)$ at a few selected time points t . This is easily derived from a full posterior sample for the survival function at each time point; the value $S_k(t)$ is simply the expected value of the exponential survival function $\exp(-\mu t)$ with respect to the relevant gamma prior; so a single random draw from the posterior for the survival function is simply $\exp(-\mu t)$ where the value of μ is sampled from this gamma. Thus, a simulation sample is generated by (a) selecting one of the K components at random, according to the weights p_k ; then (b) drawing the implied μ value and hence the value of the implied exponential survival function; and (c) repeating. The resulting sample can be summarised, in terms of quantiles, for example, to represent uncertainties in predictive survival curves of this mixture form.

III. Collections of Genes and Metagenes Identified by the Invention

The modeling methods of the invention and the analytical methods taught by the invention with respect to clinical, genomic, and biomedical inventions, allow the subject invention to be directed to a collection of genes whose expression is correlated with biological states. In one embodiment, this biological state is a disease state. Such disease states include, but are not limited to cardiovascular diseases such as atherosclerosis, breast cancer, and prostate cancer. The invention allows for the identification of any disease state caused by the interactions of multiple genetic and/or clinical factors. In one embodiment, such a disease state is one where multiple, interacting biological and environmental processes define physiological states, and individual dimensions provide only partial information.

Thus, the invention is directed to collections of phenotype determinative genes, as well as methods for using the collection or subparts thereof in various

applications. Applications in which the collection finds use, include diagnostic, therapeutic and screening applications. Also reviewed are reagents and kits for use in practicing the subject methods. Finally, a review of various methods of identifying genes whose expression correlates with a given phenotype, such as atherosclerosis and breast cancer is provided.

The subject invention provides a collection of phenotype determinative genes. By phenotype determinative genes is meant genes whose expression or lack thereof correlates with a phenotype. Thus, phenotype determinative genes include genes: (a) whose expression is correlated with the phenotype, i.e., are expressed in cells and tissues thereof that have the phenotype, and (b) whose lack of expression is correlated with the phenotype, i.e., are not expressed in cells and tissues thereof that have the phenotype. A cell is a cell with the indicated phenotype if it is obtained from tissue that is determined to display that phenotype through methods known to those skilled in the art.

The invention claims all collections and subsets thereof of phenotype determinative genes as well as metagenes disclosed herewith. The subject collections of phenotype determinative genes may be physical or virtual. Physical collections are those collections that include a population of different nucleic acid molecules, where the phenotype determinative genes are represented in the population, i.e., there are nucleic acid molecules in the population that correspond in sequence to the genomic, or more typically, coding sequence of the phenotype determinative genes in the collection. In many embodiments, the nucleic acid molecules are either substantially identical or identical in sequence to the sense strand of the gene to which they correspond, or are complementary to the sense strand to which they correspond, typically to an extent that allows them to hybridize to their corresponding sense strand under stringent conditions. An example of stringent hybridization conditions is hybridization at 50°C or higher and 0.1×SSC (15 mM sodium chloride/1.5 mM sodium citrate). Another example of stringent hybridization conditions is overnight incubation at 42°C in a solution: 50 % formamide, 5 × SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5 × Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 ×

SSC at about 65°C. Stringent hybridization conditions are hybridization conditions that are at least as stringent as the above representative conditions, where conditions are considered to be at least as stringent if they are at least about 80% as stringent, typically at least about 90% as stringent as the above specific stringent conditions.

- 5 Other stringent hybridization conditions are known in the art and may also be employed to identify nucleic acids of this particular embodiment of the invention.

The nucleic acids that make up the subject physical collections may be single-stranded or double-stranded. In addition, the nucleic acids that make up the physical collections may be linear or circular, and the individual nucleic acid
10 molecules may include, in addition to a phenotype determinative gene coding sequence, other sequences, e.g., vector sequences. A variety of different nucleic acids may make up the physical collections, e.g., libraries, such as vector libraries, of the subject invention, where examples of different types of nucleic acids include, but are not limited to, DNA, e.g., cDNA, etc., RNA, e.g., mRNA, cRNA, etc. and
15 the like. The nucleic acids of the physical collections may be present in solution or affixed, i.e., attached to, a solid support, such as a substrate as is found in array embodiments, where further description of such diverse embodiments is provided below.

Also provided are virtual collections of the subject phenotype determinative
20 genes. By virtual collection is meant one or more data files or other computer readable data organizational elements that include the sequence information of the genes of the collection, where the sequence information may be the genomic sequence information but is typically the coding sequence information. The virtual collection may be recorded on any convenient computer or processor readable
25 storage medium. The computer or processor readable storage medium on which the collection data is stored may be any convenient medium, including CD, DAT, floppy disk, RAM, ROM, etc, which medium is capable of being read by a hardware component of the device.

Also provided are databases of expression profiles of the phenotype
30 determinative genes. Such databases will typically comprise expression profiles of various cells/tissues having the phenotypes, such as various stages of a disease

negative expression profiles, prognostic profiles, etc., where such profiles are further described below.

The expression profiles and databases thereof may be provided in a variety of media to facilitate their use. "Media" refers to a manufacture that contains the expression profile information of the present invention. The databases of the present invention can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present database information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure may be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.*

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means may comprise any manufacture comprising a recording of the present information as described above, or a memory access means that can access such a manufacture.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks expression profiles possessing varying degrees of similarity to a reference expression profile. Such presentation

provides a skilled artisan with a ranking of similarities and identifies the degree of similarity contained in the test expression profile.

Specific phenotype determinative genes of the subject invention are those listed in the Tables as indicated in the specification. Of the list of genes, certain of the genes have functions that logically implicate them as being associated with the phenotype. However, the remaining genes have functions that do not readily associate them with the phenotype.

The subject invention provides collections of phenotype determinative genes as determined by the methods of the invention. Although the following disclosure describes subject collections in terms of the genes listed in the Tables relevant to each embodiment of the invention described herein, the subject collections and subsets thereof as claimed by the invention apply to all relevant genes determined by the subject invention. Thus, the subject collections and subsets thereof, as well as applications directed to the use of the aforementioned subject collections only serve as an example to illustrate the invention.

The subject collections find use in a number of different applications. Applications of interest include, but are not limited to: (a) diagnostic applications, in which the collections of the genes are employed to either predict the presence of, or the probability for occurrence of, the phenotype; (b) pharmacogenomic applications, in which the collections of genes are employed to determine an appropriate therapeutic treatment regimen, which is then implemented; and (c) therapeutic agent screening applications, where the collection of genes is employed to identify phenotype modulatory agents. Each of these different representative applications is now described in greater detail below.

Diagnostic Applications

In diagnostic applications of the subject invention, cells or collections thereof, e.g., tissues, as well as animals (subjects, hosts, etc., e.g., mammals, such as pets, livestock, and humans, etc.) that include the cells/tissues are assayed to determine the presence of and/or probability for development of, the phenotype. As such, diagnostic methods include methods of determining the presence of the phenotype. In certain embodiments, not only the presence but also the severity or stage of a phenotype is determined. In addition, diagnostic methods also include

methods of determining the propensity to develop a phenotype, such that a determination is made that the phenotype is not present but is likely to occur.

In practicing the subject diagnostic methods, a nucleic acid sample obtained or derived from a cell, tissue or subject that includes the same that is to be diagnosed is first assayed to generate an expression profile, where the expression profile includes expression data for at least two of the genes listed in each of the tables relevant to the phenotype. The number of different genes whose expression data, i.e., presence or absence of expression, as well as expression level, that are included in the expression profile that is generated may vary, but is typically at least 2, and in many embodiments ranges from 2 to about 100 or more, sometimes from 3 to about 75 or more, including from about 4 to about 70 or more.

As indicated above, the sample that is assayed to generate the expression profile employed in the diagnostic methods is one that is a nucleic acid sample. The nucleic acid sample includes a plurality or population of distinct nucleic acids that includes the expression information of the phenotype determinative genes of interest of the cell or tissue being diagnosed. The nucleic acid may include RNA or DNA nucleic acids, e.g., mRNA, cRNA, cDNA etc., so long as the sample retains the expression information of the host cell or tissue from which it is obtained. The sample may be prepared in a number of different ways, as is known in the art, e.g., by mRNA isolation from a cell, where the isolated mRNA is used as is, amplified, employed to prepare cDNA, cRNA, etc., as is known in the differential expression art. The sample is typically prepared from a cell or tissue harvested from a subject to be diagnosed, e.g., via biopsy of tissue, using standard protocols, where cell types or tissues from which such nucleic acids may be generated include any tissue in which the expression pattern of the to be determined phenotype exists, including, but not limited, to, monocytes, endothelium, and/or smooth muscle.

The expression profile may be generated from the initial nucleic acid sample using any convenient protocol. While a variety of different manners of generating expression profiles are known, such as those employed in the field of differential gene expression analysis, one representative and convenient type of protocol for generating expression profiles is array based gene expression profile generation protocols. Such applications are hybridization assays in which a nucleic acid that

displays "probe" nucleic acids for each of the genes to be assayed/profiled in the profile to be generated is employed. In these assays, a sample of target nucleic acids is first prepared from the initial nucleic acid sample being assayed, where preparation may include labeling of the target nucleic acids with a label, e.g., a member of signal producing system. Following target nucleic acid sample preparation, the sample is contacted with the array under hybridization conditions, whereby complexes are formed between target nucleic acids that are complementary to probe sequences attached to the array surface. The presence of hybridized complexes is then detected, either qualitatively or quantitatively. Specific hybridization technology which may be practiced to generate the expression profiles employed in the subject methods includes the technology described in U.S. Patent Nos.: 5,143,854; 5,288,644; 5,324,633; 5,432,049; 5,470,710; 5,492,806; 5,503,980; 5,510,270; 5,525,464; 5,547,839; 5,580,732; 5,661,028; 5,800,992; the disclosures of which are herein incorporated by reference; as well as WO 95/21265; WO 96/31622; WO 97/10365; WO 97/27317; EP 373 203; and EP 785 280. In these methods, an array of "probe" nucleic acids that includes a probe for each of the phenotype determinative genes whose expression is being assayed is contacted with target nucleic acids as described above. Contact is carried out under hybridization conditions, e.g., stringent hybridization conditions as described above, and unbound nucleic acid is then removed. The resultant pattern of hybridized nucleic acid provides information regarding expression for each of the genes that have been probed, where the expression information is in terms of whether or not the gene is expressed and, typically, at what level, where the expression data, i.e., expression profile, may be both qualitative and quantitative.

Once the expression profile is obtained from the sample being assayed, the expression profile is compared with a reference or control profile to make a diagnosis regarding the phenotype of the cell or tissue from which the sample was obtained/derived. The reference or control profile may be a profile that is obtained from a cell/tissue known to have an phenotype, as well as a particular stage of the phenotype or disease state, and therefore may be a positive reference or control profile. In addition, the reference or control profile may be a profile from cell/tissue for which it is known that the cell/tissue ultimately developed a phenotype, and

therefore may be a positive prognostic control or reference profile. In addition, the reference/control profile may be from a normal cell/tissue and therefore be a negative reference/control profile.

In certain embodiments, the obtained expression profile is compared to a single reference/control profile to obtain information regarding the phenotype of the cell/tissue being assayed. In yet other embodiments, the obtained expression profile is compared to two or more different reference/control profiles to obtain more in depth information regarding the phenotype of the assayed cell/tissue. For example, the obtained expression profile may be compared to a positive and negative reference profile to obtain confirmed information regarding whether the cell/tissue has for example, the diseased, or normal phenotype. Furthermore, the obtained expression profile may be compared to a series of positive control/reference profiles each representing a different stage/level of the phenotype (for example, a disease state), so as to obtain more in depth information regarding the particular phenotype of the assayed cell/tissue. The obtained expression profile may be compared to a prognostic control/reference profile, so as to obtain information about the propensity of the cell/tissue to develop the phenotype.

The comparison of the obtained expression profile and the one or more reference/control profiles may be performed using any convenient methodology, where a variety of methodologies are known to those of skill in the array art, e.g., by comparing digital images of the expression profiles, by comparing databases of expression data, etc. Patents describing ways of comparing expression profiles include, but are not limited to, U.S. Patent Nos. 6,308,170 and 6,228,575, the disclosures of which are herein incorporated by reference. Methods of comparing expression profiles are also described above.

The comparison step results in information regarding how similar or dissimilar the obtained expression profile is to the control/reference profiles, which similarity/dissimilarity information is employed to determine the phenotype of the cell/tissue being assayed. For example, similarity with a positive control indicates that the assayed cell/tissue has the phenotype. Likewise, similarity with a negative control indicates that the assayed cell/tissue does not have the phenotype.

Depending on the type and nature of the reference/control profile(s) to which the obtained expression profile is compared, the above comparison step yields a variety of different types of information regarding the cell/tissue that is assayed. As such, the above comparison step can yield a positive/negative determination of an
5 phenotype of an assayed cell/tissue. In addition, where appropriate reference profiles are employed, the above comparison step can yield information about the particular stage of the phenotype of an assayed cell/tissue. Furthermore, the above comparison step can be used to obtain information regarding the propensity of the cell or tissue to develop a phenotype.

10 In many embodiments, the above obtained information about the cell/tissue being assayed is employed to diagnose a host, subject or patient with respect to the presence of, state of or propensity to develop, a disease state. For example, where the cell/tissue that is assayed is determined to have the phenotype, the information may be employed to diagnose a subject from which the cell/tissue was obtained as
15 having the phenotype state, for example, a disease.

Pharmaco/Surgicogenomic Applications

Another application in which the subject collections of phenotype determinative genes find use in is pharmacogenomic and/or surgicogenomic applications. In these applications, a subject/host/patient is first diagnosed for the
20 phenotype, e.g., presence or absence of a disease, propensity to develop the disease, etc., using a protocol such as the diagnostic protocols known to those skilled in the art.

The subject is then treated using a pharmacological and/or surgical treatment protocol, where the suitability of the protocol for a particular subject/patient is
25 determined using the results of the diagnosis step. A variety of different pharmacological and surgical treatment protocols are known to those of skill in the art. Such protocols include, but are not limited to: surgical treatment protocols known to those skilled in the art. Pharmacological protocols of interest include treatment with a variety of different types of agents, including but not limited to:
30 thrombolytic agents, growth factors, cytokines, nucleic acids (e.g. gene therapy agents); etc.

Assessment of Therapy (Therapeutics)

Another application in which the subject collections of phenotype determinative genes find use is in monitoring or assessing a given treatment protocol. In such methods, a cell/tissue sample of a patient undergoing treatment for a disease condition is monitored using the procedures described above in the
5 diagnostic section, where the obtained expression profile is compared to one or more reference profiles to determine whether a given treatment protocol is having a desired impact on the disease being treated. For example, periodic expression profiles are obtained from a patient during treatment and compared to a series of reference/controls that includes expression profiles of various phenotype (for
10 example, a disease) stages and normal expression profiles. An observed change in the monitored expression profile towards a normal profile indicates that a given treatment protocol is working in a desired manner.

Therapeutic Agent Screening Applications

The present invention also encompasses methods for identification of agents
15 having the ability to modulate a disease phenotype, e.g., enhance or diminish the phenotype, which finds use in identifying therapeutic agents for a disease. Identification of compounds that modulate a phenotype can be accomplished using any of a variety of drug screening techniques. The screening assays of the invention are generally based upon the ability of the agent to modulate an expression profile of
20 phenotype determinative genes.

The term "agent" as used herein describes any molecule, e.g., protein or pharmaceutical, with the capability of modulating a biological activity of a gene product of a differentially expressed gene. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential
25 response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection. Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate agents comprise
30 functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The

candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including, but not limited to: peptides, saccharides, fatty acids, steroids, purines, pyrimidines,
5 derivatives, structural analogs or combinations thereof.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and
10 oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts (including extracts from human tissue to identify endogenous factors affecting differentially expressed gene products) are available or readily produced. Additionally, natural or synthetically produced libraries and
15 compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, etc. to produce structural analogs.

Exemplary candidate agents of particular interest include, but are not limited
20 to, antisense polynucleotides, and antibodies, soluble receptors, and the like. Antibodies and soluble receptors are of particular interest as candidate agents where the target differentially expressed gene product is secreted or accessible at the cell-surface (e.g., receptors and other molecule stably-associated with the outer cell membrane).

25 Screening assays can be based upon any of a variety of techniques readily available and known to one of ordinary skill in the art. In general, the screening assays involve contacting a cell or tissue known to have the phenotype with a candidate agent, and assessing the effect upon a gene expression profile made up of phenotype determinative genes. The effect can be detected using any convenient
30 protocol, where in many embodiments the diagnostic protocols described above are employed. Generally such assays are conducted in vitro, but many assays can be adapted for in vivo analyses, e.g., in an animal model of the cancer.

Screening for Drug Targets

In another embodiment, the invention contemplates identification of genes and gene products from the subject collections of determinative genes as therapeutic targets. In some respects, this is the converse of the assays described above for
5 identification of agents having activity in modulating (*e.g.*, decreasing or increasing) a phenotype, and is directed towards identifying genes that are phenotype determinative genes as therapeutic targets.

In this embodiment, therapeutic targets are identified by examining the effect(s) of an agent that can be demonstrated or has been demonstrated to modulate
10 a phenotype (*e.g.*, inhibit or suppress a disease phenotype). For example, the agent can be an antisense oligonucleotide that is specific for a selected gene transcript. For example, the antisense oligonucleotide may have a sequence corresponding to a sequence of a gene appearing in any of the tables relevant to the disease prediction as taught by the instant invention.

15 Assays for identification of therapeutic targets can be conducted in a variety of ways using methods that are well known to one of ordinary skill in the art. For example, a test cell that expresses or overexpresses a candidate gene, *e.g.*, a gene found in Table 1, is contacted with the known agent, the effect upon a disease phenotype and a biological activity of the candidate gene product assessed. The
20 biological activity of the candidate gene product can be assayed by examining, for example, modulation of expression of a gene encoding the candidate gene product (*e.g.*, as detected by, for example, an increase or decrease in transcript levels or polypeptide levels), or modulation of an enzymatic or other activity of the gene product.

25 Inhibition or suppression of the disease phenotype indicates that the candidate gene product is a suitable target for therapy. Assays described herein and/or known in the art can be readily adapted in for assays for identification of therapeutic targets. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an appropriate, art-accepted animal
30 model of the disease state.

Reagents and Kits

Also provided are reagents and kits thereof for practicing one or more of the above described methods. The subject reagents and kits thereof may vary greatly. Reagents of interest include reagents specifically designed for use in production of the above described expression profiles of phenotype determinative genes.

- 5 One type of such reagent is an array probe nucleic acids in which the phenotype determinative genes of interest are represented. A variety of different array formats are known in the art, with a wide variety of different probe structures, substrate compositions and attachment technologies. Representative array structures of interest include those described in U.S. Patent Nos.: 5,143,854; 5,288,644;
10 5,324,633; 5,432,049; 5,470,710; 5,492,806; 5,503,980; 5,510,270; 5,525,464; 5,547,839; 5,580,732; 5,661,028; 5,800,992; the disclosures of which are herein incorporated by reference; as well as WO 95/21265; WO 96/31622; WO 97/10365; WO 97/27317; EP 373 203; and EP 785 280. In many embodiments, the arrays include probes for at least 2 of the genes listed in the relevant tables. In certain
15 embodiments, the number of genes that are from the relevant tables that are represented on the array is at least 5, at least 10, at least 25, at least 50, at least 75 or more, including all of the genes listed in the appropriate table. Where the subject arrays include probes for such additional genes, in certain embodiments the number % of additional genes that are represented does not exceed about 50%, usually does
20 not exceed about 25 %. In many embodiments a great majority of genes in the collection are phenotype determinative genes, where by great majority is meant at least about 75%, usually at least about 80 % and sometimes at least about 85, 90, 95 % or higher, including embodiments where 100% of the genes in the collection are phenotype determinative genes. In many embodiments, at least one of the genes
25 represented on the array is a gene whose function does not readily implicate it in the production of the disease phenotype. Another type of reagent that is specifically tailored for generating expression profiles of phenotype determinative genes is a collection of gene specific primers that is designed to selectively amplify such genes. Gene specific primers and methods for using the same are described in
30 U.S. Patent No. 5,994,076, the disclosure of which is herein incorporated by reference. Of particular interest are collections of gene specific primers that have primers for at least 2 of the genes listed in Table 1, above. In certain embodiments,

the number of genes that are from Table 1 that have primers in the collection is at least 5, at least 10, at least 25, at least 50, at least 75 or more, including all of the genes listed in the relevant table. . Where the subject gene specific primer collections include primers for such additional genes, in certain embodiments the number % of additional genes that are represented does not exceed about 50%, usually does not exceed about 25 %.

The kits of the subject invention may include the above described arrays and/or gene specific primer collections. The kits may further include one or more additional reagents employed in the various methods, such as primers for generating target nucleic acids, dNTPs and/or rNTPs, which may be either premixed or separate, one or more uniquely labeled dNTPs and/or rNTPs, such as biotinylated or Cy3 or Cy5 tagged dNTPs, gold or silver particles with different scattering spectra, or other post synthesis labeling reagent, such as chemically active derivatives of fluorescent dyes, enzymes, such as reverse transcriptases, DNA polymerases, RNA polymerases, and the like, various buffer mediums, *e.g.* hybridization and washing buffers, prefabricated probe arrays, labeled probe purification reagents and components, like spin columns, etc., signal generation and detection reagents, *e.g.* streptavidin-alkaline phosphatase conjugate, chemifluorescent or chemiluminescent substrate, and the like.

In addition to the above components, the subject kits will further include instructions for practicing the subject methods. These instructions may be present in the subject kits in a variety of forms, one or more of which may be present in the kit. One form in which these instructions may be present is as printed information on a suitable medium or substrate, *e.g.*, a piece or pieces of paper on which the information is printed, in the packaging of the kit, in a package insert, etc. Yet another means would be a computer readable medium, *e.g.*, diskette, CD, etc., on which the information has been recorded. Yet another means that may be present is a website address which may be used via the internet to access the information at a removed site. Any convenient means may be present in the kits.

Compounds and Methods Fortreatment of a Disease Phenotype

Also provided are methods and compositions whereby relevant disease symptoms may be ameliorated. The subject invention provides methods of

ameliorating, e.g., treating, disease conditions, by modulating the expression of one or more target genes or the activity of one or more products thereof, where the target genes are one or more of the phenotype determinative genes as determined by the invention.

5 Certain cardiovascular diseases and cancers are brought about, at least in part, by an excessive level of gene product, or by the presence of a gene product exhibiting an abnormal or excessive activity. As such, the reduction in the level and/or activity of such gene products would bring about the amelioration of cardiovascular disease symptoms. Techniques for the reduction of target gene
10 expression levels or target gene product activity levels are discussed below.

 Alternatively, certain other cardiovascular diseases are brought about, at least in part, by the absence or reduction of the level of gene expression, or a reduction in the level of a gene product's activity. As such, an increase in the level of gene expression and/or the activity of such gene products would bring about the
15 amelioration of cardiovascular disease symptoms. Techniques for increasing target gene expression levels or target gene product activity levels are discussed below.

Compounds That Inhibit Expression, Synthesis or Activity of Mutant Target Gene Activity

 As discussed above, target genes involved in relevant disease disorders can
20 cause such disorders via an increased level of target gene activity. A number of genes are now known to be up-regulated in cells/tissues under disease conditions. A variety of techniques may be utilized to inhibit the expression, synthesis, or activity of such target genes and/or proteins. For example, compounds such as those identified through assays described which exhibit inhibitory activity, may be used in
25 accordance with the invention to ameliorate cardiovascular disease symptoms. As discussed, above, such molecules may include, but are not limited to small organic molecules, peptides, antibodies, and the like. Inhibitory antibody techniques are described, below.

 For example, compounds can be administered that compete with an
30 endogenous ligand for the target gene product, where the target gene product binds to an endogenous ligand. The resulting reduction in the amount of ligand-bound gene target will modulate endothelial cell physiology. Compounds that can be

particularly useful for this purpose include, for example, soluble proteins or peptides, such as peptides comprising one or more of the extracellular domains, or portions and/or analogs thereof, of the target gene product, including, for example, soluble fusion proteins such as Ig-tailed fusion proteins. (For a discussion of the production of Ig-tailed fusion proteins, see, for example, U.S. Pat. No. 5,116,964.).
5 Alternatively, compounds, such as ligand analogs or antibodies that bind to the target gene product receptor site, but do not activate the protein, (e.g., receptor-ligand antagonists) can be effective in inhibiting target gene product activity. Furthermore, antisense and ribozyme molecules which inhibit expression of the target gene may also be used in accordance with the invention to inhibit the aberrant target gene activity. Such techniques are described, below. Still further, also as described, below, triple helix molecules may be utilized in inhibiting the aberrant target gene activity.

Inhibitory Antisense, Ribozyme and Triple Helix Approaches

15 Among the compounds which may exhibit the ability to ameliorate disease symptoms are antisense, ribozyme, and triple helix molecules. Such molecules may be designed to reduce or inhibit mutant target gene activity. Techniques for the production and use of such molecules are well known to those of skill in the art. Anti-sense RNA and DNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. With respect
20 to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the target gene nucleotide sequence of interest, are preferred. Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to
25 complementary target RNA, followed by an endonucleolytic cleavage. The composition of ribozyme molecules must include one or more sequences complementary to the target gene mRNA, and must include the well known catalytic sequence responsible for mRNA cleavage. For this sequence, see U.S. Pat. No. 5,093,246, which is incorporated by reference herein in its entirety. As such within
30 the scope of the invention are engineered hammerhead motif ribozyme molecules that specifically and efficiently catalyze endonucleolytic cleavage of RNA

sequences encoding target gene proteins. Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the molecule of interest for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides

5 corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features, such as secondary structure, that may render the oligonucleotide sequence unsuitable. The suitability of candidate sequences may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays. Nucleic acid

10 molecules to be used in triple helix formation for the inhibition of transcription should be single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides must be designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of either purines or pyrimidines to be present on one strand of a duplex.

15 Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC+ triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, containing a

20 stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex. Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic

25 acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex. It is possible that the antisense, ribozyme, and/or triple helix molecules described herein may reduce or inhibit the transcription (triple

30 helix) and/or translation (antisense, ribozyme) of mRNA produced by both normal and mutant target gene alleles. In order to ensure that substantially normal levels of target gene activity are maintained, nucleic acid molecules that encode and express

target gene polypeptides exhibiting normal activity may be introduced into cells via gene therapy methods such as those described, below, that do not contain sequences susceptible to whatever antisense, ribozyme, or triple helix treatments are being utilized. Alternatively, it may be preferable to co-administer normal target gene
5 protein into the cell or tissue in order to maintain the requisite level of cellular or tissue target gene activity.

Anti-sense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing
10 oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase
15 promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Various well-known modifications to the DNA molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications
20 include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

Antibodies for Target Gene Products

25 Antibodies that are both specific for target gene protein and interfere with its activity may be used to inhibit target gene function. Such antibodies may be generated using standard techniques known in the art against the proteins themselves or against peptides corresponding to portions of the proteins. Such antibodies include but are not limited to polyclonal, monoclonal, Fab fragments, single chain
30 antibodies, chimeric antibodies, etc.

In instances where the target gene protein is intracellular and whole antibodies are used, internalizing antibodies may be preferred. However, lipofectin

- liposomes may be used to deliver the antibody or a fragment of the Fab region which binds to the target gene epitope into cells. Where fragments of the antibody are used, the smallest inhibitory fragment which binds to the target protein's binding domain is preferred. For example, peptides having an amino acid sequence
- 5 corresponding to the domain of the variable region of the antibody that binds to the target gene protein may be used. Such peptides may be synthesized chemically or produced via recombinant DNA technology using methods well known in the art (e.g., see Creighton, 1983, *supra*; and Sambrook et al., 1989, *supra*). Alternatively, single chain neutralizing antibodies which bind to intracellular target gene epitopes
- 10 may also be administered. Such single chain antibodies may be administered, for example, by expressing nucleotide sequences encoding single-chain antibodies within the target cell population by utilizing, for example, techniques such as those described in Marasco et al. (Marasco, W. et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:7889-7893).
- 15 In some instances, the target gene protein is extracellular, or is a transmembrane protein. Antibodies that are specific for one or more extracellular domains of the gene product, for example, and that interfere with its activity, are particularly useful in treating cardiovascular disease. Such antibodies are especially efficient because they can access the target domains directly from the bloodstream.
- 20 Any of the administration techniques described, below which are appropriate for peptide administration may be utilized to effectively administer inhibitory target gene antibodies to their site of action.

Methods for Restoring Target Gene Activity

- Target genes that cause the relevant disease may be underexpressed within
- 25 known disease situations. Several genes are now known to be down-regulated under disease conditions. Alternatively, the activity of target gene products may be diminished, leading to the development of cardiovascular disease symptoms. Described in this section are methods whereby the level of target gene activity may be increased to levels wherein cardiovascular disease symptoms are ameliorated.
- 30 The level of gene activity may be increased, for example, by either increasing the level of target gene product present or by increasing the level of active target gene product which is present.

For example, a target gene protein, at a level sufficient to ameliorate disease symptoms may be administered to a patient exhibiting such symptoms. Any of the techniques discussed, below, may be utilized for such administration. One of skill in the art will readily know how to determine the concentration of effective, non-toxic doses of the normal target gene protein, utilizing techniques known to those of ordinary skill in the art.

Additionally, RNA sequences encoding target gene protein may be directly administered to a patient exhibiting cardiovascular disease symptoms, at a concentration sufficient to produce a level of target gene protein such that cardiovascular disease symptoms are ameliorated. Any of the techniques discussed, below, which achieve intracellular administration of compounds, such as, for example, liposome administration, may be utilized for the administration of such RNA molecules. The RNA molecules may be produced, for example, by recombinant techniques as is known in the art.

Further, patients may be treated by gene replacement therapy. One or more copies of a normal target gene, or a portion of the gene that directs the production of a normal target gene protein with target gene function, may be inserted into cells using vectors which include, but are not limited to adenovirus, adeno-associated virus, and retrovirus vectors, in addition to other particles that introduce DNA into cells, such as liposomes. Additionally, techniques such as those described above may be utilized for the introduction of normal target gene sequences into human cells.

Cells, preferably, autologous cells, containing normal target gene expressing gene sequences may then be introduced or reintroduced into the patient at positions which allow for the amelioration of cardiovascular disease symptoms. Such cell replacement techniques may be preferred, for example, when the target gene product is a secreted, extracellular gene product.

Pharmaceutical Preparations and Methods Of Administration

The identified compounds that inhibit target gene expression, synthesis and/or activity can be administered to a patient at therapeutically effective doses to treat or ameliorate the relevant disease. A therapeutically effective dose refers to

that amount of the compound sufficient to result in amelioration of symptoms of disease.

Effective Dose

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g.,
5 for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are
10 preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in
15 formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be
20 estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be
25 measured, for example, by high performance liquid chromatography.

Formulations and Use

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients.

30 Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g.,
5 lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions,
10 or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., almond oil,
15 oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the
20 compositions may take the form of tablets or lozenges formulated in conventional manner. For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane,
25 dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of e.g. gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

30 The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers,

with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Before the subject invention is described further, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

In this specification and the appended claims, the singular forms "a," "an" and "the" include plural reference unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the

same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range, and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and materials are now described. All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the subject components of the invention that are described in the publications, which components might be used in connection with the presently described invention.

Example 1: Analysis of Biscuit Dough Data

A first example concerns the application of biscuit dough data (publicly available at Osborne, B.G., Fearn, T., Miller, A.R. and Douglas, S., Applications of near infrared reflectance spectroscopy to compositional analysis of biscuits and biscuit doughs, *J. Sci. Food Agric.*, 35, 99-105 (1984); Brown, P.J., Fearn, T. and Vannucci, M., The choice of variables in multivariate regression: A non-conjugate Bayesian decision theory approach, *Biometrika*, 86, 635-648 (1999)) in which interest lies in relating aspects of near infrared ("NIR") spectra of dough to the fat content of the resulting biscuits. The data set provides 78 samples, of which 39 are taken as training data and the remaining 39 as validation cases to be predicted, precisely as in Brown *et al* (1999). The binary outcome is 0/1 according to whether

the measured fat content exceeds a threshold, where the threshold is the mean of the sample of fat values. As predictors, each x_i comprises 300 values of the spectrum of dough sample i , augmented by the set of singular factors (principal components) of the 78 sample spectra, so that $p = 378$; with singular factors indexed 301; : : : ; 378.

5 The analysis was developed repeatedly exploring aspects of model fit and prediction of the validation sample as the number of control parameters were varied. The particular parameters of key interest varied were the Bayes' factor thresholds that define splits, and controls on the number of such splits that may be made at any one node. It was determined that across ranges of these control parameters, that there
10 was a good degree of robustness. The Bayes' factor threshold was fixed at 3 on the log scale, after which and two-level trees were explored allowing at most 10 splits of the root node and then at most 4 splits of each of nodes 1 and 2. This allowed up to 160 trees, with this analysis generating 148 trees.

 Many of the trees identified had one or two of the predictors in common, and
15 represent variation in the threshold values for those predictors. Figures 1-3 display some summaries. Figure 1 represents one of the 148 trees, split at the root node by the spectral predictor labeled factor 92 (corresponding to a wavelength of 1566 nm). Multiple wavelength values appear in the 148 trees, with values close to this appearing commonly, reflecting the underlying continuity of the spectra. The key
20 second level predictor is factor 305, one of the principal component predictors. The data are scatter plotted on these two predictors in Figure 2 with corresponding levels of the predictor-specific thresholds from this tree marked.

 The data appears also against the three predictors in this tree in Figure 3. Evidently there is substantial overlap in predictor space between the 0/1 outcomes,
25 and cases close to the boundaries defined by any single tree are hard to accurately predict. Nevertheless, in terms of posterior predictive probabilities for the 39 validation samples, accuracy is good. By simply establishing the predictive probability threshold at 0.5 it is determined that 18 of 20 (90%) low fat (blue) cases are "correctly" predicted, as are 19 of 20 (95%) high fat (red) cases.

30 Predictive accuracy is high in this example with considerable overlap between predictor patterns among the two outcome groups. This is a positive example of the use of the predictive tree approach in a context where standard

methods, such as logistic regression, would be less useful. Furthermore, the We end with a note that the 50:50 split of the 78 samples into training and validation sets followed the previous authors as references. Curious about this, we reran the analysis 500 times, each time randomly splitting the data 50:50 into training and validation samples. Predictive accuracy, as measured above, was generally not so good as reported for the initial sample split, varying from a little below 50% to 100% across this set of 500 analyses. The average accuracy for low fat (blue) cases was 80%, and that for high fat (red) cases 76%.

Example 2: Metagene Expression Profiling to Predict Estrogen Receptor Status of Breast Cancer Tumors

This example illustrates not only predictive utility but also exploratory use of the tree analysis framework in exploring data structure. Here, the tree analysis is used to predict estrogen receptor ("ER") status of breast tumors using gene expression data. Prior analyses of such data involved binary regression models which utilized Bayesian generalized shrinkage approaches to factor regression. Specifically, prior statistical models involved the use of probit linear regression linking principal components of selected subsets of genes to the binary (ER positive/negative) outcomes. See West, M., Blanchette, C., Dressman, H., Ishida, S., Spang, R., Zuzan, H., Marks, J.R. and Nevins, J.R. Utilization of gene expression profiles to predict the clinical status of human breast cancer. *Proc. Natl. Acad. Sci.*, 98, 11462-11467 (2001). However, the tree model taught in the instant invention presents some distinct advantages over Bayesian linear regression models in the analysis of large non-linear data sets such as these in terms of predictive accuracy and analytical capabilities.

Primary breast tumors from the Duke Breast Cancer SPORE frozen tissue bank were selected for this study on the basis of several criteria. Tumors were either positive for both the estrogen and progesterone receptors or negative for both receptors. Each tumor was diagnosed as invasive ductal carcinoma and was between 1.5 and 5 cm in maximal dimension. In each case, a diagnostic axillary lymph node dissection was performed. Each potential tumor was examined by hematoxylin/eosin staining and only those that were > 60% tumor (on a per-cell basis), with few

infiltrating lymphocytes or necrotic tissue, were carried on for RNA extraction. The final collection of tumors consisted of 13 estrogen receptor (ER)+ lymph node (LN)+ tumors, 12 ER LN+ tumors, 12 ER+ LN tumors, and 12 ER LN tumors

The RNA was derived from the tumors as follows: Approximately 30 mg of frozen breast tumor tissue was added to a chilled BioPulverizer H tube (Bio101) (Q-Biogene, La Jolla, CA). Lysis buffer from the Qiagen (Chatsworth, CA) RNeasy Mini kit was added, and the tissue was homogenized for 20 sec in a MiniBeadbeater (Biospec Products, Bartlesville, OK). Tubes were spun briefly to pellet the garnet mixture and reduce foam. The lysate was transferred to a new 1.5-ml tube by using a syringe and 21-gauge needle, followed by passage through the needle 10 times to shear genomic DNA. Total RNA was extracted by using the Qiagen RNeasy Mini kit. Two extractions were performed for each tumor, and total RNA was pooled at the end of the RNeasy protocol, followed by a precipitation step to reduce volume. Quality of the RNA was checked by visualization of the 28S:18S ribosomal RNA ratio on a 1% agarose gel. After the RNA preparation, the samples were subject to Affymetrix GENECHIP analysis.

Affymetrix GENECHIP Analysis: The targets for Affymetrix DNA microarray analysis were prepared according to the manufacturer's instructions. All assays used the human HuGeneFL GENECHIP microarray. Arrays were hybridized with the targets at 45°C for 16 h and then washed and stained by using the GENECHIP Fluidics. DNA chips were scanned with the GENECHIP scanner, and signals obtained by the scanning were processed by GENECHIP Expression Analysis algorithm (version 3.2) (Affymetrix, Santa Clara, CA).

A set of $n = 49$ breast cancer samples is analyzed in this study, using predictors based on metagene summaries of the expression levels of many genes. Metagenes, as defined above, are useful aggregate, summary measures of gene expression profiles. The evaluation and summarization of large-scale gene expression data in terms of lower dimensional factors of some form is utilized for two main purposes: first, to reduce dimension from typically several thousand, or tens of thousands of genes to a more practical dimension; second, to identify multiple underlying "patterns" of variation across samples that small subsets of genes share, and that characterize the diversity of patterns evidenced in the full

sample. Although, the analysis is conducive to the use of various factor model approaches known to those skilled in the art, a cluster-factor approach is used here to define empirical metagenes. This defines the predictor variables x utilized in the tree model.

5 Metagenes can be obtained by combining clustering with empirical factor methods. The metagene summaries used in the ER example in this disclosure, are based on the following steps.

- Assume a sample of n profiles of p genes;
- Screen genes to reduce the number by eliminating genes that show limited
10 variation across samples or that are evidently expressed at low levels that are not detectable at the resolution of the gene expression technology used to measure levels. This removes noise and reduces the dimension of the predictor variable;
- Cluster the genes using k _means, correlated-based clustering. Any standard
15 statistical package may be used. This analysis uses the xcluster software created by Gavin Sherlock (<http://genomewww.stanford.edu/sherlock/cluster.html>). A large number of clusters are targeted so as to capture multiple, correlated patterns of variation across samples, and generally small numbers of genes within clusters;
- Extract the dominant singular factor (principal component) from each of the
20 resulting clusters. Again, any standard statistical or numerical software package may be used for this; this analysis uses the efficient, reduced singular value decomposition function ("SVD") in the Matlab software environment (<http://www.mathworks.com/products/matlab>).

25 In the analysis of the ER data in this disclosure, the original data was developed using Affymetrix arrays with 7129 sequences, of which 7070 were used (following removal of Affymetrix controls from the data.). The expression estimates used were log₂ values of the signal intensity measures computed using the dChip software for post-processing Affymetrix output data (See Li, C. and Wong, W.H.
30 Model-based analysis of oligonucleotide arrays: Expression index computation and outlier detection. *Proc. Natl. Acad. Sci.*, 98, 31-36 (2001), and the software site <http://www.biostat.harvard.edu/complab/dchip/>). With a target of 500 clusters, the

xcluster software implementing the correlation-based *k*_means clustering produced $p = 491$ clusters. The corresponding p metagenes were then evaluated as the dominant singular factors of each of these clusters, as referenced above. See Table that provide tables detailing the 491 metagenes.

- 5 The data comprised 40 training samples and 9 validation cases. Among the latter, 3 were initial training samples that presented conflicting laboratory tests of the ER protein levels, so casting into question their actual ER status; these were therefore placed in the validation sample to be predicted, along with an initial 6 validation cases selected at random. These three cases are numbers 14, 31 and 33.
- 10 The color coding in the graphs is based on the first laboratory test (immunohistochemistry). Additional samples of interest are cases 7, 8 and 11, cases for which the DNA microarray hybridizations were of poor quality, with the resulting data exhibiting major patterns of differences relative to the rest.

- The metagene predictor has dimension $p = 491$: the analysis generated trees
- 15 based on a Bayes' factor threshold of 3 on the log scale, allowing up to 10 splits of the root node and then up to 4 at each of nodes 1 and 2. Some pertinent summaries appear in the following figures. Figures 4 and 5 display 3-D and pairwise 2-D scatterplots of three of the key metagenes, all clearly strongly related to the ER status and also correlated. However, there are in fact five or six metagenes that quite
- 20 strongly associate with ER status and it is evident that they reflect multiple aspects of this major biological pathway in breast tumors. In the study reported in West *et al* (2001), Bayesian probit regression models were utilized with singular factor predictors which identified a single major factor predictive of ER. That analysis identified ER negative tumors 16, 40 and 43 as difficult to predict based on the gene
- 25 expression factor model; the predictive probabilities of ER positive versus negative for these cases were near or above 0.5, with very high uncertainties reflecting real ambiguity.

- In contrast to the more more traditional regression models, the current tree model identifies several metagene patterns that together combine to define an ER
- 30 profile of tumors, and that when displayed as in Figures 4 and 5 isolate these three cases as quite clearly consistent with their designated ER negative status in some aspects, yet conflicting and much more in agreement with the ER positive patterns

on others. Metagene 347 is the dominant ER signature; the genes involved in defining this metagene include two representations of the ER gene, and several other genes that are coregulated with, or regulated by, the ER gene. Many of these genes appeared in the dominant factor in the regression prediction. This metagene strongly
5 discriminates the ER 11 negatives from positives, with several samples in the mid-range. Thus, it is no surprise that this metagene shows up as defining root node splits in many high-likelihood trees. This metagene also clearly defines these three cases – 16, 40 and 43 – as appropriately ER negative. However, a second ER associated metagene, number 352, also defines a significant discrimination. In this
10 dimension, however, it is clear that the three cases in question are very evidently much more consistent with ER positives; a number of genes, including the ER regulated PS2 protein and androgen receptors, play roles in this metagene, as they did in the factor regression; it is this second genomic pattern that, when combined together with the first as is implicit in the factor regression model, breeds the
15 conflicting information that fed through to ambivalent predictions with high uncertainty.

The tree model analysis here identifies multiple interacting patterns and allows easy access to displays such as those shown in Figures 4 to 6 that provide insights into the interactions, and hence to interpretation of individual cases. In the
20 full tree analysis, predictions based on averaging multiple trees are in fact dominated by the root level splits on metagene 347, with all trees generated extending to two levels where additional metagenes define subsidiary branches. Due to the dominance of metagene 347, the three interesting cases noted above are perfectly in accord with ER negative status, and so are well predicted, even though they exhibit additional,
25 subsidiary patterns of ER associated behaviour identified in the figures. Figure 6 displays summary predictions. The 9 validation cases are predicted based on the analysis of the full set of 40 training cases. Predictions are represented in terms of point predictions of ER positive status with accompanying, approximate 90% intervals from the average of multiple tree models. The training cases are each
30 predicted in an honest, cross-validation sense: each tumor is removed from the data set, the tree model is then refitted completely to the remaining 39 training cases only, and the hold-out case is predicted, *i.e.*, treated as a validation sample.

Excellent predictive performance is observed for both these one-at-a-time honest predictions of training samples and for the out of sample predictions of the 9 validation cases. One ER negative, sample 31, is firmly predicted as having metagene expression patterns completely consistent with ER positive status. This is in fact one of the three cases for which the two laboratory tests conflicted. The other two such cases, however agree with the initial ER negative test result - number 33, for which the predictions firmly agree with the initial ER negative test result, and number 14, for which the predictions agree with the initial ER positive result though not quite so forcefully. The lack of conformity of expression patterns in some cases (Case 8, 11 and 7) are due to major distortions in the data on the DNA microarray due to hybridization problems.

Example 3A: Prediction of Lymph Node Metastases and Cancer

Recurrence

This study assesses complex, multivariate patterns in gene expression data from primary breast tumor samples that can accurately predict nodal metastatic states and relapse for the individual patient using the statistical tree model of the invention.

DNA microarray data on samples of primary breast tumors was generated to which non-linear statistical analyses embodied by the tree model of the invention was applied to evaluate multiple patterns of interactions of groups of genes that have true predictive value, at the individual patient level, with respect to lymph node metastasis and cancer recurrence. For both lymph node metastasis and cancer recurrence, patterns of gene expression (metagenes) were identified that associate with outcome. Much more importantly, these patterns were capable of honestly predicting outcomes in individual patients with about 90% accuracy, based on a simple threshold of 0.5 probability in each case. The metagenes that predict lymph node metastasis and recurrence identify distinct groups of genes, suggesting different biological processes underlying these two characteristics of breast cancer.

Patients and biopsy specimens: The analyses of gene expression phenotypes drew samples from 171 primary tumor biopsies at the Koo Foundation Sun Yat-Sen Cancer Center (KF-SYSCC) in Taipei, Taiwan, collected and banked from 1991 to

2001. Samples from eleven patients who received preoperative chemotherapy and one with *in-situ* carcinoma were excluded from analysis. These 159 samples represent a heterogeneous population, though patient selection was enriched with cases of longer-term follow-up and observed recurrences. For a final analysis, only
5 89 samples were used. The median follow-up was 49 months. Full details of clinical characteristics are shown in Table 1.

Microarray analysis: Tumor total RNA was extracted with Qiagen RNEasy kits, and assessed for quality with an Agilent Lab-on-a-Chip 2100 Bioanalyzer. Hybridization targets were prepared from total RNA according to Affymetrix
10 protocols and hybridized to Affymetrix Human U95 GeneChip arrays See West M, Blanchette C, Dressman H, Huang E, Ishida S, Spang R et al. Predicting the clinical status of human breast cancer by using gene expression profiles, *Proc Natl Acad Sci*, 98:11462-11467 (2001).

Hybridization procedures and parameters. The amount of starting total
15 RNA for each reaction was 20 µmcg. Briefly, first strand cDNA synthesis was generated using a T7-linked oligo-dT primer, followed by second strand synthesis. An in vitro transcription reaction was performed to generate the cRNA containing biotinylated UTP and CTP, which was subsequently chemically fragmented at 95°C for 35 min. The fragmented, biotinylated cRNA was hybridized in MES buffer (2-
20 [N-morpholino]ethanesulfonic acid) containing 0.5 mg/ml acetylated bovine serum albumin to Affymetrix GeneChip Human U95Av2 arrays at 45°C for 16hr, according to the Affymetrix protocol (www.affymetrix.com and www.affymetrix.com/products/arrays/specific/hgu95.affx). The arrays contain over 12,000 genes and ESTs. Arrays were washed and stained with streptavidin-
25 phycoerythrin (SAPE, Molecular Probes). Signal amplification was performed using a biotinylated anti-streptavidin antibody (Vector Laboratories, Burlingame, CA) at 3 µmcg/ml. This was followed by a second staining with SAPE. Normal goat IgG (2 mg/ml) was used as a blocking agent.

Measurement data and specifications. Scans were performed with an
30 Affymetrix GeneChip scanner and the expression value for each gene was calculated using the Affymetrix Microarray Analysis Suite (v5.0), computing the expression intensities in 'signal' units defined by software. Scaling factors were determined for

each hybridization based on an arbitrary target intensity of 500. Scans were rejected if the scaling factor exceeded a factor of 25, resulting in only one reject. *Array design.* All assays employed the Affymetrix Human U95Av2 GeneChip. The characteristics of the array are detailed on the Affymetrix web site
5 (www.affymetrix.com/products/arrays/specific/hgu95.affx).

Statistical analysis: This analysis used the predictive statistical tree model of this invention. The method of the invention first screens genes to reduce noise, applies k-means correlation-based clustering targeting a large number of clusters,
10 and then uses singular value decompositions ("SVD") to extract the single dominant factor (principal component) from each cluster. This generated 496 cluster-derived singular factors (metagenes) that characterize multiple patterns of expression of the genes across samples. The strategy aimed to extract multiple such patterns while reducing dimension and smoothing out gene-specific noise through the aggregation
15 within clusters. Formal predictive analysis then uses these metagenes in a Bayesian classification tree analysis. This generates multiple recursive partitions of the sample into subgroups (the "leaves" of the classification tree), and associates Bayesian predictive probabilities of outcomes with each subgroup. Overall predictions for an individual sample are then generated by averaging predictions, with appropriate
20 weights, across many such tree models. Iterative out-of-sample, cross-validation predictions are then performed leaving each tumor out of the data set one at a time, refitting the model from the remaining tumors and using it to predict the hold-out case. This rigorously tests the predictive value of a model and mirrors the real-world prognostic context where prediction of new cases as they arise is the major
25 goal.

Although, clinico-pathologic parameters such as the presence or absence of positive axillary nodes represent the best means available to classify patients into broad subgroups by recurrence and survival, such methods remain an imperfect tool. Among patients with no detectable lymph node involvement, a population thought to
30 be in a low risk category, between 22 and 33% develop recurrent disease after a 10-year follow-up. See Polychemotherapy for early breast cancer: an overview of the randomized trials, Early Breast Cancer Trialists' Collaborative Group, *Lancet*;

352:930-942 (2001). Thus, properly identifying individuals out of this group who are at risk for recurrence is beyond the current capabilities of most predictive diagnostics.

Details of the statistical analysis as taught by the instant invention are as follows:

- 5 • Raw data are the 12,625 signal intensity measures of expression of genes on the Affymetrix HU95aV2 DNA microarray, with signal intensities based on the Affymetrix V5 software then transformed to the log-base 2 scale. An initial screen reduces this to a total of 7,030 genes to remove sequences that vary at low levels or minimally. Specifically, this screens out genes whose
10 expression levels across all samples varies by less than two-fold, and whose maximum signal intensity value is lower than nine on a log-base 2 scale.
- The set of samples on these 7,030 genes are clustered using k-means correlated-based clustering. Any standard statistical package may be used for this; our analysis uses the xcluster software created by Gavin Sherlock at
15 Stanford University (<http://genome-www.stanford.edu/~sherlock/cluster.html>). We defined a target of 500 clusters and the xcluster routine delivered 496 in this analysis.
- The dominant singular factor (principal component) from each of the 496 clusters is extracted. Again, any standard statistical or numerical software
20 package may be used for this; this analysis uses the reduced singular value decomposition function (svd) in Matlab.
(<http://www.mathworks.com/products/matlab>).
- These 496 metagene predictors are input to the tree model analysis. A key ingredient is the generalized likelihood ratio, or Bayes' factor, measure of
25 association between metagenes and binary outcomes. An initial ordering of metagenes is provided by the Bayes' factor values on all the data (at the root node of the tree). "Top" metagenes are those with highest Bayes' factor in this sense, and several "top" metagenes were selected to define the lists of genes (accompanying material) as described further below. Specifics
30 parameters defined to create the precise tree models in the two breast examples are as follows. The tree model analysis as reported utilised a Bayes' factor threshold of 3 on the log scale, allowed up to 10 splits of the

root node and then up to 4 at each of nodes 1 and 2. Trees were allowed to grow to at most 2 levels consistent with the relatively small sample size of the data sets.

- Predictions for individual patients were performed as described in the paper:
5 the analysis was repeated for each patient, holding out from the model fitting the expression and outcome data for that patient, and then developing the statistical tree model analysis based on only the remaining data. Then, the hold-out patient was predicted. We note that the model fitting, including the statistical evaluation of which metagenes are most predictive and the roles
10 they play in the analysis (i.e., the "feature selection process") is repeated anew for each of these analyses. Were this not done, and metagene selection based on all the data, then the predictions would appear much more accurate, but incorrectly and misleadingly so. This critical perspective, which we have terms "honest prediction" in the cross-validation context, is one we have
15 taken pains to stress in our work (e.g., reference 11) and one that defines our approach to critical model evaluation when prediction is a primary focus.
- The lists of genes were generated precisely as follows, for each of the recurrence and metastasis analyses separately. From the statistical tree model fit to all the data, the "top" 4 metagenes were selected, based on the marginal
20 Bayes' factor association measure as described. This defines 4 clusters of genes that are the initial basis of the list. The list was extended by adding in additional genes that are most highly correlated (standard linear correlation) with each of these 4 metagenes; the set of unique genes in the resulting lists are reported and form part of this supplementary material, as are full details
25 of all genes defining each of the 496 metagenes.
- In the lymph node metastasis external validation test, the predictions of the sample of cancers from the Duke 2001 PNAS study were performed directly using the tree model fitted only to the data from the current study (as
30 described). That is, predictions were performed entirely out-of-sample with no modification at all to the definition of metagenes, the model or the details of analysis, so paralleling the "real life" circumstances of predicting new

patients and providing a completely honest out-of-sample assessment of generalization and predictive validity.

- The metagene data for the Duke breast cancer samples used for external validation via out-of-sample prediction were evaluated as follows. The samples are from a 2000 study and gene expression profiles are on the early Affymetrix HU6800 array. The first step was then to identify all genes on that array (7,129 genes) that are also represented among the 12,625 genes on the U95av2 array. This was done using the chip-to-chip key available at the Affymetrix web site. This allows for the identification of genes on the HU6800 array that map to genes within each of the 496 metagene clusters from the current study. For example, the key metagenes 330, 146 and 130 have precisely 30, 37 and 8 genes, respectively; mapping these genes to the earlier HU6800 array identifies sets of 26, 42 and 4 genes, respectively (note that there are duplicates in some cases, as for metagene 146 here). These sets of genes on the HU6800 array define the metagene clusters and the corresponding value of the metagenes are evaluated precisely as described, using the dominant singular factor (principal component) from each of the 496 clusters.

The question of lymph node diagnosis is part of the broader issue of more accurately predicting breast cancer disease course and recurrence. Recently, genomic-scale measures of gene expression, using microarrays and other technologies have opened a new avenue for cancer diagnosis. They identify patterns of gene activity that sub-classify tumors, and such patterns may correlate with the biological and clinical properties of the tumors. The utility of such data in improving prognosis will relies on analytical methods that accurately predict the behavior of the tumors based on expression patterns. Credible predictive evaluation is critical in establishing valid and reproducible results and implicating expression patterns that do indeed reflect underlying biology. This predictive perspective is a key step towards integrating complex data into the process of prognosis for the individual patient, a step that can be accomplished through the practice of the present invention.

Furthermore, an ultimate goal is to integrate molecular and genomic information with traditional clinical risk factors, including lymph node status, patient age, hormone receptor status, and tumor size, in comprehensive models for predicting disease outcomes. Rather than supplant traditional clinical appraisal, genomic data adds data to traditional risk factors, and assessing individuals based on combinations of relevant traditional risk factors with identified genomic factors could potentially improve predictions. The present invention allows this goal to be realized by demonstrating the ability of genomic data to accurately predict lymph node involvement and disease recurrence in defined patient subgroups. Most importantly, these predictions are relevant for the individual patient and can provide a quantitative measure of the probability for the clinical phenotype and outcome of disease. Such predictions may ultimately facilitate treating patients as individuals rather than as unidentifiable members of a risk profile as described in the following examples.

The present invention was applied to the analysis of gene expression patterns in primary breast tumors that predict lymph node metastasis, as well as tumor recurrence. The first study compares traditional "low-risk" versus "high-risk" patients, primarily based on age, primary tumor size, lymph node status, and Estrogen receptor ("ER") status. Among ER positive individuals, the "high-risk" clinical profile is represented by advanced lymph node metastases (10 or more positive nodes); the "low-risk profile" identifies node-negative women of age greater than 40 years with tumor size below 2cm. The number of samples in the tumor collection that met these criteria reduced down to 18 high-risk and 19 low-risk cases (37 of the 89 samples in Table 1). Expression data were generated and metagenes identified and used in the Bayesian statistical tree analysis. Figure 7 displays summary predictions from the resulting total of 37 cross-validation analyses. For each individual tumor, this graph illustrates the predicted probability for "high-risk" versus "low-risk" (red versus blue) together with an approximate 90% confidence interval, based on analysis of the 36 remaining tumors performed successively 37 times as each tumor prediction is made. It is important to recognize that each sample in the data set, when assayed in this manner, constitutes a validation set that accurately assesses the robustness of the predictive model. The

metagene model accurately predicts metastatic potential; about 90% of cases are accurately predicted based on a simple threshold at 0.5 on the estimated probability in each case. Case number 7 is in the intermediate zone, exhibiting patterns of expression of the selected metagenes that relate equally well to those of “high-“ and “low-risk” cases, while case 22 is a clinical “high-risk” case with genomic expression patterns that relate more closely to “low-risk” cases. In contrast, node negative patients 5 and 11 have gene expression patterns more strongly indicative of “high-risk”, and are key cases for follow-up investigations. The details of clinical information in these apparently discordant cases are shown in Table 2.

Clinical features of these “discordant” cases are illuminating, and suggestive of how a broader investigation of clinical data combined with molecular model-based predictions may aid in the eventual decision-making process. Although case 22 did in fact recur, 6 years post-surgery; this patient’s clinical classification as high risk for recurrence based on purely clinical parameters was moderated by a lower risk based on metagenes, as demonstrated by this patient having survived recurrence-free for a longer time. Thus the lower probability prediction assigned to patient 22 based on the gene expression profiles is reflected in the clinical behavior of her disease. The “low-risk” patient 7 recurred at 31 months, and patient 11 at 38 months, whereas case 5 is currently disease-free after only 12 months of follow-up. Again, case 7, and to some degree case 11, thus partly corroborate the predictions based on genomic criteria. data. With such predictions as part of a prognostic model, more intensive or innovative post-surgical therapy should perhaps have been recommended for these two cases.

A critical aspect of the analyses described here is allowing the complexity of distinct gene expression patterns to enter the predictive model. Tumors are graphed against metagene levels for three of the highest scoring metagene factors (Figure 8). This analysis highlights the need to analyze multiple aspects of gene expression patterns. For example, if the low-risk cases 1, 3 and 11 are assessed against metagene 146 alone, their levels are more consistent with high-risk cases. However, when additional dimensions are considered, the picture changes. The second frame (upper right) shows that low-risk is consistent with low levels of metagene 130 or high levels of metagene 146; hence, cases 1 and 3 are not inconsistent in the overall

pattern, though case 11 is consistent. An analysis that selects one set of genes, summarized here as one metagene, as a “predictor” would be potentially misleading, as it ignores the broader picture of multiple interlocked genomic patterns that together characterize a state. In the predictions, these two metagenes play key roles: low levels of metagene 146 coupled with higher levels of metagene 130 are strongly predictive of high-risk cases. Metagene 330 also plays a role and it is the combined use of multiple metagenes, in the context of the tree selection model building process that ultimately yields a pattern that has the capacity to accurately predict the clinical outcome.

10 This analysis was validated using data from a study conducted in a prior study. To extend this analysis to an independent data set, we used a small but relevant subset of the patient samples studied in a previous Duke breast cancer analysis (West et al., Predicting the Clinical Status of Human Breast Cancer by Using Gene Expression Profiles, Proc. Natl. Acad. Sci., USA 2001; 98:11462, hereinafter called the “Duke PNAS 2001 Study”). This is a limited initial study conducted using binary regression analysis, but also supportive of the basic conclusion of predictive value of multiple metagene patterns. Relative to the samples used in this analysis which were based entirely on an East Asian cohort, and thus racially homogeneous, the Duke PNAS 2001 study patients had rather different characteristics: the racial difference, and the facts that the US women were generally much older and had much larger tumors at surgery than East Asian women. Furthermore, the numbers of extreme (>9) lymph nodes are very small, so the criteria for the two risk groups were relaxed (ignoring age, reducing the number of positive nodes for the high-risk group, and substantially increasing the maximum tumor size for the low-risk group) in order to generate meaningful numbers of cases for study. This led to 6 low-risk cases (lymph node negative, ER+, tumor sizes less than 3.5cm which is the median size of the whole group) and 7 high-risk cases (at least 4 positive nodes, rather than 10). Additional complications are due to the fact that the expression data for this older study were obtained on an earlier Affymetrix microarray, so they represent different though overlapping genes. In spite of these complications, and the resulting expectation that predictive accuracy would be reduced, the predictions based on precisely the model fitted to the Asian data are

very accurate: one of the low-risks cases appears more consistent, in terms of metagene expression, with the high-risk cases, whereas the remaining 12 cases are very accurately predicted to lie within their defined risk groups. Interestingly, the apparently discrepant low-risk case (#42) has the largest tumor (3.5cm) of the group.

- 5 Figure 9 exhibits the three key metagenes, in a format similar to Figure 8 but now including also these external validation cases, where concordance with the Asian samples is clear.

The second analysis concerns 3 year recurrence following primary surgery among the challenging and varied subset of patients with 1-3 positive lymph nodes.

- 10 Such patients typically receive adjuvant chemotherapy alone, and uniformly across this risk group, so that it is of interest to explain variations in outcome within this subgroup based on predictors other than treatment regimen. This is a critical subgroup as more than 20% suffer relapse within five years (See Cheng et al., Unique Features of Breast Cancer in Taiwan, Breast Cancer Res. Treat.
- 15 2000:63:213-23). Hence, improved prognosis for this heterogeneous group is of critical importance; patients identified with a high probability of relapse could be targeted for more intensive treatment. The data set used in this analysis provides expression profiles on 52 cases in this lymph node category (34 non-recurrent, 18 recurrent). The aggregate predictions from the sets of generated statistical tree
- 20 models defines a rather accurate picture; once again, there is an approximate 90% (with 95% CI 82-99%) overall predictive accuracy in the 52 separate one-at-a-time, cross-validation prediction assessments (Figure 10).

- Based on the gene expression analysis, the 3 year non-recurrent cases 6 and 23, having profiles more akin to recurrent cases, would be candidates for intensive
- 25 treatment. These patients did receive adjuvant chemotherapy based on additional clinical risk factors (especially tumor size). Thus traditional clinical risk factors other than lymph node status also indicate higher risk of recurrence for these two cases, consistent with the molecular predictions. Each actually survived recurrence-free for over three years; case 6 recurred at 42 months and case 23 remains disease-
- 30 free after over 6 years. Cases with low genomic criteria for recurrence would be 36, 38 and 42. They, however, each recurred within three years. These are cases that, under prognosis informed by only the genomic model, would have been indicated as

more benign and not candidates for intensive treatment, whereas such a treatment might have proven to be more beneficial.

Genes implicated in lymph node and recurrence studies

Subsets of genes related to the metagene predictors of lymph node
 5 involvement are replete with those involved in cellular immunity including a high proportion of genes that function in the interferon pathway. Genes associated with metagene predictors of lymph node metastasis are provided in Table 3. Genes associated with metagene predictors of breast cancer recurrence are provided in Table 4. A Full list of genes defining all metagenes is shown in Table 6. Table 6 is
 10 provided at the end of the specification for the purpose of convenience.

They include genes that are induced by interferon such as various chemokines and chemokine receptors (Rantes, CXCL10, CCR2), other interferon-induced genes (IFI30, IFI35, IFI27, IFI44, IFIT1, IFIT4, IFITM3), as well as
 15 interferon effectors (2'-5' oligoA synthetase), and genes encoding proteins mediating the induction of these genes in response to interferon (STAT1 and IRF1). This connection is intriguing given the role of interferon as a mediator of the anti-tumor response and, together with the fact that many genes involved in T cell function (TCRA, CD3D, IL2R, MHC) are also included within the group that predict lymph node metastasis. Possibly, this may reflect the distinct nature of these
 20 tumors that have acquired a metastatic potential that elicits an anti-tumor response that is ultimately unsuccessful or an aberration of the normal anti-tumor response. Both of the key metagenes, 146 and 330, contain a number of these interferon related genes.

There is little intersection between the lists of genes defined by key
 25 metagenes here and those from the Duke 2001 PNAS lymph node study, which is perhaps not surprising given the relative heterogeneity of the patients in the Duke study. However, when the method of analysis used previously is reapplied to the restricted subset of 6 low versus 7 high risk cases identified in the external validation study reported above, the 100 genes that most strongly relate to the
 30 categorization of lymph node status do indeed overlap with the top few metagenes of the current study. In particular, these include several genes already noted that are

involved in an interferon response (STAT1, MX1, IFIT1, ISG115, IFI27, and IFI44).

Genes implicated in recurrence prediction do not exhibit such a striking functional clustering but do include many examples previously associated with breast cancer. Moreover, this group of genes is clearly distinct set from those that predict lymph node involvement. They include genes associated with cell proliferation control, both cell cycle specific activities (CDKN2D, Cyclin F, E2F4, DNA primase, DNA ligase), more general cell growth and signaling activities (MK2, JAK3, MAPK8IP, and EF1 α), and a number of growth factor receptors and G-protein coupled receptors, some of which have been shown to facilitate breast tumor growth (EpoR). Possibly, the poor prognosis with respect to survival reflects a more vigorous proliferative capacity of the tumor.

We conclude that genes implicated in the prediction of lymph node metastasis and overall recurrence of disease, although clearly representing interrelated phenomena, nevertheless reflect the participation of distinct biological processes. The modeling approach we take here is flexible in this regard. The tree models select only those metagenes that are most relevant to the prediction in hand and also enable a more accurate analysis.

The instant invention by allowing the integration of clinical and genomic factors, allows for personalized medicine that aims to characterize those variables unique to the individual that determine disease susceptibility, response to therapy, and eventual disease outcome. It does so by addressing this in assessing complex, multivariate patterns in gene expression data from primary tumor biopsies, and in exploring the value of such patterns in predicting lymph node metastasis and relapse. The resulting predictive accuracy of about 90%, and additional understanding of individual outcomes generated by the analysis, confirm the utility of gene expression patterns as prognostic factors in breast cancer. The invention stresses the focus on predictions made in terms of numerical probabilities of outcomes for individual patients, with associated measures of uncertainties.

The lymph node risk group analysis defines metagene patterns capable of predicting high versus low risk cases with good accuracy, in both internal and external validation studies. In a reanalysis of the small subset of samples from the

Duke 2001 PNAS Study that relate most closely to the risk categories defined in this current study, it is determined that improved predictions relative to earlier methods were seen, but also that a number of genes, including interferon-induced genes and others, were in common. This provides additional support for the biological

5 relevance of the metagene predictors identified, and suggests potential areas for further pathway studies. In one embodiment, the present invention would allow for the prediction of drug metabolism pathways that occur in a individual patient. The concordance between genomic predictors found between the Asian and US samples, though preliminary, is also a positive finding.

10 A related recurrence study (T. Van Veer et al., Gene Expression Profiling Predicts Clinical Outcome of Breast Cancer, Nature, 2002, 4154:530-6) defines a single summary of gene expression related to breast cancer recurrence (though not nodal metastasis), generating a 70 gene predictor. The methods of the instant invention do not identify more than 17 of these 70 genes on the Affymetrix array
15 used here, and none of these appears in the key metagenes in the recurrence study. The analysis approach used in T. Van Veer et al follows the work of the Duke 2001 PNAS Study in developing a single predictor based on an initial screen for genes most correlated with outcome. However, a major distinction of the current invention relative to these prior studies is the finding that multiple measures of gene
20 expression – multiple metagenes – may be found that are involved in explaining differences and, most importantly, defining predictions. Investigation of several metagenes, defining distinct patterns in the data relevant to the outcome, show how the combined effect of several views of clinico-biological data can highlight the similarities between patients while also identifying their differences. The non-linear
25 statistical analysis aids in the elucidation of such patterns as they shed light on individual cases, as well as providing for informed predictions based on multiple patterns.

This latter point relates to the broader question of utilizing gene expression profiles into prognostic settings. The present invention allows for the integration of
30 genomic data with clinical risk factors that will determine the strategy for treating patients as individuals with distinct genomic disease features. Although, genomic data may not replace traditional clinical risk factors, it will add significant detail to

this clinical information, especially in a context such as breast cancer where multiple, interacting biological and environmental processes define physiological states, and individual dimensions provide only partial information. As one initial example, the recurrence study here focuses on the 1-3 positive lymph node group
5 where the analysis defines metagenes optimized for prediction within that group; predicting other subgroups, such as higher-risk cases in terms of lymph node count or subgroups stratified by additional clinical factors, will involve exploration of metagenes that optimally relate to outcomes within those subgroups.

Reliably improved predictions of disease course, including lymph node
10 metastasis or recurrence, will profoundly affect the clinical decision process. Several studies indicate that 22-33% of node negative tumors behave in a manner similar to node positive tumors (Polychemotherapy for Early Breast Cancer: An overview of the randomized trials, Early Breast Cancer Trialists Collaborative Group, Lancet 2001: 352:930-42). Whether an issue of timing or of the inability to recognize
15 histopathologic involvement of tumor material in the lymph nodes, a capacity to identify these cases as requiring more intensive clinical intervention could lead to an improvement in cancer survival. Previous attempts to correlate characteristics of primary tumors such as S-phase fraction, tumor grade, ploidy, *c-erbB-2* overexpression, and hormone receptor status with lymph node metastasis have
20 proven unsuccessful (See Mittra I, MacRae KD. A Meta-analysis of reported correlations between prognostic factors in breast cancer: does axillary lymph node metastasis represent biology or chronology, Eur.J.Cancer 1991;27:1574-83; McGuire WL. Prognostic factors for recurrence and survival in human breast cancer. Breast Cancer Res Treat. 1987;10:5-9; Tandon AK, Clark GM, Chamness GC,
25 Ullrich A, McGuire WL. HER-2/neu oncogene protein and prognosis in breast cancer. J.Clin.Oncol. 1989;7:1120-8). The ability to appropriately utilize gene expression profiles provides opportunity to add enormous additional detail to the few, currently used biological attributes in tumor characterization. Finally, genes implicated in these analyses generate information of value for future pathway
30 studies, with the potential to identify new targets that may feed into improved therapeutic strategies as well as improved understanding of genes related to the biology of metastasis and tumor evolution.

Table 1. Clinical characteristics of patients in the study

	Number	Percentage
Age		
< 40	27	30.3
41-50	26	29.2
51-60	19	21.4
> 60	17	19.1
Histology type		
Infiltrating Ductal Carcinoma	78	87.6
Infiltrating Lobular Carcinoma	2	2.3
Papillary Carcinoma	2	2.3
Tubular Carcinoma	1	1.1
Cribriform Carcinoma	1	1.1
Apocrine Carcinoma	1	1.1
Others (mixed of histologies)	4	4.5
Pathological tumor size		
	Number	Percentage
< 1 cm	6	6.8
1 – 2 cm	31	34.8
2 – 5 cm	47	52.8
> 5 cm	5	5.6
Lymph node positive		
0	19	21.4
1 – 3	52	58.4
4 – 9	0	0
> 10	18	20.2
Nuclear grade		
Grade I	15	16.8
Grade II	24	27.0

Grade III	50	56.2
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LVI (peritumoral and intratumoral)

Absent	35	39.3
Focal	16	18.0
Prominent	38	42.7

ER status

Positive	74	83.1
Negative	15	16.9

Table 2. Clinical information on discordant cases

Case #	Surgery	RT	CT	Histology	Tumor		Nodes	ER	PR	Relapse
					size					
			CM							
LN-5	MRM	N	F	IDC	2	0	+++	++		NED, 12 months
LN-7	MRM	N	No	IDC	1.7	0	+++	+++		Yes, 32 months
LN-11	BCS	Y	No	IDC	0.5	0	+	+++		Yes, 38 months
LN-22	MRM	Y	CEF	IDC	3	10	+	+		Yes, 75 months

Case #	Surgery	R	T	CT	Histology	Tumor		Nodes	ER	PR	Relapse
						size					
Rec-38	MRM	N	No	TC		1.8	2	+	++		Yes, 11 months
Rec-23	MRM	N	CAF	IDC		3	1	-	-		NED, 74 months
Rec-6	MRM	N	CMF	ILC		3.1	2	+	+		Yes, 44 months
Rec-36	MRM	N	No	IDC		3.5	1	+	-		Yes, 6 months
Rec-42	MRM	N	CEF	IDC		3	2	+	+		Yes, 16 months

5

Abbreviations: MRM, modified radical mastectomy; RT, adjuvant Radiotherapy; CT, adjuvant chemotherapy; BCS, breast conserving surgery; NED, no evidence of disease; IDC, infiltrating ductal carcinoma; ILC, infiltrating lobular carcinoma; TC, tubular carcinoma.

10 Table 3: Genes associated with metagene predictors of lymph node metastasis

Table 4: Genes associated with Metagene Predictors of Breast Cancer Recurrence

Table 5: Full List of Genes Defining All 496 Metagenes as Determined in Example

15 3A (See End of Disclosure)

Example 3B: Prediction of Outcomes in Individual Breast Cancer**Patients****(i) *Combining multiple metagene signatures to improve the accuracy of Breast Cancer Recurrence Prediction***

5 The analyses employing the method of the invention utilizes the data from 158 breast cancer patients registered at the Koo Foundation Sun Yat-Sen Cancer Center (KF-SYSCC) in Taipei during 1991-2001 (*See Chen, S.H. et al. Unique features of breast cancer in Taiwan. Breast Cancer Res Treat. 63, 213-223 (2000)*), with detailed clinical records of traditional risk factors -- axillary lymph node status, ER status, age, tumor size, nuclear grade, recurrence, and others (*See Table 1*).
 10 Gene expression assays provide data summarized in terms of multiple metagenes (*See Huan, E. et al. Gene expression predictors of breast cancer outcomes. Lancet in press, (2003); Seo, D.M. et al.*).

Samples used, extract preparation, and labeling. The case study involved
 15 158 primary tumor biopsies at the Koo Foundation Sun Yat-Sen Cancer Center (KF-SYSCC) in Taipei, collected and banked between 1991-2001. Samples were collected under Duke (IRB# 3157-01) and KF-SYSCC (9/21/01) Institutional Review Board guidelines. Total RNA was extracted from tumor tissue with Qiagen RNEasy kits, and assessed for quality with an Agilent Lab-on-a-Chip 2100
 20 Bioanalyzer. Hybridization targets (probes for hybridization) were prepared from total RNA according to standard Affymetrix protocols.

Hybridization procedures and parameters. The amount of starting total RNA for each reaction was 20 µg. Briefly, first strand cDNA synthesis was generated using a T7-linked oligo-dT primer, followed by second strand synthesis.
 25 An in vitro transcription reaction was performed to generate the cRNA containing biotinylated UTP and CTP, which was subsequently chemically fragmented at 95°C for 35 min. The fragmented, biotinylated cRNA was hybridized in MES buffer (2-[N-morpholino]ethanesulfonic acid) containing 0.5 mg/ml acetylated bovine serum albumin to Affymetrix GeneChip Human U95Av2 arrays at 45°C for 16hr,
 30 according to the Affymetrix protocol (www.affymetrix.com and Pittman Ms -NG 21

www.affymetrix.com/products/arrays/specific/hgu95.affx). The arrays contain over 12,000 genes and ESTs. Arrays were washed and stained with streptavidin-phycoerythrin (SAPE, Molecular Probes). Signal amplification was performed using a biotinylated antistreptavidin antibody (Vector Laboratories, Burlingame, CA) at 3 µg/ml. This was followed by a second staining with SAPE. Normal goat IgG (2 mg/ml) was used as a blocking agent. Each sample was hybridized once.

Measurement data and specifications. Scans were performed with an Affymetrix GeneChip scanner and the expression value for each gene was calculated using the Affymetrix Microarray Analysis Suite (v5.0), computing the expression intensities in 'signal' units defined by software. Scaling factors were determined for each hybridization based on an arbitrary target intensity of 500. Scans were rejected if the scaling factor exceeded a factor of 25, resulting in only one reject. Files containing the computed single intensity value for each probe cell on the arrays (CEL files), files containing experimental and sample information (control info files), and files providing the signal intensity values for each probe set, as derived from the Affymetrix Microarray Analysis Suite (v5.0) software (pivot files), can be found in the Supplementary Material on the project web site.

Array design. All assays employed the Affymetrix Human U95Av2 GeneChip. The characteristics of the array are detailed on the Affymetrix web site (www.affymetrix.com/products/arrays/specific/hgu95.affx).

Statistical analysis. Statistical analysis of the gene expression data involves a number of approaches. Initial exploratory analyses of clinical and genomic patterns associated with recurrence are based on traditional Kaplan-Meier and proportional hazards models. The core methodology that underlies our comprehensive clinico-genomic models uses statistical prediction tree models, and the gene expression data enters into these models in the form of what we term *metagenes*. As previously described, metagenes represent the aggregate patterns of variation of subsets of potentially related genes. Our current approach is to cluster genes with similar patterns of expression and evaluate a single underlying "signature" of each cluster; this signature is termed a metagene for that cluster and serves as a candidate predictive factor in statistical models. Complete technical

details of the clustering analysis methods, the construction of metagene summaries, and the development and implementation of statistical analysis via predictive classification tree models, are given in the accompanying Supplementary Material.

Survival curve estimation using Kaplan-Meier estimates and Cox
5 proportional hazards models illustrates the traditional view of stratifying patients into high versus low risk of recurrence based on clinical factors such as lymph node involvement (*See* Figure 12A). Similar survival rate summaries using any one of a number of metagenes indicate stronger association with recurrence. Metagene 440 (Mg440) provides a strongly discriminating genomic signature (*See* Figure 12B):
10 individuals in the “low Mg440” group exhibit a raw 3-year survival rate of about 20%, compared to about 65% in the “high Mg440” group. This is similar to a recent study described in the previous section employing a single 70-gene predictor that classified breast cancer patients into risk categories based on a “good” or “poor” signature. However, although the prediction of low-risk (good signature) was
15 accurate, the prediction of high-risk (poor signature) was highly uncertain since individuals in this group had a 50-50 probability of recurrence at 10 years (*See* van de Vijver, M.J. *et al.* A gene-expression signature as a predictor of survival in breast cancer. *N. Engl. J. Med.* 347, 1999-2009 (2002). The Mg440 predictor alone is more accurate, in this sense, at the shorter (and more challenging) 3-year horizon,
20 but this analysis only begins the process of understanding personal-level recurrence risks. Further factors are available to substantially refine these risk categories towards customized, personal prediction and to generate improved understanding of uncertainties for the individual patient.

An examination of the gene expression pattern defined by the Mg440 split
25 (*See* Figure 13) reveals substantial heterogeneity in the patterns in the two subgroups. Considering that additional gene expression patterns might resolve this heterogeneity, metagenes were examined for further, statistically significant categorization. As a result, the “low Mg440” group splits further on Mg408, while the “high Mg440” group splits on Mg109 (*See* Figure 13). In each case, the
30 expression patterns were further divided into more homogeneous subgroups based on the expression patterns of a second metagene.

The value of this refinement is clear in the Kaplan-Meier estimate in which the incorporation of additional metagenes markedly changes the survival estimates (See Figures 12D & 12E). This combination of multiple metagenes via further categorization of patients into refined risk groups underlies our statistical tree models and leads to substantially improved predictions -- suggested by the figure. The same applies to combining clinical factors with metagenes (See Figure 12C). Also, multiple metagenes are capable of playing significant roles in such analyses (See Tables 2 and 3). Thus, it is clear that there is a resulting potential for different models to generate different, even potentially conflicting predictions.

10 Understanding this is vital in developing an appreciation of the true nature of the genomic state, reflected in multiple, related measures of expression. Hence there is a need to consider multiple models that define successive partitions of patient groups with a mechanism to formally compare, contrast and combine them.

15 (ii) *Statistical tree models utilizing multiple metagenes to predict cancer recurrence*

To explore multiple metagenes for optimal predictions, the invention uses extensions of regression and classification trees determined by the statistical model. A single tree defines successive partitions of the sample into more homogenous subgroups. At any node of the tree, the corresponding subset of patients may be divided into two at a threshold on a chosen metagene, analogous to the standard low/high-risk grouping already discussed. The analysis shown in Figure 13 represents one node of a tree in which Mg440 splits the samples into two groups that are then further split by additional metagenes. The logical extension is to tree models with more levels, and also to multiple trees. At any node, the optimal metagene/threshold pair for dividing the sample in the node is chosen by screening all metagenes, and evaluated by a test statistic for the significance of splits across a range of possible thresholds. A split is made if the significance exceeds a specified level. Tree growth is restricted, and ended, when no metagene can be found to define a significant split. Multiple possible splits generate copies of the tree and so underlie the generation of forests of trees. The specific statistical test used is a Bayes' factor (integrated likelihood ratio) test (See Kass, R.E. & Raftery, A.E. Bayes'

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factors. *J. Am. Stat. Assoc.* 90, 773-795 (1998)) that is generally conservative relative to standard significance tests and so tends to generate less elaborate trees than traditional tree programs.

Two highly significant tree models, involving several metagenes are shown in Figure 14A, where the development of branches involving additional metagenes, and the resulting predictions of recurrence within the population subgroups are defined by each leaf. The boxes at nodes of a tree indicate the number of patients together with the model-based estimate of 4-year recurrence-free survival probability. These simple point estimates of recurrence probabilities help to illustrate the implications of the tree model; as a patient is successively categorized down the tree, these node probabilities show the "current" prediction at each node and how those predictions change as additional predictor variables are used. It must be borne in mind, of course, that these point estimates are subject to uncertainty generated by the analyses (see Figures 16 and 17). For example, the 50% probability indicated in the extreme left-hand terminal node of the first tree in frame (A) is in fact very uncertain, with associated confidence intervals spanning up to much higher values well above 90%.

At any given node of a tree model, there may be several metagenes defining significant subgroups, so it is important to consider multiple tree models. A resulting set of tree models is evaluated statistically by computing the implied value of the statistical likelihood function for each tree; the set of likelihood values are then converted to tree probabilities by summing and normalizing with respect to all selected trees. Predictions are based on all trees in combination, via weighted averages of predictions from individual trees with the tree probabilities acting as weights. This "model averaging" is well known to generally improve prediction accuracy relative to choosing one "best" model (*See* Hoeting, J., Madigan, D., Raftery, A.E. & Volinsky, C.T. Bayesian model averaging. *Statistical Science* in press, (1999); Clyde, M. Bayesian Statistics 6. Bernardo, J.M. (ed.), pp. 157-185 (Oxford University Press, 1999)) especially when several or many models fit the data comparably. In exploring and evaluating trees, several hundreds are generated and

weighted; very low probability trees are discarded and the remaining are summarized and averaged to compute resulting predictions.

(iii) *Statistical prediction tree models combining metagenes and clinical risk factors predict individual breast recurrence most accurately*

5 The tree models were extended to explore all forms of input data, both genomic and clinical. Key clinical factors are lymph node status, represented as 0, 1-3, 4-9, and 10 or more positive nodes, ER status (0,1,2+), tumor size, and treatment factors. Figure 3B displays two of the most highly significant trees that play important roles in contributing to the prediction of recurrence. The key clinical
10 variable identified by these trees is nodal status; its appearance in these most highly weighted trees indicates that it supersedes some of the metagene predictors selected in the exclusively genomic analysis. ER status defines secondary aspects of some of the top trees. Of hundreds of trees generated in the model search, others involve clinical predictors and also treatment variables, but these trees receive low relative
15 statistical likelihood measures and resulting tree probabilities. Treatment protocols follow closely the traditional clinical risk groups that are dominated by lymph node status, and so, though some lesser weighted trees involve variants of treatments in appropriate ways, the inclusion of nodal status stands-in for treatments in highly weighted trees.

20 Once lymph node status is a candidate predictor, it defines key aspects of predictive trees and reduces the number of metagenes required to achieve accurate predictions. ER status (ER level) is the second clinical factor selected in some of the top trees, and appears here in conjunction with Mg20 that in fact defines a group of genes related to the known risk factor Her-2-nu/Erb-b2. One minor feature (lowest
25 level, right branch) of the first tree is worth noting - a final split according to node negatives versus nodes 1-3 positive. This represents a partition of this subgroup into the traditional two lowest lymph node risk categories, but associates higher risk with the subgroup of node negatives in this final branch of this path in the tree. The reason is twofold: first, the sample design overrepresented short-term recurrences
30 among the lymph node negatives, second, the 1-3 lymph node positives tend to have some form of adjuvant chemotherapy so are treated more aggressively. The model

isolates these subgroups and identifies the differential risk related to this specific aspect of sample selection for this data set, though this feature would be refined in further analysis of a larger, more balanced sample.

Figure 15A summarizes the tree model-predictor variable for the most highly weighted trees based solely on metagenes; Figure 15B summarizes that using both metagenes and clinical factors. These represent subsets of hundreds of trees that were evaluated, and account for most of the resulting predictive value. The figures indicate the predictor variables (columns) that appear in the selected top trees (rows), and the levels (boxed numbers) of the trees in which they define node splits. The probability of each tree and the overall probability of occurrence of each of the clinical and metagene factors across the set of trees are also given. Metagenes dominate the initial splits. Other tree models -- with lesser relative weights but nevertheless representing interesting combinations of predictor variables -- include additional metagenes that are strongly related to those in the top few trees. Although each of the two models (metagenes only versus combined metagenes and clinical factors) defines significant models and are substantially accurate in cross-validated prediction assessments, the combined models have a significantly higher statistical likelihood (difference in log-model likelihoods is greater than 11, which represents a very substantial weight of evidence in favor of the clinico-genomic model).

(iv) *Predicting risk of recurrence based on tree model summaries*

Honest assessment of true predictive accuracy of the models can be made based on a one-at-a-time cross-validation study in which the analysis is repeatedly performed -- for example, holding out one tumor sample at each reanalysis and predicting the recurrence time distribution for that holdout patient. Importantly, the entire model building process -- selection of metagenes and clinical factors, and their combination in sets of trees to be weighted by the data analysis -- must form part of each reanalysis in order to obtain a truly honest predictive evaluation. No pre-selection of predictor variables, or pre-specification of aspects of the model, may be made based on an examination of all the data prior to these repeat validation analyses, as such would bias the results towards what will generally be a gross overstatement of predictive accuracy and validity.

Figure 16 displays summaries of this honest predictive assessment for 5-year survival probabilities (panel A) and 4-year survival probabilities (panel B).

Corresponding to the point estimates, receiver-operator characteristic (ROC) curves were computed that indicate the capacity to predict 4-year survivors with over 90%

5 accuracy, and 5-year survivors with about 95% accuracy. That is, by simply classifying a patient as "high-risk" versus "low-risk" based on her predicted recurrence probability, about 90% (or 95%) of cases are correctly predicted in the sense of low-risk cases not recurring and high-risk cases recurring. Although this is a very crude summary of overall prediction accuracy a more detailed analysis is
10 available in the next example. Nevertheless, serves to indicate a very high degree of model accuracy. Consistent with the fitted model, the combined clinico-genomic analysis exceeds the predictive accuracy of the exclusively genomic analysis. In addition to providing predictive evaluation, this provides an initial illustration of the use of such models in individual patient-level predictions.

15 Although a number of patients with shorter follow-up do not appear in the figures, because their status as 4- or 5-year survivors is undetermined the models directly predict their survival distributions and provide assessment of survival chances conditional on the observed time of recurrence-free follow-up (See Figure 18) again at the individual level.

20 (v) *Metagenes can predict and substitute for clinical risk factors*

The combined clinico-genomic predictive tree analyses reveal that lymph node involvement appears in the key predictive trees, consistent with the wide recognition of lymph node involvement as the most significant clinical risk factor in breast cancer (See Jatoi, I., Hilsenbeck, S.G., Clark, G.M. & Osborne, C.K.

25 Significance of axillary lymph node metastasis in primary breast cancer. *J Clin Oncol* 17, 2334-2340 (1999); McGuire, W.L. Prognostic factors for recurrence and survival in human breast cancer. *Breast Cancer Res Treat.* 10, 5-9 (1987)). Since axillary node dissection carries significant morbidity, the invention uses a metagene analysis as a preferable alternative to clinical lymph node diagnosis. The metagene
30 signatures have the capacity to replace nodal counts although the latter still aids in constructing the most significant models. Nevertheless, when tree analyses are

carried out without the use of clinical factors, including lymph node status, the predictive capability is very good indeed, almost comparable to the combined model though still overshadowed to a degree, in terms of statistical fit and predictive accuracy.

5 Metagene 408 is a key feature of one major "branch" of the most significant trees (See Figure 14A, the left branch of trees beginning with Mg440). The association of Mg408 as a strong predictor of lymph node status (see, Huang, E. *et al.* Gene expression predictors of breast cancer outcomes. *Lancet* in press, (2003)) indicates that it can, to some degree, substitute for lymph node status subject to
 10 verification and comparison by the model of the invention. In the model with genomic data alone, the picture is less clear as many more metagenes are required to define a larger set of relatively equally well weighted trees, representing multiple patterns that each partially substitute for the clinical predictors. Among these is Mg328, an additional genomic predictor of lymph node status.

15 Also included are Mg315 and Mg351 that correlate with genes within the estrogen pathway substitute for ER status in the genomic-only analysis. See Example 2.

A further case, Mg20 that appears with ER status in the combined model, is based on 15 genes that define the Her-2-neu/Erb-b2 metagene cluster (See Table 4).
 20 Her-2-neu/Erb-b2 has previously been defined as a risk factor primarily among ER negative cases (see, Tandon, A.K., Clark, G.M., Chamness, G.C., Ullrich, A. & McGuire, W.L. HER-2/neu oncogene protein and prognosis in breast cancer. *J. Clin. Oncol.* 7, 1120-1128 (1989)) so its appearance here within a subset of ER positive cases implicates Her-2-neu/Erb-b2 more broadly. Its strength as a prognostic factor
 25 is, however, only marginal and it is strongly dominated by preceding metagenes.

(vi) *Prediction of recurrence to achieve personalized prognosis*

The 4- and 5-year survival probability predictions in Figure 16 are taken from the full survival distributions that result from the statistical model analysis. At each terminal leaf of each tree, the analysis estimates a full survival time distribution

that represents the survival characteristics of individuals assigned to the subpopulation with predictors defining that leaf. Formal predictions for an individual are based on averaging these survival distributions across tree models, each tree weighted by its corresponding data-based probability. The analysis also provides assessments of uncertainty about predicted survival curves; communicating these uncertainties along with estimates is critical to interpretation and assessment of survival prospects at an individual level. To illustrate this, Figure 17 displays the resulting predictions for four patients whose clinical and metagene factors match a chosen four of the patients in the data base. Each panel gives the predicted survival curve for one patient. At a number of time points, the vertical intervals represent approximate 95% uncertainty intervals for the predicted survival probabilities at those time points. Also, the estimated 5-year survival probability is highlighted.

A critical aspect of predictive analysis is that models must properly evaluate uncertainties associated with predictions of probabilities of recurrence and other outcomes. Uncertainties arise from multiple sources, including the usual sampling variability and the limitations of samples sizes. Uncertainty also arises when the patient characteristics that define predictions show evidence of conflict. The tree model framework utilizes multiple trees and, in cases of apparent conflict within or between the genomic and clinical predictor sets, different trees may suggest different outcomes. It is then important that an overall prediction summary recognizes and represents this via high uncertainty intervals about probability predictions, and that the model be open to investigation so that the specifics of such cases can be explored.

Cases 15 and 158 are examples in which the confidence of prediction, whether for early recurrence (Case #15) or disease-free survival (Case #158), is very high -- indicated by the narrow prediction intervals. In contrast, the two additional cases are examples where uncertainty is high. For example, Patient #98 is a younger woman with 10 positive nodes and a reasonably large tumor at biopsy. She was, by choice, not treated aggressively, but in spite of her high clinical risk profile survived recurrence-free up to 75 months. The model predictions clearly indicated substantial conflict among the metagene-clinical predictors, resulting in a very uncertain

predictive distribution. A second patient, #148, is an older woman who had one positive node and only a modest sized tumor, so was apparently clinically low-risk and indeed survived recurrence free for at least 6.5 years. The prediction for this individual from the full model was quite uncertain, favoring higher-risk but
5 generating very wide intervals and so suggesting caution and further detailed investigation at the point of evaluation. In fact, the pathology reports for this woman indicated a range of characteristics that defined her as very high-risk (4B by T-staging-15), in contrast to the generally, but not exclusively, lower-risk clinical factors. Further detailed investigations revealed that, in fact, the clinical
10 determinations were highly unusual, with evidence of an invasive, more aggressive tumor, to the extent that the clinical classification of this patient is also, alone, quite controversial. However, the metagene predictors are capable of capturing a very high degree of conflicting information in genomic patterns, perfectly consistent with this very unusual, and complex, mix of conflicting clinical and pathological
15 characteristics. Although the clinico-genomic model dominates the metagene-only model overall, the predictions for Patient #148 in the latter, while similarly uncertain, generate higher point estimates of survival probabilities, and so represent, postfacto, a more accurate prediction for this one individual.

Patient #148 is unusual. Other patients with low (0-3) positive lymph node
20 counts are similarly predicted with low recurrence-free survival probabilities, but much less uncertainty, and in fact recur within four or five years. These cases, and others in the low lymph node count categories that in fact survived much longer, are all very accurately predicted based on the amalgam of risk factors represented in the model.

25 The analysis framework has the capacity to evaluate the relative contributions of multiple forms of data, both clinical and genomic, to predict disease outcomes. This provides a mechanism to substantially refine predictions to be specific for individual patients. Multiple, related patterns of gene expression -- metagene signatures -- provide strong and predictively valid associations with breast
30 cancer recurrence. Several key metagenes are each individually capable of defining very highly significant population differences, and their value as population risk

factors far exceeds that of previously published genomic risk factors. When combined in predictive models, small sets of multiple metagenes together define improved predictions via successive stratification of the patient set into smaller, more homogeneous subgroups with associated survival distributions defined by interactions of metagenes.

Prediction accuracy can be improved by combining clinical factors with the genomic data. Key metagenes can, to a degree, replace traditional risk factors in terms of individual association with recurrence, but the combination of metagenes and clinical factors, notably axillary lymph node status, defines models most predictive of recurrence. The resulting tree models provide an integrated clinico-genomic analysis that is most highly supported by the data analysis and also generate substantially accurate, crossvalidated predictions at the individual patient level.

The models deliver formal predictive survival assessments, in terms of estimates of survival distributions for future patients, and current patients being followed-up, together with measures of uncertainty about the predictions. The latter are critical in advising clinical decisions. A point prediction of a survival probability, such as a 5-year recurrence probability, is only part of the story; it is critical to also communicate how uncertain that probability estimate is, as measured by an interval estimate that integrates uncertainty due to sample size and sampling fluctuations together with uncertainty arising from potentially conflicting predictors. The specific approach using tree models highlights the latter issue, helping to identify individual patients for whom there is evidence of conflict among the predictors, within or between the genomic and clinical predictors, that is reflected in increased uncertainty about the resulting recurrence predictions.

Genomic data, particularly gene expression profiles, clearly has the capacity to significantly improve clinical predictions. Further, genomic information potentially identifies relevant genes and pathways providing clues to the pathophysiology underlying the disease. Key metagenes that provide predictive power also define sets of genes suggestive of biologically relevant pathways associated with clinical phenotypes. Most striking are the lymph node metagenes,

especially Mg408, that involve genes generally associated with tumor immunosurveillance. This indicates that characteristics of the tumor that predict lymph node metastasis, and ultimately disease recurrence as we have shown, relate to the involvement of processes associated with immunological response to the tumor. Immunologically, this may represent an incomplete or failed immunological response, one that allows tumor cells to escape. Alternatively, the immunological response itself may contribute to tumor progression by contributing to local tissue breakdown. Other metagenes highly weighted in predicting disease recurrence, such as Mg440, identify growth-signaling pathways that are altered in a variety of oncogenic settings. Highly related metagenes that have similar weights and contributions to the tree prediction models, such as Mg440 and Mg307, also exhibit similarities in gene function; for example, Mg307 exhibits additional genes associated with growth factor signaling. In contrast, other implicated metagenes identify distinct biological properties suggesting that different aspects of biology are contributing to the prediction and ultimately reflecting the heterogeneity of the disease process. The identification of multiple genes of potential biological relevance to tumor development in breast cancer, and their predictive value in individual-level prognostics models, represents a key and distinctive finding.

In complex diseases such as breast cancer, clinical endpoints reflect the accumulative or aggregate action of multiple genomic patterns – representing multiple gene pathways and their interactions. Individual prognosis must recognize and evaluate such patterns in combination with clinical factors, especially when multiple factors involve conflicting prognostic signals. The invention evaluates and uses multiple, related genomic patterns in combination with clinical factors, rather than a single genomic pattern to the exclusion of other informative factors. Thus, the invention teaches that not only do that multiple factors define the most accurate predictions, also permit the analysis of what may be deemed to be conflicting biological predictors at the clinical evaluation stage.

The modeling process provides a framework in which other forms of clinical data including, but not limited to improvements in clinical phenotyping, new forms of genomic data (for example, DNA structure, protein patterns, metabolic profiles,

- single nucleotide polymorphisms [SNPs] and haplotype data could be incorporated that will likely make significant contributions to the ultimate prediction of outcome. The generation of predictive models that can evaluate multiple, distinct forms of data thus has the added advantage of being able to integrate any form of quantifiable
- 5** information. This adaptability is immediately relevant in the context of developing extended studies that aim to refine and evolve the understanding of multiple forms of data relevant to moving genomic analysis through clinical trials to clinical practice.

Table 3: 175 genes related to top few metagenes in lymph node analysis

	32435_at	Cluster Incl. X63527:H.sapiens mRNA for ribosomal protein L19 /cds=(28,
	33611_g_at	Cluster Incl. AL049977:Homo sapiens mRNA; cDNA DKFZp564C122 (from clo
5	34585_at	Cluster Incl. L07919:Human homeodomain protein DLX-2 mRNA, 3 end /cds=
	35055_at	Cluster Incl. X53281:H.sapiens BTF3b mRNA /cds=(239,727) /gb=X53281 /gi
	35061_at	Cluster Incl. AF030514:Homo sapiens interferon stimulated T-cell alpha
	35099_at	Cluster Incl. AF019225:Homo sapiens apolipoprotein L mRNA, complete cds
	35583_at	Cluster Incl. X99699:H.sapiens mRNA for XIAP associated factor-1 /cds=(
10	36412_s_at	Cluster Incl. U53831:Homo sapiens interferon regulatory factor 7B mRN
	34491_at	Cluster Incl. AJ225089:Homo sapiens mRNA for 2-5 oligoadenylate synthe
	34974_at	Cluster Incl. Y13323:Homo sapiens mRNA for disintegrin-protease /cds=(6
	35008_at	Cluster Incl. AB002345:Human mRNA for KIAA0347 gene, complete cds /cds=
	35428_g_at	Cluster Incl. W28256:44b9 Homo sapiens cDNA /gb=W28256 /gi=1308204 /u
15	35926_s_at	Cluster Incl. AF004230:Homo sapiens monocyte/macrophage Ig-related re
	36280_at	Cluster Incl. U26174:Human pre-granzyme 3 mRNA, complete cds /cds=(40,8
	36776_at	Cluster Incl. X51985:Human LAG-3 mRNA for CD4-related protein involved
	36804_at	Cluster Incl. M34455:Human interferon-gamma-inducible indoleamine 2,3-d
	37126_at	Cluster Incl. M62800:Human 52-kD SS-A/Ro autoantigen mRNA, complete cds
20	37137_at	Cluster Incl. M17016:Human serine protease-like protein mRNA, complete
	37145_at	Cluster Incl. M85276:Homo sapiens NKG5 gene, complete cds /cds=(128,565
	37149_s_at	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (c
	37168_at	Cluster Incl. AB013924:Homo sapiens mRNA for TSC403 protein, complete c
	37420_i_at	Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex,
25	37454_at	Cluster Incl. AJ001634:Homo sapiens mRNA for CC-chemokine MCP-4 /cds=(4
	37873_g_at	Cluster Incl. AF072468:Homo sapiens (JH8) mRNA, partial cds /cds=(0,1
	37874_at	Cluster Incl. Z47553:H.sapiens mRNA for flavin-containing monooxygenase
	38241_at	Cluster Incl. U90548:Human butyrophilin (BTF3) mRNA, complete cds /cds=
	38517_at	Cluster Incl. M87503:Human IFN-responsive transcription factor subunit
30	38549_at	Cluster Incl. AF026941:Homo sapiens cig5 mRNA, partial sequence /cds=UN
	38584_at	Cluster Incl. AF026939:Homo sapiens CIG49 (cig49) mRNA, complete cds /c
	38850_at	Cluster Incl. M11119:Human endogenous retrovirus envelope region mRNA (
	38922_at	Cluster Incl. AF097738:Homo sapiens non-receptor tyrosine kinase (TNK1)
	39263_at	Cluster Incl. M87434:Human 71 kDa 25 oligoadenylate synthetase (p69 2-
35	39264_at	Cluster Incl. M87284:Human 69 kDa 25 oligoadenylate synthetase (P69 2-
	39266_at	Cluster Incl. AF070632:Homo sapiens clone 24405 mRNA sequence /cds=UNKN
	39665_at	Cluster Incl. U33267:Human glycine receptor beta subunit (GLRB) mRNA, c
	39939_at	Cluster Incl. D21337:Human mRNA for collagen /cds=(234,5270) /gb=D21337
	39959_at	Cluster Incl. AL031983:dJ271M21.6 (Diubiquitin) /cds=(18,515) /gb=AL031

	39988_at	Cluster Incl. M74447:Human PSF-2 mRNA, complete cds /cds=(96,2207) /gb=
	40035_at	Cluster Incl. AB012917:Homo sapiens mRNA for serine protease (TLSP), co
	40385_at	Cluster Incl. U64197:Homo sapiens chemokine exodus-1 mRNA, complete cds
	40738_at	Cluster Incl. M16336:Human T-cell surface antigen CD2 (T11) mRNA, compl
5	41679_at	Cluster Incl. AF035282:Homo sapiens clone 23703 mRNA sequence /cds=UNKN
	31891_at	Cluster Incl. U58515:Human chitinase (HUMTCHIT) mRNA, exon 1b form, par
	32664_at	Cluster Incl. D37931:Human mRNA for RNase 4, complete cds /cds=(27,470)
	32668_at	Cluster Incl. AL080076:Human sapiens mRNA; cDNA DKFZp564C0362 (from clon
10	32700_at	Cluster Incl. M55543:Human guanylate binding protein isoform II (GBP-2)
	33236_at	Cluster Incl. AF060228:Homo sapiens retinoic acid receptor responder 3
	33304_at	Cluster Incl. U88964:Human HEM45 mRNA, complete cds /cds=(37,582) /gb=U
	33788_at	Cluster Incl. AB002390:Human mRNA for KIAA0392 gene, partial cds /cds=(
	33811_at	Cluster Incl. AI761567:wg66a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
15	34767_at	Cluster Incl. AI670788:tz10c02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35253_at	Cluster Incl. AB011143:Homo sapiens mRNA for KIAA0571 protein, complete
	35622_at	Cluster Incl. AB001451:Homo sapiens mRNA for Sck, partial cds /cds=(0,1
	35630_at	Cluster Incl. X87342:H.sapiens mRNA for human giant larvae homolog /cds
	35992_at	Cluster Incl. AF087036:Homo sapiens musculin mRNA, partial cds /cds=(0,
20	36013_at	Cluster Incl. AF006621:Homo sapiens embryonic lung protein (HUEL) mRNA,
	36057_at	Cluster Incl. AB011084:Homo sapiens mRNA for KIAA0512 protein, complete
	36092_at	Cluster Incl. AL080213:Homo sapiens mRNA; cDNA DKFZp586I1823 (from clon
	36506_at	Cluster Incl. AJ131693:Homo sapiens mRNA for AKAP450 protein /cds=(222,
	36879_at	Cluster Incl. M63193:Human platelet-derived endothelial cell growth fac
25	36890_at	Cluster Incl. AF001691:Homo sapiens 195 kDa cornified envelope precurs
	36891_at	Cluster Incl. AL022237:bK1191B2.3.1 (PUTATIVE novel Acyl Transferase si
	36927_at	Cluster Incl. AB000115:Homo sapiens mRNA expressed in osteoblast, compl
	37219_at	Cluster Incl. X72755:H.sapiens Humig mRNA /cds=(39,416) /gb=X72755 /gi=
	37281_at	Cluster Incl. D87071:Human mRNA for KIAA0233 gene, complete cds /cds=(2
30	37567_at	Cluster Incl. X98834:H.sapiens mRNA for zinc finger protein, Hsa12 /cds
	37641_at	Cluster Incl. D28915:Human gene for hepatitis C-associated microtubular
	37934_at	Cluster Incl. AL080078:Homo sapiens mRNA; cDNA DKFZp564D1462 (from clon
	37944_at	Cluster Incl. U19523:Human GTP cyclohydrolase I mRNA, complete cds /cds
35	37992_s_at	Cluster Incl. AI436567:ti03b09.x1 Homo sapiens cDNA, 3 end /clone=IM
	38287_at	Cluster Incl. AA808961:nw16h03.s1 Homo sapiens cDNA /clone=IMAGE-124066
	38319_at	Cluster Incl. AA919102:ol84h02.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	38662_at	Cluster Incl. AL047596:DKFZp586G0421_s1 Homo sapiens cDNA /clone=DKFZp5

	38976_at	Cluster Incl. D44497:Human mRNA for actin binding protein p57, complete
	38990_at	Cluster Incl. AL031178:Human DNA sequence from clone 341E18 on chromoso
	39061_at	Cluster Incl. D28137:Human mRNA for BST-2, complete cds /cds=(9,551) /g
	39341_at	Cluster Incl. AJ001902:Homo sapiens mRNA for TRIP6 (thyroid receptor in
5	39412_at	Cluster Incl. U09825:Human acid finger protein mRNA, complete cds /cds=
	39717_g_at	Cluster Incl. AI597616:tn15f08.x1 Homo sapiens cDNA, 3 end /clone=IM
	40087_at	Cluster Incl. AF020202:Homo sapiens Munc13 mRNA, complete cds /cds=(224
	40153_at	Cluster Incl. X57522:H.sapiens RING4 cDNA /cds=(30,2456) /gb=X57522 /gi
	40471_at	Cluster Incl. Y09048:H.sapiens PxF gene /cds=(10,909) /gb=Y09048 /gi=25
10	40505_at	Cluster Incl. AA883502:am25h07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	40518_at	Cluster Incl. Y00062:Human mRNA for T200 leukocyte common antigen (CD45
	40824_at	Cluster Incl. AB018288:Homo sapiens mRNA for KIAA0745 protein, partial
	41140_at	Cluster Incl. U05875:Human clone pSK1 interferon gamma receptor accesso
	41171_at	Cluster Incl. D45248:Human mRNA for proteasome activator hPA28 subunit
15	41184_s_at	Cluster Incl. X87344:H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LM
	41225_at	Cluster Incl. AL049417:Homo sapiens mRNA; cDNA DKFZp586O1919 (from
	clon	
	41237_at	Cluster Incl. D32129:Human mRNA for HLA class-I (HLA-A26) heavy chain,
	41745_at	Cluster Incl. X57352:Human 1-8U gene from interferon-inducible gene fam
20	41755_at	Cluster Incl. AB023194:Homo sapiens mRNA for KIAA0977 protein, complete
	32148_at	Cluster Incl. AI701049:wc78b08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	32244_at	Cluster Incl. AB018280:Homo sapiens mRNA for KIAA0737 protein, complete
	32778_at	Cluster Incl. D26070:Human mRNA for type 1 inositol 1,4,5-trisphosphate
	32814_at	Cluster Incl. M24594:Human interferon-inducible 56 Kd protein mRNA, com
25	32859_at	Cluster Incl. M97935:Homo sapiens transcription factor ISGF-3 mRNA, com
	32860_g_at	Cluster Incl. M97935:Homo sapiens transcription factor ISGF-3 mRNA, c
	33338_at	Cluster Incl. M97936:Human transcription factor ISGF-3 mRNA sequence /c
	33339_g_at	Cluster Incl. M97936:Human transcription factor ISGF-3 mRNA sequence
	34800_at	Cluster Incl. AL039458:DKFZp434N0910_s1 Homo sapiens cDNA, 3 end /clon
30	34821_at	Cluster Incl. AL050197:Homo sapiens mRNA; cDNA DKFZp586D0623 (from
	clon	
	34851_at	Cluster Incl. AF011468:Homo sapiens serine/threonine kinase (BTAK) mRNA
	34892_at	Cluster Incl. AF016266:Homo sapiens TRAIL receptor 2 mRNA, complete cds
	35280_at	Cluster Incl. Z15008:H.sapiens mRNA for laminin /cds=(117,3698) /gb=Z15
35	35298_at	Cluster Incl. U54558:Homo sapiens translation initiation factor eIF3 p6
	35735_at	Cluster Incl. M55542:Human guanylate binding protein isoform I (GBP-2)
	35810_at	Cluster Incl. AI525393:PT1.1_07_A11.r Homo sapiens cDNA, 5 end /clone_
	35839_at	Cluster Incl. D78130:Homo sapiens mRNA for squalene epoxidase, complete
	36118_at	Cluster Incl. AJ000882:Homo sapiens mRNA for steroid receptor coactivat

	36689_at	Cluster Incl. AL040446:DKFZp434D1414_r1 Homo sapiens cDNA, 5' end /clone
	36938_at	Cluster Incl. U70063:Human acid ceramidase mRNA, complete cds /cds=(17,
	37014_at	Cluster Incl. M33882:Human p78 protein mRNA, complete cds /cds=(345,233
	37023_at	Cluster Incl. J02923:Human 65-kilodalton phosphoprotein (p65) mRNA, com
5	37383_f_at	Cluster Incl. X58536:Human mRNA for HLA class I locus C heavy chain /
	37754_at	Cluster Incl. L13210:Human Mac-2 binding protein mRNA, complete cds /cd
	38013_at	Cluster Incl. AL096842:Homo sapiens mRNA; cDNA DKFZp586D1519 (from clone
	38079_at	Cluster Incl. AL049367:Homo sapiens mRNA; cDNA DKFZp586B0918 (from clone
10	38121_at	Cluster Incl. X59892:H.sapiens mRNA for IFN-inducible gamma2 protein /c
	38388_at	Cluster Incl. M11810:Human (2-5) oligo A synthetase E gene /cds=(0,120
	38389_at	Cluster Incl. X04371:Human 1.6Kb mRNA for 2-5A synthetase induced by in
	38432_at	Cluster Incl. AA203213:zx57e04.r1 Homo sapiens cDNA, 5' end /clone=IMAG
15	38759_at	Cluster Incl. U97502:Homo sapiens butyrophilin (BT3.3) gene /cds=(73,22
	38760_f_at	Cluster Incl. U90546:Human butyrophilin (BTF4) mRNA, complete cds /cd
	38792_at	Cluster Incl. AD001528:Homo sapiens spermidine aminopropyltransferase m
	38837_at	Cluster Incl. W26226:22e3 Homo sapiens cDNA /gb=W26226 /gi=1306637 /ug=
	39811_at	Cluster Incl. AA402538:zu48g06.r1 Homo sapiens cDNA, 5' end /clone=IMAG
20	39864_at	Cluster Incl. D78134:Homo sapiens mRNA for CIRP, complete cds /cds=(80,
	40196_at	Cluster Incl. D88153:Homo sapiens mRNA for HYA22, complete cds /cds=(14
	40619_at	Cluster Incl. M91670:Human ubiquitin carrier protein (E2-EPF) mRNA, com
	40639_at	Cluster Incl. AL021683:Homo sapiens cDNA homologous to Yeast SCO1 & SCO
	40916_at	Cluster Incl. AL035494:Human DNA sequence from clone 635G19 on chromoso
25	40936_at	Cluster Incl. AI651806:wb55f10.x1 Homo sapiens cDNA, 3' end /clone=IMAG
	41837_at	Cluster Incl. AA149431:zl26a08.s1 Homo sapiens cDNA, 3' end /clone=IMAG
	32510_at	Cluster Incl. AF026947:Homo sapiens aflatoxin aldehyde reductase AFAR m
	33126_at	Cluster Incl. L13435:Human chromosome 3p21.1 gene sequence /cds=UNKNOWN
30	1985_s_at	X73066 /FEATURE=cds /DEFINITION=HSNM23H1A H.sapiens NM23-H1 mRNA
	1878_g_at	M13194 /FEATURE=mRNA /DEFINITION=HUMERCC1 Human excision repair protei
	1854_at	X13293 /FEATURE=cds /DEFINITION=HSBMYB Human mRNA for B-myb gene
35	1782_s_at	M31303 /FEATURE=mRNA /DEFINITION=HUMOP18A Human oncoprotein 18 (Op18)
	1651_at	U73379 /FEATURE= /DEFINITION=HSU73379 Human cyclin-selective ubiquitin c
	1592_at	J04088 /FEATURE= /DEFINITION=HUMTOPII Human DNA topoisomerase II (top2)
	1505_at	D00596 /FEATURE=cds /DEFINITION=HUMTS1 Homo sapiens gene for thymidylate

- 1506_at D11086 /FEATURE= /DEFINITION=HUMIL2RG Human mRNA for interleukin 2 recep
 1498_at L05148 /FEATURE= /DEFINITION=HUMTYRKIN Human protein tyrosine kinase rel
 1403_s_at M21121 /FEATURE= /DEFINITION=HUMTCSM Human T cell-specific protein
 (RA
- 5** 1358_s_at U22970 /FEATURE=mRNA#1 /DEFINITION=HSU22970 Human interferon-
 inducible
 1291_s_at L03840 /FEATURE= /DEFINITION=HUMFGFR4X Human fibroblast growth
 factor
- 1183_at D43767 /FEATURE= /DEFINITION=HUMAR Human mRNA for chemokine, complete cd
10 1184_at D45248 /FEATURE= /DEFINITION=HUMHPA28A Human mRNA for proteasome
 activa
 1106_s_at M12959 /FEATURE= /DEFINITION=HUMTCAXB Human T-cell receptor active
 alp
 1107_s_at M13755 /FEATURE=mRNA /DEFINITION=HUMIFN15K Human interferon-
15 induced 17
 973_at Y10032 /FEATURE=cds /DEFINITION=HSRNASTPK H.sapiens mRNA for putative ser
 925_at J03909 /FEATURE= /DEFINITION=HUMIIP Human gamma-interferon-inducible prot
 915_at M24594 /FEATURE=mRNA /DEFINITION=HUMIL56KD Human interferon-inducible 56
 879_at M30818 /FEATURE=mRNA /DEFINITION=HUMMXB Human interferon-induced
20 cellular
 893_at M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier protein (E2
 894_g_at M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier
 protein (
 766_at AB006782 /FEATURE= /DEFINITION=AB006782 Homo sapiens mRNA for galectin-9
- 25** 776_at D13435 /FEATURE= /DEFINITION=HUMPIGF Human mRNA for PIG-F (phosphatidyl-i
 675_at J04164 /FEATURE= /DEFINITION=HUM927A Human interferon-inducible protein 9
 669_s_at L05072 /FEATURE=expanded_cds /DEFINITION=HUMIFNRF1A Homo sapiens
 interfe
 631_g_at L39874 /FEATURE=expanded_cds /DEFINITION=HUMDODDA Homo sapiens
30 deoxycyt
 626_s_at L78833 /FEATURE=cds#5 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7
 and vatI g
 464_s_at U72882 /FEATURE= /DEFINITION=HSU72882 Human interferon-induced
 leucine
- 35** 431_at X02530 /FEATURE=cds /DEFINITION=HSINFGER Human mRNA for gamma-interferon
 425_at X67325 /FEATURE=cds /DEFINITION=HSP27 H.sapiens p27 mRNA
 343_s_at D12485 /FEATURE=cds#1 /DEFINITION=HUMNPP Human mRNA for
 nucleotide pyro
 348_at D14678 /FEATURE= /DEFINITION=HUMMHCB Human mRNA for kinesin-related prote

324_f_at Transcription Factor Btf3b

291_s_at J04152 /FEATURE=mRNA /DEFINITION=HUMGA733A Human
gastrointestinal tumor

269_at L40387 /FEATURE=cds /DEFINITION=HUMTRIP14G Homo sapiens thyroid receptor

5 189_s_at U09937 /FEATURE=mRNA /DEFINITION=HSUROKR7 Human urokinase-type
plasmino

195_s_at U28014 /FEATURE= /DEFINITION=HSU28014 Human cysteine protease
(ICErel-I

176_at U37352 /FEATURE= /DEFINITION=HSU37352 Human protein phosphatase 2A B alph

10 1
6

Table 4: 216 genes related to top few metagenes in Recurrence analysis

	31410_at	Cluster Incl. AF023614:Homo sapiens transmembrane activator and CAML in
5	31426_at	Cluster Incl. U34806:Human G protein-coupled receptor (GPR15) gene, com
	31559_at	Cluster Incl. U26209:Human renal sodium/dicarboxylate cotransporter (NA
	31590_g_at	Cluster Incl. AL031983:dJ271M21.2 (hs6M1-12 (7 transmembrane receptor
	31594_at	Cluster Incl. Y16788:Homo sapiens hHa3-I gene, complete CDS /cds=(0,121
	31626_i_at	Cluster Incl. AF047485:Homo sapiens amine oxidase pseudogene mRNA, sp
10	31681_at	Cluster Incl. X57282:H.sapiens mRNA for soluble erythropoietin receptor
	31700_at	Cluster Incl. AF027957:Homo sapiens G protein-coupled receptor (GPR35)
	31745_at	Cluster Incl. AF007194:Homo sapiens mucin (MUC3) mRNA, partial cds /cds
	31930_f_at	Cluster Incl. X63096:H.sapiens mRNA for rhesus polypeptide (RhVIII) /
	31947_r_at	Cluster Incl. X74143:H.sapiens HBF-2 mRNA for transcription factor /c
15	31975_at	Cluster Incl. X55503:H.sapiens pseudogene for metallothionein and AG/CT
	31993_f_at	Cluster Incl. U80764:Human EST clone 122887 mariner transposon Hsmar1
	32000_g_at	Cluster Incl. AI344681:qp09h03.x1 Homo sapiens cDNA, 3 end /clone=IM
	32010_at	Cluster Incl. Z82180:Human DNA sequence from clone E81G9 on chromosome
	32407_f_at	Cluster Incl. U92818:Homo sapiens c33.28 unnamed HERV-H protein mRNA,
20	32498_at	Cluster Incl. L35318:Human rearranged metabotropic glutamate receptor t
	33016_at	Cluster Incl. AI052224:oz21a02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	33069_f_at	Cluster Incl. U06641:Human UDP glucuronosyltransferase mRNA, partial
	33080_s_at	Cluster Incl. AB007943:Homo sapiens mRNA for KIAA0474 protein, comple
	33670_at	Cluster Incl. X74439:H.sapiens mRNA for estrogen receptor gene 5flankin
25	33685_at	Cluster Incl. AC004755:Homo sapiens chromosome 19, fosmid 37502 /cds=(0
	34066_at	Cluster Incl. AJ012590:Homo sapiens mRNA for glucose 1-dehydrogenase /c
	34089_at	Cluster Incl. AB028953:Homo sapiens mRNA for KIAA1030 protein, partial
	34139_at	Cluster Incl. AL049651:Human DNA sequence from clone 753D10 on chromoso
	34166_at	Cluster Incl. S80071:hPROT=brain-specific L-proline transporter [human,
30	34167_s_at	Cluster Incl. AA984230:am82g03.s1 Homo sapiens cDNA, 3 end /clone=IM
	34558_at	Cluster Incl. U30185:Human orphan opioid receptor mRNA, complete cds /c
	34568_at	Cluster Incl. X82634:Homo sapiens mRNA for hair keratin acidic 3-II /cd
	34573_at	Cluster Incl. U14187:Human receptor tyrosine kinase ligand LERK-3 (EPLG
	35505_at	Cluster Incl. AI290660:qm12b10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35	35590_s_at	Cluster Incl. X81832:H.sapiens mRNA for glucose-dependant insulinotro
	36332_at	Cluster Incl. U40391:Human serotonin N-acetyltransferase gene, complete
	36375_at	Cluster Incl. X74614:H.sapiens ODF2 (allele 2) gene for outer dense fib
	36407_at	Cluster Incl. AL050220:Homo sapiens mRNA; cDNA DKFZp586J1923 (from clon

	36411_s_at	Cluster Incl. U29943:Human ELAV-like neuronal protein-2 Hel-N2 mRNA,
	32269_at	Cluster Incl. W26805:13a12 Homo sapiens cDNA /gb=W26805 /gi=1305889 /ug
	32877_i_at	Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-9542
	32878_f_at	Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-9542
5	32897_at	Cluster Incl. AJ237672:Homo sapiens mRNA for methylenetetrahydrofolate
	32915_at	Cluster Incl. AL109730:Homo sapiens mRNA full length insert cDNA clone
	32923_r_at	Cluster Incl. M58378:Human synapsin I (SYN1) gene /cds=(0,2117) /gb=M
	33470_at	Cluster Incl. AF052177:Homo sapiens clone 24510 mRNA sequence /cds=UNKN
	33521_at	Cluster Incl. M63962:Human gastric H,K-ATPase catalytic subunit gene, c
10	33568_at	Cluster Incl. U48861:Human beta 4 nicotinic acetylcholine receptor subu
	33967_at	Cluster Incl. M31525:Human MHC class II lymphocyte antigen (HLA-DNA) ge
	34005_at	Cluster Incl. X73079:Homo sapiens encoding Polymeric immunoglobulin rec
	34469_at	Cluster Incl. X84746:H.sapiens Histo-blood group AB0 gene, exon 1 /cds=
	34906_g_at	Cluster Incl. AA977136:oaq24f02.s1 Homo sapiens cDNA, 3 end /clone=IM
15	34963_at	Cluster Incl. AA557228:nl75c09.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	35492_at	Cluster Incl. AC004523:Homo sapiens chromosome 19, cosmid F22329 /cds=(
	35864_at	Cluster Incl. Y00970:Human mRNA for acrosin (EC 3.4.21.10) /cds=(16,128
	35910_f_at	Cluster Incl. AJ003147:Homo sapiens complete genomic sequence between
	35912_at	Cluster Incl. AJ010901:Homo sapiens MUC4 gene, 3 flanking region /cds=(
20	35950_at	Cluster Incl. U90841:Homo sapiens SSX4 (SSX4) mRNA, complete cds /cds=(
	35961_at	Cluster Incl. AL049390:Homo sapiens mRNA; cDNA DKFZp586O1318 (from
	clon	
	35963_at	Cluster Incl. AI201243:qf70f09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	36237_at	Cluster Incl. AB009698:Homo sapiens mRNA for hOAT1-2, complete cds /cds
25	36276_at	Cluster Incl. X67734:H.sapiens mRNA for transient axonal glycoprotein (
	36732_at	Cluster Incl. AI004207:ot94g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	36747_at	Cluster Incl. AF052172:Homo sapiens clone 24617 mRNA sequence /cds=UNKN
	37070_at	Cluster Incl. D14720:Homo sapiens gene for peripheral myelin protein ze
	37138_at	Cluster Incl. AB018352:Homo sapiens mRNA for KIAA0809 protein, partial
30	37415_at	Cluster Incl. AB018258:Homo sapiens mRNA for KIAA0715 protein, partial
	37429_g_at	Cluster Incl. AI140857:qa83c11.s1 Homo sapiens cDNA, 3 end /clone=IM
	37853_at	Cluster Incl. AI857458:wl57e02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	38157_at	Cluster Incl. AF059252:Homo sapiens clone 1 HLA class III protein Dom3z
	38530_at	Cluster Incl. W26021:18c10 Homo sapiens cDNA /gb=W26021 /gi=1306306 /ug
35	38550_at	Cluster Incl. AB021638:Homo sapiens X11L2 mRNA for X11-like protein 2,
	38558_at	Cluster Incl. M29273:Human myelin-associated glycoprotein (MAG) mRNA, c
	38599_s_at	Cluster Incl. AD001530:Homo sapiens XAP-5 mRNA, complete cds /cds=(75
	38607_at	Cluster Incl. AF027204:Homo sapiens putative tetraspan transmembrane pr

	38851_at	Cluster Incl. M63394:Human 3 nucleotide sequence mRNA /cds=UNKNOWN /gb=
	38897_at	Cluster Incl. AJ000730:Homo sapiens mRNA for cationic amino acid transp
	39290_f_at	Cluster Incl. W28257:44c1 Homo sapiens cDNA /gb=W28257 /gi=1308205 /u
5	39645_r_at	Cluster Incl. AF033105:Homo sapiens X-arrestin mRNA, complete cds /cd
	39657_at	Cluster Incl. X07695:Human mRNA for cytokeratin 4 C-terminal region /cd
	40295_at	Cluster Incl. AB009288:Homo sapiens mRNA for N-copine, complete cds /cd
	40299_at	Cluster Incl. AF091890:Homo sapiens G-protein coupled receptor RE2 mRNA
	40300_g_at	Cluster Incl. AF091890:Homo sapiens G-protein coupled receptor RE2 mR
10	40317_at	Cluster Incl. U57352:Human sodium channel 1 (hBNaC1) mRNA, complete cds
	40685_at	Cluster Incl. U10868:Human aldehyde dehydrogenase ALDH7 mRNA, complete
	41382_at	Cluster Incl. AJ000342:Homo sapiens mRNA for DMBT1 6 kb transcript vari
	31802_at	Cluster Incl. D86979:Human mRNA for KIAA0226 gene, complete cds /cds=(6
	31819_at	Cluster Incl. AI796281:wh49a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
15	31845_at	Cluster Incl. U32645:Human myeloid elf-1 like factor (MEF) mRNA, comple
	31861_at	Cluster Incl. L14754:Human DNA-binding protein (SMBP2) mRNA, complete c
	32029_at	Cluster Incl. AF017995:Homo sapiens 3-phosphoinositide dependent protei
	32100_r_at	Cluster Incl. U06088:Human N-acetylgalactosamine 6-sulphatase (GALNS)
	32699_s_at	Cluster Incl. X64116:H.sapiens PVR gene for poliovirus receptor (exon
20	32702_at	Cluster Incl. U04810:Human tastin mRNA, complete cds /cds=(110,2446) /g
	32710_at	Cluster Incl. X83127:H.sapiens mRNA for voltage gated potassium channel
	32734_at	Cluster Incl. L76703:Homo sapiens protein phosphatase 2A B56-epsilon (P
	33293_at	Cluster Incl. AB023167:Homo sapiens mRNA for KIAA0950 protein, partial
	33719_at	Cluster Incl. AF010242:AF010242 Homo sapiens cDNA /gb=AF010242 /gi=2612
25	33744_at	Cluster Incl. AL080150:Homo sapiens mRNA; cDNA DKFZp434D174 (from clone
	34261_at	Cluster Incl. D84307:Homo sapiens mRNA for phosphoethanolamine cytidily
	34708_at	Cluster Incl. D88587:Homo sapiens mRNA for Hakata antigen, complete cds
	35141_at	Cluster Incl. Z97029:Homo sapiens mRNA for ribonuclease H I large subun
30	35225_at	Cluster Incl. M91592:Human zinc-finger protein (ZNF76) gene, partial cd
	35626_at	Cluster Incl. U30894:Human N-sulphoglucosamine sulphohydrolase mRNA, co
	35685_at	Cluster Incl. Z14000:H.sapiens RING1 gene /cds=(75,1208) /gb=Z14000 /gi
	36011_at	Cluster Incl. AF035531:Homo sapiens syntaxin 10 mRNA, complete cds /cds
	36037_g_at	Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /c
35	36485_at	Cluster Incl. U85647:Homo sapiens small optic lobes homolog (SOLH) mRNA
	36520_at	Cluster Incl. AB014590:Homo sapiens mRNA for KIAA0690 protein, partial
	36567_at	Cluster Incl. W26700:11h4 Homo sapiens cDNA /gb=W26700 /gi=1305802 /ug=
	36847_r_at	Cluster Incl. AA121509:zk88c10.s1 Homo sapiens cDNA, 3 end /clone=IM
	36883_at	Cluster Incl. X14640:Human mRNA for keratin 13 /cds=(42,1418) /gb=X1464

	36907_at	Cluster Incl. M88468:Homo sapiens mevalonate kinase mRNA, complete cds
	37191_at	Cluster Incl. D87463:Human mRNA for KIAA0273 gene, complete cds /cds=(4
	37285_at	Cluster Incl. X60364:Human ALAS mRNA for 5-aminolevulinate synthase pre
	38309_r_at	Cluster Incl. AA805659:nz41b04.s1 Homo sapiens cDNA /clone=IMAGE-1290
5	38706_at	Cluster Incl. AA552140:ng48e07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	38707_r_at	Cluster Incl. S75174:E2F-4=transcription factor [human, Nalm6 and HeL
	38981_at	Cluster Incl. AA203354:zx58b07.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	39335_at	Cluster Incl. AI074025:oy66g12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39398_s_at	Cluster Incl. AB023205:Homo sapiens mRNA for KIAA0988 protein, comple
10	39412_at	Cluster Incl. U09825:Human acid finger protein mRNA, complete cds /cds=
	39418_at	Cluster Incl. AJ007398:Homo sapiens mRNA for PBK1 protein /cds=(5,1558)
	39689_at	Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	40164_at	Cluster Incl. X69550:H.sapiens mRNA for rho GDP-dissociation Inhibitor
	40868_at	Cluster Incl. AA442799:zv69b10.r1 Homo sapiens cDNA, 5 end /clone=IMAG
15	32162_r_at	Cluster Incl. AI817548:wk24e08.x1 Homo sapiens cDNA, 3 end /clone=IM
	32166_at	Cluster Incl. AB028950:Homo sapiens mRNA for KIAA1027 protein, partial
	32211_at	Cluster Incl. AB009398:Homo sapiens mRNA for 26S proteasome subunit p40
	32228_at	Cluster Incl. AB020706:Homo sapiens mRNA for KIAA0899 protein, partial
	32831_at	Cluster Incl. AA453183:zx46b09.r1 Homo sapiens cDNA, 5 end /clone=IMAG
20	33416_at	Cluster Incl. AI332820:qp96e06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	33449_at	Cluster Incl. AF054185:Homo sapiens proteasome subunit HSPC mRNA, compl
	34338_at	Cluster Incl. D49738:Human cytoskeleton associated protein (CG22) mRNA,
	34361_at	Cluster Incl. U33849:Human lymphoma proprotein convertase (LPC) mRNA, c
	34405_at	Cluster Incl. U47927:Human isopeptidase T (ISOT) mRNA, complete cds /cd
25	35338_at	Cluster Incl. X17094:Human fur mRNA for furin /cds=(216,2600) /gb=X1709
	36150_at	Cluster Incl. AB020649:Homo sapiens mRNA for KIAA0842 protein, partial
	36169_at	Cluster Incl. N47307:yy87a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	36586_at	Cluster Incl. U78521:Homo sapiens immunophilin homolog ARA9 mRNA, compl
	36615_at	Cluster Incl. M83751:Human arginine-rich protein (ARP) gene, complete c
30	37323_r_at	Cluster Incl. X82460:H.sapiens mRNA for 15-hydroxy prostaglandin dehy
	37746_r_at	Cluster Incl. U15131:Human p126 (ST5) mRNA, complete cds /cds=(114,35
	38027_at	Cluster Incl. X53742:H.sapiens mRNA for fibulin-1 B /cds=(10,1815) /gb=
	38043_at	Cluster Incl. X55448:H.sapiens G6PD gene for glucose-6-phosphate dehydr
	38048_at	Cluster Incl. D84110:Homo sapiens mRNA for RBP-MS/type 4, complete cds
35	38058_at	Cluster Incl. Z22865:H.sapiens dermatopontin mRNA, complete CDS /cds=(1
	38375_at	Cluster Incl. AF112219:Homo sapiens esterase D mRNA, complete cds /cds=
	38752_r_at	Cluster Incl. AA426364:zv61b06.s1 Homo sapiens cDNA, 3 end /clone=IM
	39451_i_at	Cluster Incl. AF050145:Homo sapiens iduronate-2-sulfatase (IDS) mRNA,
	39472_s_at	Cluster Incl. W25985:17e6 Homo sapiens cDNA /gb=W25985 /gi=1306252 /u

- 39473_r_at Cluster Incl. W29065:56g2 Homo sapiens cDNA /gb=W29065 /gi=1309094 /u
- 39474_s_at Cluster Incl. AF045800:Homo sapiens gremlin mRNA, complete cds /cds=(
- 39490_f_at Cluster Incl. W26381:29b11 Homo sapiens cDNA /gb=W26381 /gi=1307098 /
- 39838_at Cluster Incl. AB014522:Homo sapiens mRNA for KIAA0622 protein, partial
- 5 39846_at Cluster Incl. AF071748:Homo sapiens cathepsin F (CATSF) mRNA, complete
- 39868_at Cluster Incl. AL046394:DKFZp434M217_r1 Homo sapiens cDNA, 5 end /clone
- 39921_at Cluster Incl. AI526089:DU3.2-7.H07.r Homo sapiens cDNA, 5 end /clone_e
- 40565_at Cluster Incl. AI358867:qy24a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 40595_at Cluster Incl. AI345337:tb81g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 10 40622_r_at Cluster Incl. AL096740:Homo sapiens mRNA; cDNA DKFZp586K2123 (from cl
- 40886_at Cluster Incl. L41498:Homo sapiens longation factor 1-alpha 1 (PTI-1) mR
- 40888_f_at Cluster Incl. W28170:43a12 Homo sapiens cDNA /gb=W28170 /gi=1308118 /
- 40905_s_at Cluster Incl. AL050369:Homo sapiens mRNA; cDNA DKFZp566J153 (from clo
- 40923_at Cluster Incl. AA290994:zs45d07.r1 Homo sapiens cDNA, 5 end /clone=IMAG
- 15 41001_at Cluster Incl. AB023202:Homo sapiens mRNA for KIAA0985 protein, complete
- 41279_f_at Cluster Incl. AF007134:Homo sapiens clone 23565 unknown mRNA, partial
- 41351_at Cluster Incl. AA885106:am31h01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 41500_at Cluster Incl. AI761818:wi62g02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 41525_at Cluster Incl. N25429:yx76b02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
- 20 41584_at Cluster Incl. AF062529:Homo sapiens clone 486790 diphosphoinositol poly
- 41799_at Cluster Incl. W28595:48h8 Homo sapiens cDNA /gb=W28595 /gi=1308543 /ug=
- 41825_at Cluster Incl. W26652:34c6 Homo sapiens cDNA /gb=W26652 /gi=1307495 /ug=
- 41829_at Cluster Incl. AB018274:Homo sapiens mRNA for KIAA0731 protein, partial
- 32525_r_at Cluster Incl. W29012:55a6 Homo sapiens cDNA /gb=W29012 /gi=1308969 /u
- 25 32567_at Cluster Incl. D10704:Human mRNA for choline kinase /cds=(27,1397) /gb=D
- 33110_at Cluster Incl. AI356682:qy22a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 33178_at Cluster Incl. AF003837:Homo sapiens Jagged1 (JAG1) mRNA, complete cds /
- 33211_at Cluster Incl. AW051889:wz04f05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 2032_s_at U07375 /FEATURE=cds /DEFINITION=HSU07375 Human integrin alpha v gene;
- 30 2005_s_at U31317 /FEATURE= /DEFINITION=HSU31317 Human JAK family tyrosine
- protei
- 2013_at U35117 /FEATURE= /DEFINITION=HSU35117 Human transcription factor Dp-2 mR
- 1967_f_at U18334 /FEATURE=cds /DEFINITION=HSUNOSIIC1 Human nitric oxide
- synthase
- 35 1925_at Z36714 /FEATURE=mRNA /DEFINITION=HSCYCLF H.sapiens mRNA for cyclin F
- 1894_f_at Neurofibromatosis 2 Tumor Suppressor
- 1797_at U40343 /FEATURE= /DEFINITION=HSU40343 Human CDK inhibitor p19INK4d
- mRNA,
- 1804_at X07730 /FEATURE= /DEFINITION=HSPSA Human mRNA for prostate specific anti

- 1775_at L24559 /FEATURE= /DEFINITION=HUMDNSPOLA Homo sapiens DNA polymerase
alph
- 1663_at Retinoic Acid Receptor, Gamma 2
- 1627_at Tyrosine Kinase
- 5** 1552_i_at U22028 /FEATURE=expanded_cds /DEFINITION=HSU22028 Human
cytochrome P45
- 1561_at U27193 /FEATURE= /DEFINITION=HSU27193 Human protein-tyrosine phosphatase
- 1483_at L34059 /FEATURE= /DEFINITION=HUMCA4A Homo sapiens cadherin-4 mRNA, compl
- 1469_at U12779 /FEATURE= /DEFINITION=HSU12779 Human MAP kinase activated protein
- 10** 1432_s_at D16105 /FEATURE= /DEFINITION=HUMLTCLP2 Human mRNA for leukocyte
tyrosi
- 1415_at D26561 /FEATURE=cds#3 /DEFINITION=D26561 Homo sapiens cellular DNA conta
- 1376_at M36067 /FEATURE=mRNA /DEFINITION=HUMLIGAA Human DNA ligase I mRNA,
compl
- 15** 1353_g_at U11870 /FEATURE=mRNA /DEFINITION=HSU11870 Human interleukin-8
receptor
- 1256_at L38929 /FEATURE=mRNA /DEFINITION=HUMPTPD Homo sapiens protein tyrosine p
- 1259_at L76568 /FEATURE=exons#13-14 /DEFINITION=HUMERCC4G Homo sapiens excision
- 1177_at Dna-Binding Protein Ap-2, Alt. Splice 3
- 20** 1155_at J03069 /FEATURE=mRNA /DEFINITION=HUMMYCL2A Human MYCL2 gene,
complete cd
- 1122_f_at K03183 /FEATURE=cds /DEFINITION=HUMCGBBA3 Human chorionic
gonadotropin
- 1047_s_at U37055 /FEATURE=mRNA /DEFINITION=HSU37055 Human hepatocyte
- 25** growth fact
- 1008_f_at U50648 /FEATURE=mRNA /DEFINITION=HSIIPKR17 Human interferon-
inducible
- 882_at M37435 /FEATURE= /DEFINITION=HUMCSDF1 Human macrophage-specific colony-st
- 888_s_at M62302 /FEATURE=cds#1 /DEFINITION=HUMGDF1 Human
- 30** growth/differentiation
- 726_f_atChorionic Somatomammotropin Hormone Cs-5
- 729_i_atMucin 3, Intestinal
- 730_r_atMucin 3, Intestinal
- 731_f_atMucin 3, Intestinal
- 35** 678_at J04948 /FEATURE=mRNA /DEFINITION=HUMALP1GC Human alkaline phosphatase
(AL
- 534_s_at U20391 /FEATURE=mRNA#1 /DEFINITION=HSU20391 Human folate receptor
(FOLR
- 420_at X65633 /FEATURE=cds /DEFINITION=HSACTHR H.sapiens ACTH-R gene for adrenoc

385_at X71874 /FEATURE=cds#2 /DEFINITION=HSPROSCHY H.sapiens genes for proteasom

396_f_atX97671 /FEATURE=cds /DEFINITION=HSERYTHR H.sapiens mRNA for erythropoie

336_at D38081 /FEATURE= /DEFINITION=HUMHTAR Human mRNA for thromboxane A2
recept

5 240_at M64231 /FEATURE=mRNA /DEFINITION=HUMSPERSYN Human spermidine synthase
gen

121_at X69699 /FEATURE= /DEFINITION=HSPAX8A H.sapiens Pax8 mRNA

Table 5: 496 Metagenes Related to Breast Cancer Study

Metagene 1		
5	38573_at	Cluster Incl. U72209:Human YY1-associated factor 2 (YAF2) mRNA, complet
	38908_s_at	Cluster Incl. AL096744:Homo sapiens mRNA; cDNA DKFZp566H033 (from clo
	34288_at	Cluster Incl. U67784:Human orphan G protein-coupled receptor (RDC1) mRN
	34752_at	Cluster Incl. AL080111:Homo sapiens mRNA; cDNA DKFZp586G2222 (from
	clon	
10	34763_at	Cluster Incl. AF020043:Homo sapiens chromosome-associated polypeptide (
	34768_at	Cluster Incl. AL080080:Homo sapiens mRNA; cDNA DKFZp564E1962 (from
	clon	
	35656_at	Cluster Incl. AJ010346:Homo sapiens mRNA for RING-H2 protein RNF6, alte
	38993_r_at	Cluster Incl. W27522:32a12 Homo sapiens cDNA /gb=W27522 /gi=1307326 /
15	39019_at	Cluster Incl. D14696:Human mRNA for KIAA0108 gene, complete cds /cds=(1
	39354_at	Cluster Incl. D14662:Human mRNA for KIAA0106 gene, complete cds /cds=(4
	39381_at	Cluster Incl. AF055030:Homo sapiens clone 24538 mRNA sequence /cds=UNKN
	39389_at	Cluster Incl. M38690:Human CD9 antigen mRNA, complete cds /cds=(51,737)
	40128_at	Cluster Incl. D79993:Human mRNA for KIAA0171 gene, complete cds /cds=(1
20	40467_at	Cluster Incl. AB006202:Homo sapiens mRNA for cytochrome b small subunit
	40516_at	Cluster Incl. L19872:Human AH-receptor mRNA, complete cds /cds=(375,292
	40864_at	Cluster Incl. D25274:Homo sapiens mRNA, clone-PO2ST9 /cds=UNKNOWN
	/gb=D	
	33830_at	Cluster Incl. AW026535:vv14f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
25	34326_at	Cluster Incl. X82103:H.sapiens mRNA for beta-COP /cds=(0,911) /gb=X8210
	34387_at	Cluster Incl. D86960:Human mRNA for KIAA0205 gene, complete cds /cds=(2
	34392_s_at	Cluster Incl. AL050268:Homo sapiens mRNA; cDNA DKFZp564B163 (from clo
	34393_r_at	Cluster Incl. AL050268:Homo sapiens mRNA; cDNA DKFZp564B163 (from clo
	34774_at	Cluster Incl. U44772:Human palmitoyl protein thioesterase mRNA, complet
30	34781_at	Cluster Incl. D84145:Human WS-3 mRNA, complete cds /cds=(87,659) /gb=D8
	34879_at	Cluster Incl. AF007875:Homo sapiens dolichol monophosphate mannose synt
	34889_at	Cluster Incl. AA056747:zk81f02.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	35258_f_at	Cluster Incl. AF030234:Homo sapiens splicing factor Sip1 mRNA, comple
	35747_at	Cluster Incl. AF035287:Homo sapiens clone 23742 mRNA, partial cds /cds=
35	35790_at	Cluster Incl. AF054179:Homo sapiens H beta 58 homolog mRNA, complete cd
	35811_at	Cluster Incl. AF037204:Homo sapiens RING zinc finger protein (RZF) mRNA
	36107_at	Cluster Incl. AA845575:ak04e09.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	36585_at	Cluster Incl. M36341:Human ADP-ribosylation factor 4 (ARF4) mRNA, compl

	36614_at	Cluster Incl. X87949:H.sapiens mRNA for BiP protein /cds=(222,2183) /gb
	36631_at	Cluster Incl. D49396:Human mRNA for Apo1_Human (MER5(Aop1-Mouse)-like
	p	
	36981_at	Cluster Incl. AF070649:Homo sapiens clone 24452 mRNA sequence /cds=UNKN
5	37009_at	Cluster Incl. AL035079:dJ53C18.1 (Catalase) /cds=(74,1657) /gb=AL035079
	37010_at	Cluster Incl. AI203737:qf76b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	37035_at	Cluster Incl. AI557272:PT2.1_15_G02.r Homo sapiens cDNA, 3 end /clone_
	37296_at	Cluster Incl. L28997:Homo sapiens ARL1 mRNA, complete cds /cds=(144,689
	37358_at	Cluster Incl. AI039880:ox97c12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
10	37359_at	Cluster Incl. D14658:Human mRNA for KIAA0102 gene, complete cds /cds=(3
	37374_at	Cluster Incl. M82809:Human annexin IV (ANX4) mRNA, complete cds /cds=(7
	37392_at	Cluster Incl. X84908:H.sapiens mRNA for phosphorylase-kinase, beta subu
	38100_at	Cluster Incl. D87127:Homo sapiens mRNA for translocation protein-1, com
	38110_at	Cluster Incl. AF000652:Homo sapiens syntenin (sycl) mRNA, complete cds
15	38392_at	Cluster Incl. AF006088:Homo sapiens Arp2/3 protein complex subunit p16-
	38462_at	Cluster Incl. U64028:Human NADH-ubiquinone oxidoreductase subunit B13 m
	38738_at	Cluster Incl. X99584:H.sapiens mRNA for SMT3A protein /cds=(94,405) /gb
	40605_at	Cluster Incl. AA524345:ng43a06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	40988_at	Cluster Incl. AJ132637:Homo sapiens mRNA for ATP-dependent metalloprote
20	41598_at	Cluster Incl. AA890010:aj89h08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	32508_at	Cluster Incl. AL096857:Novel human mRNA from chromosome 1, which has si
	32597_at	Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488
	1874_at	D21090 /FEATURE= /DEFINITION=HUMHHR23B Human mRNA for XP-C repair
	comple	
25	1064_at	U02680 /FEATURE= /DEFINITION=HSU02680 Human protein tyrosine kinase mRNA
	924_s_at	J03805 /FEATURE= /DEFINITION=HUMALPHLB Human phosphatase 2A
	mRNA, parti	
	843_at	U48296 /FEATURE= /DEFINITION=HSU48296 Homo sapiens protein tyrosine phosp
	409_at	X56468 /FEATURE=mRNA /DEFINITION=HS1433 Human mRNA for 14.3.3 protein, a
30	Metagene 2	
	37161_at	Cluster Incl. W28948:54b12 Homo sapiens cDNA /gb=W28948 /gi=1308896 /ug
	38957_at	Cluster Incl. AB002367:Human mRNA for KIAA0369 gene, complete cds /cds=
35	31879_at	Cluster Incl. U69127:Human FUSE binding protein 3 (FBP3) mRNA, partial
	34657_at	Cluster Incl. AB014529:Homo sapiens mRNA for KIAA0629 protein, partial
	36827_at	Cluster Incl. AF020762:Homo sapiens clone 1400 unknown protein mRNA, pa
	37900_at	Cluster Incl. AF093670:Homo sapiens peroxisomal biogenesis factor (PEX1
	38649_at	Cluster Incl. AB023187:Homo sapiens mRNA for KIAA0970 protein, complete

	38667_at	Cluster Incl. AA189161:zq45g01.s1 Homo sapiens cDNA, 3' end /clone=IMAG
	38698_at	Cluster Incl. AL080070:Homo sapiens mRNA; cDNA DKFZp564M112 (from clone
	39741_at	Cluster Incl. D16481:Homo sapiens mRNA for mitochondrial 3-ketoacyl-CoA
5	39744_at	Cluster Incl. AF000982:Homo sapiens dead box, X isoform (DBX) mRNA, alt
	40779_at	Cluster Incl. U59919:Human Smg GDS-associated protein SMAP mRNA, comple
	40786_at	Cluster Incl. U37352:Human protein phosphatase 2A Balphal regulatory su
	41146_at	Cluster Incl. J03473:Human poly(ADP-ribose) synthetase mRNA, complete c
	33340_at	Cluster Incl. AB007898:Homo sapiens KIAA0438 mRNA, complete cds /cds=(1
10	33835_at	Cluster Incl. AB018264:Homo sapiens mRNA for KIAA0721 protein, partial
	33847_s_at	Cluster Incl. AI304854:qo19f03.x1 Homo sapiens cDNA, 3' end /clone=IM
	33899_at	Cluster Incl. U34252:Human gamma-aminobutyraldehyde dehydrogenase mRNA,
	34821_at	Cluster Incl. AL050197:Homo sapiens mRNA; cDNA DKFZp586D0623 (from clon
15	35325_at	Cluster Incl. AF052113:Homo sapiens clone 23675 mRNA sequence /cds=UNKN
	35754_at	Cluster Incl. L40391:Homo sapiens (clone s153) mRNA fragment /cds=UNKNO
	35762_at	Cluster Incl. AB007952:Homo sapiens mRNA for KIAA0483 protein, partial
	35793_at	Cluster Incl. AB014560:Homo sapiens mRNA for KIAA0660 protein, complete
	37718_at	Cluster Incl. D43636:Human mRNA for KIAA0096 gene, partial cds /cds=(0,
20	38035_at	Cluster Incl. AF072928:Homo sapiens myotubularin related protein 6 mRNA
	38050_at	Cluster Incl. D79986:Human mRNA for KIAA0164 gene, complete cds /cds=(2
	38075_at	Cluster Incl. X68194:H.sapiens h-Sp1 mRNA /cds=(33,812) /gb=X68194 /gi=
	38102_at	Cluster Incl. W28575:51f12 Homo sapiens cDNA /gb=W28575 /gi=1308730 /ug
	38409_at	Cluster Incl. M61199:Human cleavage signal 1 protein mRNA, complete cds
25	38837_at	Cluster Incl. W26226:22e3 Homo sapiens cDNA /gb=W26226 /gi=1306637 /ug=
	39809_at	Cluster Incl. AF019214:Homo sapiens HMG box containing protein 1 mRNA,
	40189_at	Cluster Incl. M93651:Human set gene, complete cds /cds=(3,836) /gb=M936
	1377_at	M58603 /FEATURE= /DEFINITION=HUMNFKB Human nuclear factor kappa-B DNA bi
	818_s_at	U72936 /FEATURE= /DEFINITION=HSU72936 Homo sapiens putative DNA
30	depende	
	176_at	U37352 /FEATURE= /DEFINITION=HSU37352 Human protein phosphatase 2A B alph
	Metagene 3	
35	38151_at	Cluster Incl. AF002672:Homo sapiens breast cancer suppressor candidate
	38945_at	Cluster Incl. X78710:H.sapiens MTF-1 mRNA for metal-regulatory transcri
	39295_s_at	Cluster Incl. AF049884:Homo sapiens Arg/Abl-interacting protein ArgBP
	41039_at	Cluster Incl. AL022476:dJ323M22.2.1 (novel protein similar to KIAA0173
	41640_at	Cluster Incl. AL031427:dJ167A19.1 (novel protein) /cds=(122,1042) /gb=A

	35673_at	Cluster Incl. U02082:Human guanine nucleotide regulatory protein (tim1)
	36900_at	Cluster Incl. U52426:Homo sapiens GOK (STIM1) mRNA, complete cds /cds=(
	37230_at	Cluster Incl. AB007938:Homo sapiens mRNA for KIAA0469 protein, complete
	38286_at	Cluster Incl. AB028994:Homo sapiens mRNA for KIAA1071 protein, partial
5	38685_at	Cluster Incl. AL035306:H.sapiens gene from PAC 426I6, similar to syntax
	38692_at	Cluster Incl. AF045451:Homo sapiens transcriptional regulatory protein
	38983_at	Cluster Incl. AI223047:qg70a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39001_at	Cluster Incl. AF047470:Homo sapiens malate dehydrogenase precursor (MDH
	40064_at	Cluster Incl. AB011121:Homo sapiens mRNA for KIAA0549 protein, partial
10	40133_s_at	Cluster Incl. W28944:54h12 Homo sapiens cDNA /gb=W28944 /gi=1308955 /
	40155_at	Cluster Incl. D31883:Human mRNA for KIAA0059 gene, complete cds /cds=(2
	40437_at	Cluster Incl. AL049944:Homo sapiens mRNA; cDNA DKFZp564G2022 (from
	clon	
	41775_at	Cluster Incl. AF064084:Homo sapiens prenylcysteine carboxyl methyltrans
15	32743_at	Cluster Incl. AB007922:Homo sapiens mRNA for KIAA0453 protein, partial
	33860_at	Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial
	33868_at	Cluster Incl. Z93241:dJ222E13.3.2 (PUTATIVE partial isoform 2) /cds=(0,
	34849_at	Cluster Incl. X91257:H.sapiens mRNA for seryl-tRNA synthetase /cds=(75,
	38421_at	Cluster Incl. AF070546:Homo sapiens clone 24607 mRNA sequence /cds=UNKN
20	39171_at	Cluster Incl. W21787:58b10 Homo sapiens cDNA /clone=(not-directional) /
	1386_at	M83738 /FEATURE= /DEFINITION=HUMPTPSA Human protein-tyrosine phosphatase
	Metagene 4	
25	39314_at	Cluster Incl. X77533:H.sapiens mRNA for activin type II receptor /cds=(
	31833_at	Cluster Incl. U78575:Human 68 kDa type I phosphatidylinositol-4-phospha
	34189_at	Cluster Incl. D31891:Human mRNA for KIAA0067 gene, complete cds /cds=(8
	37256_at	Cluster Incl. AI829890:wj47a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39053_at	Cluster Incl. AF016370:Homo sapiens U4/U6 small nuclear ribonucleoprote
30	40425_at	Cluster Incl. M57730:Human B61 mRNA, complete cds /cds=(73,690) /gb=M57
	1408_at	J02986 /FEATURE=exon#3 /DEFINITION=HUMHST Human transforming protein (hs
	Metagene 5	
35	41396_at	Cluster Incl. AB006629:Homo sapiens mRNA for KIAA0291 gene, partial cds
	32076_at	Cluster Incl. D83407:ZAKI-4 mRNA in human skin fibroblast, complete cds
	39327_at	Cluster Incl. D86983:Human mRNA for KIAA0230 gene, partial cds /cds=(0,
	36116_at	Cluster Incl. AJ000414:Homo sapiens mRNA for Cdc42-interacting protein
	32502_at	Cluster Incl. AL041124:DKFZp434D0316_s1 Homo sapiens cDNA, 3 end /clon

Metagene 6

- 38148_at Cluster Incl. D83702:Homo sapiens mRNA for photolyase, complete cds /cd
- 5 38204_at Cluster Incl. AB007866:Homo sapiens KIAA0406 mRNA, complete cds /cds=(1
- 36527_at Cluster Incl. AL050405:Novel human gene mapping to chomosome X /cds=(39
- 39745_at Cluster Incl. AB011139:Homo sapiens mRNA for KIAA0567 protein, partial
- 39771_at Cluster Incl. AB018283:Homo sapiens mRNA for KIAA0740 protein, complete
- 32160_at Cluster Incl. U76247:Human hSIAH1 mRNA, complete cds /cds=(186,1034) /g
- 10 36655_at Cluster Incl. L27476:Human X104 mRNA, complete cds /cds=(79,3429) /gb=L
- 37654_at Cluster Incl. D31764:Human mRNA for KIAA0064 gene, complete cds /cds=(2
- 38062_at Cluster Incl. D87467:Human mRNA for KIAA0277 gene, complete cds /cds=(5
- 32618_at Cluster Incl. X93086:H.sapiens mRNA for biliverdin IX alpha reductase /

15 Metagene 7

- 37826_at Cluster Incl. AF020761:Homo sapiens stimulator of Fe transport mRNA, co
- 38589_i_at Cluster Incl. M14630:Human prothymosin alpha mRNA, complete cds /cds=
- 39570_at Cluster Incl. W22289:65G5 Homo sapiens cDNA /clone=(not-directional) /g
- 20 32730_at Cluster Incl. AL080059:Homo sapiens mRNA; cDNA DKFZp564H142 (from
- clone
- 33759_at Cluster Incl. X04327:Human erythrocyte 2,3-bisphosphoglycerate mutase m
- 36088_at Cluster Incl. AJ006291:Homo sapiens mRNA for leucine rich protein /cds=
- 36857_at Cluster Incl. AF084513:Homo sapiens DNA repair exonuclease (REC1) mRNA,
- 25 37890_at Cluster Incl. X69398:H.sapiens mRNA for OA3 antigenic surface determina
- 38992_at Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=3
- 38999_s_at Cluster Incl. M86707:Homo sapiens myristoyl CoA-protein N-myristoyltr
- 39686_g_at Cluster Incl. AL050282:Homo sapiens mRNA; cDNA DKFZp586H2219 (from cl
- 39748_at Cluster Incl. AL050021:Homo sapiens mRNA; cDNA DKFZp564D016 (from
- 30 clone
- 39793_at Cluster Incl. AF029786:Homo sapiens GBAS (GBAS) mRNA, complete cds /cds
- 40490_at Cluster Incl. U41387:Human Gu protein mRNA, partial cds /cds=(0,2405) /
- 32214_at Cluster Incl. AF003938:Homo sapiens thioredoxin-like protein mRNA, comp
- 32850_at Cluster Incl. Z25535:H.sapiens mRNA for nuclear pore complex protein hn
- 35 33429_at Cluster Incl. AL050225:Homo sapiens mRNA; cDNA DKFZp586M1523 (from
- clon
- 34383_at Cluster Incl. AB014458:Homo sapiens hUBP mRNA for ubiquitin specific pr
- 34824_at Cluster Incl. AB015344:Homo sapiens HRIHFB2157 mRNA, partial cds /cds=(

	35750_at	Cluster Incl. AL049948:Homo sapiens mRNA; cDNA DKFZp564K0222 (from
	clon	
	35818_at	Cluster Incl. D00265:Homo sapiens mRNA for cytochrome c, partial cds /c
	36163_at	Cluster Incl. L13761:Human dihydrolipoamide dehydrogenase gene /cds=(20
5	36597_at	Cluster Incl. D21262:Human mRNA for KIAA0035 gene, partial cds /cds=(0,
	36604_at	Cluster Incl. D83004:Human epidermoid carcinoma mRNA for ubiquitin-conj
	36941_at	Cluster Incl. U16954:Human (AF1q) mRNA, complete cds /cds=(355,627) /gb
	37046_at	Cluster Incl. AI246726:qk40a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	37304_at	Cluster Incl. U35451:Homo sapiens heterochromatin protein p25 mRNA, com
10	37373_at	Cluster Incl. U27460:Human uridine diphosphoglucose pyrophosphorylase m
	37740_r_at	Cluster Incl. J02683:Human ADP/ATP carrier protein mRNA, complete cds
	38010_at	Cluster Incl. AF002697:Homo sapiens E1B 19K/Bcl-2-binding protein Nip3
	38036_at	Cluster Incl. L35035:Homo sapiens ribose 5-phosphate isomerase (RPI) mR
	38040_at	Cluster Incl. AF107463:Homo sapiens splicing factor mRNA, complete cds
15	38084_at	Cluster Incl. AA648295:ns20e08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	38123_at	Cluster Incl. D14878:Human mRNA for protein D123, complete cds /cds=(28
	38846_at	Cluster Incl. AA768912:nz82h06.s1 Homo sapiens cDNA /clone=IMAGE-130201
	39086_g_at	Cluster Incl. AA768912:nz82h06.s1 Homo sapiens cDNA /clone=IMAGE-1302
	40258_at	Cluster Incl. M55265:Human casein kinase II alpha subunit mRNA, complet
20	40610_at	Cluster Incl. AI743507:wf72a06.x2 Homo sapiens cDNA, 3 end /clone=IMAG
	40982_at	Cluster Incl. AA926957:om68h06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	41342_at	Cluster Incl. D38076:Human mRNA for RanBP1 (Ran-binding protein 1), com
	41490_at	Cluster Incl. Y00971:Human mRNA for phosphoribosyl pyrophosphate synth
	41579_s_at	Cluster Incl. AI952267:wx50d11.x1 Homo sapiens cDNA, 3 end /clone=IM
25	674_g_at	J04031 /FEATURE= /DEFINITION=HUMMDMCSF Human
	methylenetetrahydrofolate	
	652_g_at	L07493 /FEATURE= /DEFINITION=HUM14RPA Homo sapiens replication
	protein	
	171_at	U56833 /FEATURE= /DEFINITION=HSU56833 Human VHL binding protein-1 (VBP-1)
30	140_s_at	U68063 /FEATURE= /DEFINITION=HSU68063 Human transformer-2 beta (htra-
	2	
	Metagene 8	
35	31685_at	Cluster Incl. Y08976:H.sapiens mRNA for FEV protein /cds=(584,1300) /gb
	32998_at	Cluster Incl. L19315:Human cholecystokinin A receptor mRNA, complete cd
	33947_at	Cluster Incl. U18550:Human GPR3 G protein-coupled receptor gene, comple
	36328_at	Cluster Incl. M31651:Homo sapiens sex hormone-binding globulin (SHBG) g
	36737_at	Cluster Incl. U59057:Human beta-A4 crystallin (CRYBA4) mRNA, complete c

- 32104_i_at Cluster Incl. U66063:Homo sapiens calcium/calmodulin-dependent protei
 1254_at L36861 /FEATURE=expanded_cds /DEFINITION=HUMGCAPB Homo sapiens guanylate
 1170_at Colony-Stimulating Factor 1, Macrophage, Alt. Splice 3
- 5** Metagene 9
- 37117_at Cluster Incl. Z83838:Human DNA sequence from PAC 127B20 on chromosome 2
 36475_at Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosome
 41758_at Cluster Incl. AL096879:Novel human mRNA similar to C. elegans gene WP-C
10 34299_at Cluster Incl. AL096880:Novel human mRNA containing Zinc finger C2H2 typ
 34300_at Cluster Incl. AI352450:qt16g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40925_at Cluster Incl. AA554945:ni36d11.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 895_at L19686 /FEATURE=mRNA /DEFINITION=HUMMIF Homo sapiens macrophage
 migration
- 15** Metagene 10
- 36403_s_at Cluster Incl. AI434146:ti36g07.x1 Homo sapiens cDNA, 3 end /clone=IM
 34442_at Cluster Incl. U72943:U72943 Homo sapiens cDNA /gb=U72943 /gi=5763294 /u
20 36997_at Cluster Incl. J04809:Human cytosolic adenylate kinase (AK1) gene, compl
 39190_s_at Cluster Incl. AC002126:Homo sapiens DNA from chromosome 19-cosmids R3
 41537_r_at Cluster Incl. L31881:Human nuclear factor I-X mRNA, complete cds /cds
 33197_at Cluster Incl. U39226:Human myosin VIIA (USH1B) mRNA, complete cds /cds=
 1445_at AF014958 /FEATURE= /DEFINITION=AF014958 Homo sapiens chemokine receptor
25 1280_i_at Serine/Threonine Kinase
- Metagene 11
- 39943_at Cluster Incl. U27459:Human origin recognition complex protein 2 homolog
30 33245_at Cluster Incl. AF004709:Homo sapiens stress-activated protein kinase 4 m
 37569_at Cluster Incl. AF035606:Homo sapiens calcium binding protein (ALG-2) mRN
 38980_at Cluster Incl. AB018276:Homo sapiens mRNA for KIAA0733 protein, partial
 36176_at Cluster Incl. U61234:Human tubulin-folding cofactor C mRNA, complete cd
 41569_at Cluster Incl. AI680675:tx40a08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 35** Metagene 12
- 31525_s_at Cluster Incl. J00153:Human alpha globin gene cluster on chromosome 16
 31687_f_at Cluster Incl. M25079:Human sickle cell beta-globin mRNA, complete cds

- 35606_at Cluster Incl. D16583:Human gene for L-histidine decarboxylase, complete
 36749_at Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /
 36780_at Cluster Incl. M25915:Human complement cytolysis inhibitor (CLI) mRNA, c
 32052_at Cluster Incl. L48215:Homo sapiens beta-globin (HBB) gene, with a to c a
 5 36535_at Cluster Incl. U04209:Human associated microfibrillar protein mRNA, comp
 40084_at Cluster Incl. U03494:Human transcription factor LSF mRNA, complete cds
 35783_at Cluster Incl. H93123:yv05g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 37003_at Cluster Incl. X62654:H.sapiens gene for Me491/CD63 antigen /cds=(69,785
 38458_at Cluster Incl. L39945:Human cytochrome b5 (CYB5) gene /cds=(120,548) /gb
 10 2031_s_at U03106 /FEATURE= /DEFINITION=HSU03106 Human wild-type p53 activated
 fr
 529_at U15932 /FEATURE= /DEFINITION=HSU15932 Human dual-specificity protein phos
- Metagene 13
- 15 37965_at Cluster Incl. AA181053:zp66g11.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 36675_r_at Cluster Incl. J03191:Human profilin mRNA, complete cds /cds=(127,549)
 38122_at Cluster Incl. D87075:Human mRNA for KIAA0238 gene, partial cds /cds=(0,
 41288_at Cluster Incl. AL036744:DKFZp564I1663_r1 Homo sapiens cDNA, 5 end /clon
 20 1830_s_at M38449 /FEATURE= /DEFINITION=HUMTGFBA Human transforming growth
 factor
 883_s_at M54915 /FEATURE= /DEFINITION=HUMPIM1LE Human h-pim-1 protein (h-
 pim-1)
- 25 Metagene 14
- 32021_at Cluster Incl. AI560890:tq41d05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 36224_g_at Cluster Incl. AI827895:wf12b02.x1 Homo sapiens cDNA, 3 end /clone=IM
 39323_at Cluster Incl. U45974:Human phosphatidylinositol (4,5) bisphosphate 5-ph
 30 32731_at Cluster Incl. AB018247:Homo sapiens mRNA for Fe65L2, complete cds /cds=
 33698_at Cluster Incl. AB028975:Homo sapiens mRNA for KIAA1052 protein, complete
 37964_at Cluster Incl. W25793:13e7 Homo sapiens cDNA /gb=W25793 /gi=1305934 /ug=
 40050_at Cluster Incl. AF069747:Homo sapiens MTG8-like protein MTGR1a mRNA, comp
 40837_at Cluster Incl. M99436:Human transducin-like enhancer protein (TLE2) mRNA
 35 32751_at Cluster Incl. AF007140:Homo sapiens clone 23711 unknown mRNA, partial c
 36129_at Cluster Incl. AB007857:Homo sapiens KIAA0397 mRNA, complete cds /cds=(5
 36137_at Cluster Incl. X86691:H.sapiens mRNA for 218kD Mi-2 protein /cds=(89,582
 40219_at Cluster Incl. AI796944:we25b03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32591_at Cluster Incl. AI494623:qz17b06.x1 Homo sapiens cDNA, 3 end /clone=IMAG

Metagene 15

- 33620_at Cluster Incl. X16667:Human HOX2G mRNA from the Hox2 locus /cds=(363,165)
- 5** 32355_at Cluster Incl. AL050270:Homo sapiens mRNA; cDNA DKFZp564D166 (from clone
- 33723_at Cluster Incl. AL049346:Homo sapiens mRNA; cDNA DKFZp566B213 (from clone
- 37633_s_at Cluster Incl. J04129:Human placental protein 14 (PP14) mRNA, complete
- 10** 39418_at Cluster Incl. AJ007398:Homo sapiens mRNA for PBK1 protein /cds=(5,1558)
- 34779_at Cluster Incl. R90942:yp92b03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-

Metagene 16

- 15** 31481_s_at Cluster Incl. M92383:Homo sapiens thymosin beta-10 gene, 3end /cds=(0
- 37152_at Cluster Incl. L07592:Human peroxisome proliferator activated receptor m
- 37157_at Cluster Incl. X56667:Human mRNA for calretinin /cds=(43,858) /gb=X56667
- 38233_at Cluster Incl. AF093265:Homo sapiens homer-3 mRNA, complete cds /cds=(90
- 38515_at Cluster Incl. X51801:Human OP-1 mRNA for osteogenic protein /cds=(122,1
- 20** 38869_at Cluster Incl. AB028992:Homo sapiens mRNA for KIAA1069 protein, partial
- 39929_at Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial
- 40030_at Cluster Incl. Y15801:Homo sapiens mRNA for PRKY protein /cds=UNKNOWN
- /g
- 31863_at Cluster Incl. D80001:Human mRNA for KIAA0179 gene, partial cds /cds=(0,
- 25** 33764_at Cluster Incl. AF056085:Homo sapiens GABA-B receptor mRNA, complete cds
- 35694_at Cluster Incl. AB014587:Homo sapiens mRNA for KIAA0687 protein, partial
- 36014_at Cluster Incl. AL033377:Human DNA sequence from clone 287G14 on chromoso
- 37966_at Cluster Incl. AA187563:zp66g11.r1 Homo sapiens cDNA, 5 end /clone=IMAG
- 38003_s_at Cluster Incl. U94905:Human diacylglycerol kinase zeta mRNA, alternati
- 30** 32186_at Cluster Incl. M80244:Human E16 mRNA, complete cds /cds=(310,1035) /gb=M
- 33380_at Cluster Incl. AB005754:Homo sapiens mRNA for LAK-1, complete cds /cds=(
- 33394_at Cluster Incl. AA034074:zi06c05.r1 Homo sapiens cDNA, 5 end /clone=IMAG
- 35304_at Cluster Incl. AF052130:Homo sapiens clone 23704 mRNA sequence /cds=UNKN
- 36175_s_at Cluster Incl. AL023584:Human DNA sequence from clone 67K17 on chromos
- 35** 36581_at Cluster Incl. U09510:Human glycyl-tRNA synthetase mRNA, complete cds /c
- 37737_at Cluster Incl. D25547:Homo sapiens mRNA for PIMT isozyme I, complete cds
- 39827_at Cluster Incl. AA522530:ni38d12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 738_at D38524 /FEATURE= /DEFINITION=HUM5N Human mRNA for 5'-nucleotidase

Metagene 17

- 35403_at Cluster Incl. AB029017:Homo sapiens mRNA for KIAA1094 protein, complete
 35408_i_at Cluster Incl. X16281:Human mRNA for zinc finger protein (clone 431) /
5 37146_at Cluster Incl. AB007864:Homo sapiens KIAA0404 mRNA, partial cds /cds=(0,
 33314_at Cluster Incl. U69141:Human glutaryl-CoA dehydrogenase mRNA, complete cd
 34291_at Cluster Incl. U07424:Human putative tRNA synthetase-like protein mRNA,
 39729_at Cluster Incl. L19185:Human natural killer cell enhancing factor (NKEFB)
 41197_at Cluster Incl. D21235:Human mRNA for HHR23A protein, complete cds /cds=(
10 35322_at Cluster Incl. D50922:Human mRNA for KIAA0132 gene, complete cds /cds=(1
 37721_at Cluster Incl. U79262:Human deoxyhypusine synthase mRNA, complete cds /c
 37722_s_at Cluster Incl. U26266:Human deoxyhypusine synthase mRNA, complete cds
 1751_g_at AD000092 /FEATURE=cds#5 /DEFINITION=CH19HHR23 Homo sapiens DNA
 from ch

15

Metagene 18

- 38881_i_at Cluster Incl. AF096870:Homò sapiens estrogen-responsive B box protein
 31812_at Cluster Incl. M24470:Human glucose-6-phosphate dehydrogenase, complete
20 34217_at Cluster Incl. AB015132:Homo sapiens UKLF mRNA for ubiquitous Kruppel li

Metagene 19

- 35381_at Cluster Incl. AL080127:Homo sapiens mRNA; cDNA DKFZp434C013 (from
25 clone
 38922_at Cluster Incl. AF097738:Homo sapiens non-receptor tyrosine kinase (TNK1)
 32724_at Cluster Incl. AF023462:Homo sapiens peroxisomal phytanoyl-CoA alpha-hyd
 33326_at Cluster Incl. D42087:Human mRNA for KIAA0118 gene, partial cds /cds=(0,
 37214_g_at Cluster Incl. X90392:H.sapiens mRNA for DNase X gene /cds=(794,1702)
30 39022_at Cluster Incl. AL050110:Homo sapiens mRNA; cDNA DKFZp586J0619 (from clon
 37764_at Cluster Incl. D87328:Homo sapiens mRNA for HCS, complete cds /cds=(1231
 38836_at Cluster Incl. AL008583:dJ327J16.2 (human ortholog of rat Neuronal Pentr
 40527_at Cluster Incl. AF000571:Homo sapiens kidney and cardiac voltage dependen
 41349_at Cluster Incl. L43964:Homo sapiens (clone F-T03796) STM-2 mRNA, complete
35 1324_at U53174 /FEATURE= /DEFINITION=HSU53174 Human cell cycle checkpoint contro

Metagene 20

- 32880_at Cluster Incl. AW015055:UI-H-BI0-aal-c-01-0-UI.s1 Homo sapiens cDNA, 3

36329_at Cluster Incl. U33147:Human mammaglobin mRNA, complete cds /cds=(60,341)
 41066_at Cluster Incl. AF071219:Homo sapiens mammaglobin B precursor, mRNA, comp
 38348_at Cluster Incl. X95190:H.sapiens mRNA for Branched chain Acyl-CoA Oxidase

5 Metagene 21

31598_s_at Cluster Incl. L41668:Homo sapiens UDP-galactose-4-epimerase (GALE) mR
 32047_at Cluster Incl. U91985:Human DNA fragmentation factor-45 mRNA, complete c
 37927_at Cluster Incl. X12654:Human mRNA for cell cycle gene RCC1 /cds=(182,1447
 10 41249_at Cluster Incl. AL031282:dJ283E3.6.1 (PUTATIVE novel protein similar to m
 1196_at D00591 /FEATURE=exons#7-14 /DEFINITION=HUMRCC1 Homo sapiens RCC1 gene, e

Metagene 22

15 33974_at Cluster Incl. Y07847:H.sapiens mRNA for RRP22 protein /cds=(321,932) /g
 34989_at Cluster Incl. U09414:Human zinc finger protein ZNF137 mRNA, complete cd
 35484_at Cluster Incl. U95737:Human Chromosome 16 BAC clone CIT987SK-A-388D4 /cd
 36238_at Cluster Incl. Y11284:Homo sapiens AFX1 gene, exon 1 (and joined CDS) /c
 38864_at Cluster Incl. W26851:17b12 Homo sapiens cDNA /gb=W26851 /gi=1306214 /ug
 20 38956_at Cluster Incl. AF052111:Homo sapiens clone 23953 mRNA sequence /cds=UNKN
 39580_at Cluster Incl. AB014549:Homo sapiens mRNA for KIAA0649 protein, complete
 41113_at Cluster Incl. AI871396:wl81f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41464_at Cluster Incl. AB002337:Human mRNA for KIAA0339 gene, complete cds /cds=
 34661_at Cluster Incl. AB002348:Human mRNA for KIAA0350 gene, partial cds /cds=(
 25 35138_at Cluster Incl. Y11997:H.sapiens mRNA for A-kinase anchoring protein AKAP
 38253_at Cluster Incl. U84011:Human glycogen debranching enzyme isoform 6 (AGL)
 40826_at Cluster Incl. M80359:Human protein p78 mRNA, complete cds /cds=(171,231
 1188_g_at X84740 /FEATURE=mRNA /DEFINITION=HSDNALIG3 H.sapiens mRNA for
 DNA liga

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Metagene 23

35467_g_at Cluster Incl. W73046:zd54h09.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 35468_at Cluster Incl. AL050381:Homo sapiens mRNA; cDNA DKFZp586B2023 (from
 35 clon
 39989_at Cluster Incl. X90530:H.sapiens mRNA for ragB protein /cds=(442,1566) /g
 32130_at Cluster Incl. W25984:17e5 Homo sapiens cDNA /gb=W25984 /gi=1306251 /ug=
 33745_at Cluster Incl. M31606:Human phosphorylase kinase (PSK-C3) mRNA, complete
 34726_at Cluster Incl. U07139:Human voltage-gated calcium channel beta subunit m

	35621_at	Cluster Incl. L77213:Homo sapiens phosphomevalonate kinase mRNA, comple
	36516_at	Cluster Incl. AL080143:Homo sapiens mRNA; cDNA DKFZp434N043 (from
	clone	
	36529_at	Cluster Incl. AI885381:wl93b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
5	36828_at	Cluster Incl. AB002324:Human mRNA for KIAA0326 gene, partial cds /cds=(
	38251_at	Cluster Incl. AI127424:qb75b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	38332_at	Cluster Incl. U83993:Human P2X4 purinoreceptor mRNA, complete cds /cds=
	38697_at	Cluster Incl. AL050274:Homo sapiens mRNA; cDNA DKFZp566C243 (from
	clone	
10	39712_at	Cluster Incl. AI541308:pec1.2-4.F11.r Homo sapiens cDNA, 5 end /clone_
	40127_at	Cluster Incl. M95929:Human homeobox protein (PHOX1) mRNA, 3 end /cds=(
	40405_at	Cluster Incl. X70991:H.sapiens MADER mRNA /cds=(0,1427) /gb=X70991 /gi=
	34376_at	Cluster Incl. AB019517:Homo sapiens PKIG mRNA for protein kinase inhibi
	36113_s_at	Cluster Incl. AJ011712:Homo sapiens TNNT1 gene, exons 1-11 (and joine
15	37704_at	Cluster Incl. Z14093:H.sapiens mRNA for branched chain decarboxylase al
	39115_at	Cluster Incl. AL050275:Homo sapiens mRNA; cDNA DKFZp566D213 (from
	clone	
	885_g_at	M59911 /FEATURE= /DEFINITION=HUMINTA3A Human integrin alpha-3
	chain mRN	
20		
	Metagene 24	
	40674_s_at	Cluster Incl. S82986:HOXC6=homeodomain-containing protein {clone 211}
	41867_at	Cluster Incl. AF055009:Homo sapiens clone 24747 mRNA sequence /cds=UNKN
25	37578_at	Cluster Incl. D25248:Homo sapiens mRNA, clone-RES4-4 /cds=UNKNOWN
	/gb=D	
	33402_at	Cluster Incl. AL035081:H.sapiens mRNA similar to Xenopus laevis mRNA fo
	36192_at	Cluster Incl. D83777:Human mRNA for KIAA0193 gene, complete cds /cds=(3
	1092_at	M65199 /FEATURE= /DEFINITION=HUMET2A Human endothelin 2 (ET2) mRNA,
30	comp	
	553_g_at	U02570 /FEATURE= /DEFINITION=HSU02570 Human CDC42 GTPase-
	activating pro	
	Metagene 25	
35		
	36782_s_at	Cluster Incl. J03242:Human insulin-like growth factor II mRNA, complet
	38950_r_at	Cluster Incl. AJ005256:Homo sapiens mRNA for MMP-23 /cds=(38,1210) /g
	41478_at	Cluster Incl. AL033538:Human DNA sequence from clone 477H23 on chromoso
	32057_at	Cluster Incl. U32907:Human p37NB mRNA, complete cds /cds=(281,1222) /gb

	32728_at	Cluster Incl. X81438:H.sapiens mRNA for amphiphysin /cds=(74,2161) /gb=
	33240_at	Cluster Incl. AB029018:Homo sapiens mRNA for KIAA1095 protein, partial
	33767_at	Cluster Incl. X15306:H.sapiens NF-H gene, exon 1 (and joined CDS) /cds=
	34730_g_at	Cluster Incl. AB029037:Homo sapiens mRNA for KIAA1114 protein, comple
5	35168_f_at	Cluster Incl. M92642:Homo sapiens alpha-1 type XVI collagen (COL16A1)
	36073_at	Cluster Incl. U35139:Human NECDIN related protein mRNA, complete cds /c
	37951_at	Cluster Incl. AF035119:Homo sapiens deleted in liver cancer-1 (DLC-1) m
	38652_at	Cluster Incl. AF070644:Homo sapiens clone 24742 mRNA sequence /cds=UNKN
	39031_at	Cluster Incl. AA152406:zo07f01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
10	33387_at	Cluster Incl. AB007854:Homo sapiens KIAA0394 mRNA, complete cds /cds=(1
	34303_at	Cluster Incl. AL049949:Homo sapiens mRNA; cDNA DKFZp564L0822 (from clon
	39528_at	Cluster Incl. L24564:Human Rad mRNA, complete cds /cds=(123,1049) /gb=L
	32526_at	Cluster Incl. AA149644:zl39d08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
15	1767_s_at	X14885 /FEATURE=mRNA /DEFINITION=HSTGF31 H.sapiens gene for transfomi
	1664_at	Insulin-Like Growth Factor 2
	1099_s_at	L38503 /FEATURE= /DEFINITION=HUMGSTT2A Homo sapiens glutathione S- tran
20	994_at	X58288 /FEATURE=mRNA /DEFINITION=HSHRPTPU H.sapiens hR-PTPu gene for prot
	995_g_at	X58288 /FEATURE=mRNA /DEFINITION=HSHRPTPU H.sapiens hR-PTPu gene for pr
	Metagene 26	
25		
	35374_at	Cluster Incl. AB007914:Homo sapiens mRNA for KIAA0445 protein, complete
	38516_at	Cluster Incl. L10338:Human sodium channel beta-1 subunit (SCN1B) mRNA,
	39968_at	Cluster Incl. U50136:Human leukotriene C4 synthase (LTC4S) gene, comple
	41018_at	Cluster Incl. AL050015:Homo sapiens mRNA; cDNA DKFZp564O243 (from clone
30		
	41418_at	Cluster Incl. AB020628:Homo sapiens mRNA for KIAA0821 protein, complete
	35169_at	Cluster Incl. AI982638:wt53c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35675_at	Cluster Incl. AF037261:Homo sapiens SH3-containing adaptor molecule-1 m
	37201_at	Cluster Incl. D38535:Human mRNA for PK-120 /cds=(129,2921) /gb=D38535 /
35	38294_at	Cluster Incl. X17360:Human HOX 5.1 gene for HOX 5.1 protein /cds=(1243,
	38621_at	Cluster Incl. AJ012008:Homo sapiens genes encoding RNCC protein, DDAH p
	33822_at	Cluster Incl. Z11584:H.sapiens mRNA for NuMA protein /cds=(258,6563) /g
	35358_at	Cluster Incl. AB028998:Homo sapiens mRNA for KIAA1075 protein, partial
	38109_at	Cluster Incl. AF020544:Homo sapiens inactive palmitoyl-protein thioeste

	38812_at	Cluster Incl. X79683:H.sapiens LAMB2 mRNA for beta2 laminin /cds=(165,5
	39130_at	Cluster Incl. AB018313:Homo sapiens mRNA for KIAA0770 protein, partial
	39164_at	Cluster Incl. AF099149:Homo sapiens TRIAD1 type I mRNA, complete cds /c
	40165_at	Cluster Incl. AB015345:Homo sapiens HRIHFB2216 mRNA, partial cds /cds=(
5	33137_at	Cluster Incl. Y13622:Homo sapiens mRNA for latent transforming growth f
	33155_at	Cluster Incl. M95740:Human alpha-L-iduronidase gene /cds=(0,1961) /gb=M
	444_g_at	X17360 /FEATURE=mRNA /DEFINITION=HSHOX51 Human HOX 5.1 gene for
	HOX 5.1	
	387_at	X80230 /FEATURE=mRNA /DEFINITION=HSSTPKC2K H.sapiens mRNA (clone C-2k)
10	mR	
	329_s_at	Nuclear Mitotic Apparatus Protein 1, Alt. Splice Form 2
	162_at	U44839 /FEATURE= /DEFINITION=HSU44839 Human putative ubiquitin C-terminal
	Metagene 27	
15		
	40390_at	Cluster Incl. J05037:Human serine dehydratase mRNA, complete cds /cds=(
	40817_at	Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /c
	41169_at	Cluster Incl. X74039:H.sapiens mRNA for urokinase plasminogen activator
	39105_at	Cluster Incl. Z46389:Homo sapiens encoding vasodilator-stimulated phosph
20	33212_at	Cluster Incl. AF006751:Homo sapiens ES/130 mRNA, complete cds /cds=(70,
	33213_g_at	Cluster Incl. AF006751:Homo sapiens ES/130 mRNA, complete cds /cds=(7
	1375_s_at	M32304 /FEATURE= /DEFINITION=HUMMET Human metalloproteinase
	inhibitor	
25	Metagene 28	
	35038_at	Cluster Incl. Y10129:H.sapiens mybpc3 gene /cds=(33,3857) /gb=Y10129 /g
	32332_at	Cluster Incl. X69433:H.sapiens mRNA for mitochondrial isocitrate dehydr
	32893_s_at	Cluster Incl. M30474:Human kidney gamma-glutamyl transpeptidase type
30	37133_at	Cluster Incl. AF027406:Homo sapiens muscle-specific serine kinase 1 (MS
	38217_at	Cluster Incl. U97698:Homo sapiens secretory mucin MUC6 (MUC6) mRNA, par
	40042_r_at	Cluster Incl. U82381:Human proline dehydrogenase/proline oxidase (PRO
	40684_at	Cluster Incl. U78190:Human GTP cyclohydrolase I feedback regulatory pro
	41706_at	Cluster Incl. AJ130733:Homo sapiens mRNA 2-methylacyl-CoA racemase /cds
35	41868_at	Cluster Incl. J04131:Human gamma-glutamyl transpeptidase (GGT) protein
	35628_at	Cluster Incl. AF023676:Homo sapiens lamin B receptor homolog TM7SF2 (TM
	37591_at	Cluster Incl. U94592:Human uncoupling protein homolog (UCPH) mRNA, comp
	37956_at	Cluster Incl. U37519:Human aldehyde dehydrogenase (ALDH8) mRNA, complet
	41776_at	Cluster Incl. U70660:Human copper transport protein HAH1 (HAH1) mRNA, c

- 33366_at Cluster Incl. AL022238:dJ1042K10.2.1 (novel protein with probable rabGA
 37017_at Cluster Incl. M22430:Human RASF-A PLA2 mRNA, complete cds /cds=(135,569
 38780_at Cluster Incl. J04794:Human aldehyde reductase mRNA, complete cds /cds=(
 33141_at Cluster Incl. M84472:Human 17-beta-hydroxysteroid dehydrogenase (EDH17B
5 1291_s_at L03840 /FEATURE= /DEFINITION=HUMFGFR4X Human fibroblast growth
 factor
 715_s_at D87002 /FEATURE=cds#4 /DEFINITION=D87002 Homo sapiens
 immunoglobulin la

10 Metagene 29

- 34969_s_at Cluster Incl. AL096750:Homo sapiens mRNA; cDNA DKFZp434H244 (from clo
 31816_at Cluster Incl. X55079:Human lysosomal alpha-glucosidase gene exon 1 /cds
 34689_at Cluster Incl. AJ243797:Homo sapiens mRNA for deoxyribonuclease III (dm
15 37904_s_at Cluster Incl. X66436:H.sapiens hsr1 mRNA (partial) /cds=UNKNOWN /gb=X
 38647_at Cluster Incl. AJ131182:Homo sapiens mRNA for Epsilon COP /cds=(42,968)
 35763_at Cluster Incl. AB011112:Homo sapiens mRNA for KIAA0540 protein, partial
 35773_i_at Cluster Incl. AA527880:nh86h10.s1 Homo sapiens cDNA, 3 end /clone=IM
 35801_at Cluster Incl. AF026816:Homo sapiens putative oncogene protein mRNA, par
20 36125_s_at Cluster Incl. L38696:Homo sapiens autoantigen p542 mRNA, complete cds
 38069_at Cluster Incl. Z67743:H.sapiens mRNA for CLC-7 chloride channel protein
 39180_at Cluster Incl. S62140:TLS=translocated in liposarcoma [human, mRNA, 1824
 41256_at Cluster Incl. Z21507:H.sapiens EF-1delta gene encoding human elongation
 41805_g_at Cluster Incl. W80358:zh49a07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
25 33131_at Cluster Incl. X70683:H.sapiens mRNA for SOX-4 protein /cds=(350,1774) /
 1665_s_at Endothelial Cell Growth Factor 1
 1550_at U19796 /FEATURE= /DEFINITION=HSU19796 Human melanoma antigen p15 mRNA, c

Metagene 30

30

- 33993_at Cluster Incl. M22919:Human nonmuscle/smooth muscle alkali myosin light
 39211_at Cluster Incl. AF091080:Homo sapiens clone 614 unknown mRNA, complete se
 41370_at Cluster Incl. AF090988:Homo sapiens U5 snRNP-specific 40 kDa protein mR
 31868_at Cluster Incl. AF060798:Homo sapiens myristilated and palmitylated serin
35 31896_at Cluster Incl. AL050281:Homo sapiens mRNA; cDNA DKFZp586G1219 (from
 clon
 38295_at Cluster Incl. X59842:Human PBX2 mRNA /cds=UNKNOWN /gb=X59842
 /gi=35312
 101_at Y09305 /FEATURE=cds /DEFINITION=HSDYRK4 H.sapiens mRNA for protein kinase

Metagene 31

- 34897_at Cluster Incl. W26524:32g4 Homo sapiens cDNA /gb=W26524 /gi=1307385 /ug=
5 34987_s_at Cluster Incl. X79536:H.sapiens mRNA for hnRNPcore protein A1 /cds=(26
 32635_at Cluster Incl. AB029036:Homo sapiens mRNA for KIAA1113 protein, partial
 32713_at Cluster Incl. U51587:Homo sapiens Golgi complex autoantigen golgin-97 m
 36459_at Cluster Incl. AB020686:Homo sapiens mRNA for KIAA0879 protein, complete
 40469_at Cluster Incl. AB011144:Homo sapiens mRNA for KIAA0572 protein, partial
10 41222_at Cluster Incl. AF067575:untitled /cds=(21,2564) /gb=AF067575 /gi=3789867
 32236_at Cluster Incl. AF032456:Homo sapiens ubiquitin conjugating enzyme G2 (UB
 32820_at Cluster Incl. U71267:Human potential transcriptional repressor NOT4Hp (
 37650_at Cluster Incl. U41315:Human ring zinc-finger protein (ZNF127-Xp) gene an
 38748_at Cluster Incl. U76421:Human dsRNA adenosine deaminase DRADA2b
15 (DRADA2b)
 38771_at Cluster Incl. D50405:Human mRNA for RPD3 protein, complete cds /cds=(63
 33188_at Cluster Incl. U37221:Human cyclophilin-like protein mRNA, partial cds /
 1357_at U20657 /FEATURE= /DEFINITION=HSU20657 Human ubiquitin protease (Unph) pr

20 Metagene 32

- 31488_s_at Cluster Incl. S81916:phosphoglycerate kinase {alternatively spliced}
 38899_s_at Cluster Incl. U95822:Human putative transmembrane GTPase mRNA, partia
 39628_at Cluster Incl. AI671547:wb33e07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
25 41855_at Cluster Incl. AF030424:Homo sapiens histone acetyltransferase 1 mRNA, c
 32111_at Cluster Incl. AL050164:Homo sapiens mRNA; cDNA DKFZp586C1622 (from
 clon
 35218_at Cluster Incl. AF022385:Homo sapiens apoptosis-related protein TFAR15 (T
 37208_at Cluster Incl. AJ001612:Homo sapiens mRNA for L-3-phosphoserine-phosphat
30 37209_g_at Cluster Incl. AJ001612:Homo sapiens mRNA for L-3-phosphoserine-phosph
 39009_at Cluster Incl. N98670:yy66d08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 40876_at Cluster Incl. U31525:Human glycogenin mRNA, complete cds /cds=(127,1128
 41223_at Cluster Incl. M22760:Homo sapiens nuclear-encoded mitochondrial cytochr
 41760_at Cluster Incl. AA978033:oq55e04.s1 Homo sapiens cDNA, 3 end /clone=IMAG
35 32232_at Cluster Incl. AF047181:Homo sapiens NADH-ubiquinone oxidoreductase subu
 32829_at Cluster Incl. X97544:H.sapiens mRNA for TIM17 preprotein translocase /c
 33456_at Cluster Incl. U24166:Homo sapiens EB1 mRNA, complete cds /cds=(64,870)
 33932_at Cluster Incl. X17644:Human GST1-Hs mRNA for GTP-binding protein /cds=(6
 34401_at Cluster Incl. L32977:Homo sapiens (clone fl7252) ubiquinol cytochrome c

- 34811_at Cluster Incl. U09813:Human mitochondrial ATP synthase subunit 9, P3 gen
 35751_at Cluster Incl. U17886:Human succinate dehydrogenase iron-protein subunit
 35759_at Cluster Incl. AF026166:Homo sapiens chaperonin-containing TCP-1 beta su
 37324_at Cluster Incl. X01060:Human mRNA for transferrin receptor /cds=(263,2545
5 37347_at Cluster Incl. AA926959:om68h08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 37350_at Cluster Incl. AL031177:dJ889N15.2.1 (26S Proteasome subunit p28 (Ankyri
 37675_at Cluster Incl. X60036:H.sapiens mRNA for mitochondrial phosphate carrier
 37742_at Cluster Incl. M34423:Human beta-galactosidase (GLB1) mRNA, complete cds
 38031_at Cluster Incl. D21853:Human mRNA for KIAA0111 gene, complete cds /cds=(2
10 38380_at Cluster Incl. Y18863:Homo sapiens mRNA for ribonuclease P protein subun
 38413_at Cluster Incl. D15057:Human mRNA for DAD-1, complete cds /cds=(66,407) /
 38435_at Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cd
 38732_at Cluster Incl. X91788:H.sapiens mRNA for Icln protein /cds=(88,801) /gb=
 38839_at Cluster Incl. AL096719:Homo sapiens mRNA; cDNA DKFZp566N043 (from
15 clone
 40587_s_at Cluster Incl. AF054186:Homo sapiens p18 protein mRNA, complete cds /c
 1840_g_at Ras-Like Protein Tc4
 1515_at Rad2
 1446_at D00760 /FEATURE= /DEFINITION=HUMPSC3 Human mRNA for proteasome subunit H
20 1166_at D78151 /FEATURE= /DEFINITION=HUM26SPSP Human mRNA for 26S proteasome sub
 1054_at M87339 /FEATURE= /DEFINITION=HUMACT1A Human replication factor C, 37-kDa
 945_at D50063 /FEATURE= /DEFINITION=HUMP40MOV Human mRNA for proteasome
 subunit
 651_at L07493 /FEATURE= /DEFINITION=HUM14RPA Homo sapiens replication protein A
25
 Metagene 33
 38571_at Cluster Incl. Y18046:Homo sapiens mRNA for FOP (FGFR1 oncogene partner)
 40873_at Cluster Incl. D86963:Human mRNA for KIAA0208 gene, complete cds /cds=(1
30 39519_at Cluster Incl. AB014592:Homo sapiens mRNA for KIAA0692 protein, partial
 1225_g_at X66363 /FEATURE=cds /DEFINITION=HSSTHPKD H.sapiens mRNA
 PCTAIRE-1 for
 429_f_atX00734 /FEATURE=cds /DEFINITION=HSREP10 Human beta-tubulin gene (5-beta
35 Metagene 34
 38142_at Cluster Incl. U38904:Human zinc finger protein C2H2-25 mRNA, complete c
 35704_at Cluster Incl. X92814:H.sapiens mRNA for rat HREV107-like protein /cds=(
 37986_at Cluster Incl. M60459:Human erythropoietin receptor mRNA, complete cds /

	34377_at	Cluster Incl. J05096:Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, c
	35266_at	Cluster Incl. AL049288:Homo sapiens mRNA; cDNA DKFZp564M053 (from clone
	35809_g_at	Cluster Incl. AL031681:dJ862K6.2.2 (splicing factor, arginine/serine-
5	35831_at	Cluster Incl. AB014511:Homo sapiens mRNA for KIAA0611 protein, partial
	37008_r_at	Cluster Incl. M68516:Human protein C inhibitor gene, complete cds /cd
	1243_at	U18300 /FEATURE= /DEFINITION=HSU18300 Human damage-specific DNA binding
	1087_at	M60459 /FEATURE= /DEFINITION=HUMERYTH Human erythropoietin receptor mRNA
10	Metagene 35	
	35961_at	Cluster Incl. AL049390:Homo sapiens mRNA; cDNA DKFZp586O1318 (from clon
	35963_at	Cluster Incl. AI201243:qf70f09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
15	36732_at	Cluster Incl. AI004207:ot94g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	38157_at	Cluster Incl. AF059252:Homo sapiens clone 1 HLA class III protein Dom3z
	38550_at	Cluster Incl. AB021638:Homo sapiens X11L2 mRNA for X11-like protein 2,
	38599_s_at	Cluster Incl. AD001530:Homo sapiens XAP-5 mRNA, complete cds /cds=(75
	40685_at	Cluster Incl. U10868:Human aldehyde dehydrogenase ALDH7 mRNA, complete
20	31802_at	Cluster Incl. D86979:Human mRNA for KIAA0226 gene, complete cds /cds=(6
	31845_at	Cluster Incl. U32645:Human myeloid elf-1 like factor (MEF) mRNA, comple
	34261_at	Cluster Incl. D84307:Homo sapiens mRNA for phosphoethanolamine cytidyly
	35141_at	Cluster Incl. Z97029:Homo sapiens mRNA for ribonuclease H I large subun
	35225_at	Cluster Incl. M91592:Human zinc-finger protein (ZNF76) gene, partial cd
25	36485_at	Cluster Incl. U85647:Homo sapiens small optic lobes homolog (SOLH) mRNA
	36520_at	Cluster Incl. AB014590:Homo sapiens mRNA for KIAA0690 protein, partial
	36847_r_at	Cluster Incl. AA121509:zk88c10.s1 Homo sapiens cDNA, 3 end /clone=IM
	38706_at	Cluster Incl. AA552140:ng48e07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	39398_s_at	Cluster Incl. AB023205:Homo sapiens mRNA for KIAA0988 protein, comple
30	32211_at	Cluster Incl. AB009398:Homo sapiens mRNA for 26S proteasome subunit p40
	34338_at	Cluster Incl. D49738:Human cytoskeleton associated protein (CG22) mRNA,
	35338_at	Cluster Incl. X17094:Human fur mRNA for furin /cds=(216,2600) /gb=X1709
	36150_at	Cluster Incl. AB020649:Homo sapiens mRNA for KIAA0842 protein, partial
	36169_at	Cluster Incl. N47307:yy87a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
35	36586_at	Cluster Incl. U78521:Homo sapiens immunophilin homolog ARA9 mRNA, compl
	38043_at	Cluster Incl. X55448:H.sapiens G6PD gene for glucose-6-phosphate dehydr
	39838_at	Cluster Incl. AB014522:Homo sapiens mRNA for KIAA0622 protein, partial
	39921_at	Cluster Incl. AI526089:DU3.2-7.H07.r Homo sapiens cDNA, 5 end /clone_e
	40905_s_at	Cluster Incl. AL050369:Homo sapiens mRNA; cDNA DKFZp566J153 (from clo

	40923_at	Cluster Incl. AA290994:zs45d07.r1 Homo sapiens cDNA, 5' end /clone=IMAG
	41584_at	Cluster Incl. AF062529:Homo sapiens clone 486790 diphosphoinositol poly
	41829_at	Cluster Incl. AB018274:Homo sapiens mRNA for KIAA0731 protein, partial
	32567_at	Cluster Incl. D10704:Human mRNA for choline kinase /cds=(27,1397) /gb=D
5	1797_at U40343	/FEATURE= /DEFINITION=HSU40343 Human CDK inhibitor p19INK4d mRNA,
	1561_at U27193	/FEATURE= /DEFINITION=HSU27193 Human protein-tyrosine phosphatase
	1376_at M36067	/FEATURE=mRNA /DEFINITION=HUMLIGAA Human DNA ligase I mRNA, compl
10	Metagene 36	
	33484_at	Cluster Incl. Y10571:H.sapiens mRNA for dinG gene /cds=(12,1022) /gb=Y1
	40349_at	Cluster Incl. AL049442:Homo sapiens mRNA; cDNA DKFZp586N1720 (from
15	clon	
	40710_at	Cluster Incl. D86322:Homo sapiens mRNA for calmegin, complete cds /cds=
	41457_at	Cluster Incl. AB007883:Homo sapiens KIAA0423 mRNA, partial cds /cds=(0,
	32084_at	Cluster Incl. AF057164:Homo sapiens organic cation transporter OCTN2 (O
	32654_g_at	Cluster Incl. AW020536:df11b12.y1 Homo sapiens cDNA, 5' end /clone=IM
20	32676_at	Cluster Incl. M93405:Human methylmalonate semialdehyde dehydrogenase ge
	34728_g_at	Cluster Incl. AI800578:wg12b07.x1 Homo sapiens cDNA, 3' end /clone=IM
	34764_at	Cluster Incl. D21851:Human mRNA for KIAA0028 gene, partial cds /cds=(18
	35180_at	Cluster Incl. AL050205:Homo sapiens mRNA; cDNA DKFZp586F1323 (from
	clon	
25	35232_f_at	Cluster Incl. AI056696:oz26h05.x1 Homo sapiens cDNA, 3' end /clone=IM
	35642_at	Cluster Incl. AF053551:Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene
	36910_at	Cluster Incl. L36870:Homo sapiens MAP kinase kinase 4 (MKK4) mRNA, comp
	37616_at	Cluster Incl. X79888:H.sapiens AUH mRNA /cds=(4,1023) /gb=X79888 /gi=78
	38659_at	Cluster Incl. AB020669:Homo sapiens mRNA for KIAA0862 protein, complete
30	40046_r_at	Cluster Incl. AF009426:Homo sapiens clone 22 mRNA, alternative splice
	40859_at	Cluster Incl. AI561196:tq27a01.x1 Homo sapiens cDNA, 3' end /clone=IMAG
	41759_at	Cluster Incl. Z47087:H.sapiens mRNA for RNA polymerase II elongation fa
	33355_at	Cluster Incl. AL049381:Homo sapiens mRNA; cDNA DKFZp586J2118 (from clon
	33358_at	Cluster Incl. W29087:56b8 Homo sapiens cDNA /gb=W29087 /gi=1309053 /ug=
35	33375_at	Cluster Incl. AB002387:Human mRNA for KIAA0389 gene, complete cds /cds=
	34876_at	Cluster Incl. U65090:Human carboxypeptidase D mRNA, complete cds /cds=(
	37031_at	Cluster Incl. D80005:Human mRNA for KIAA0183 gene, partial cds /cds=(0,
	37038_at	Cluster Incl. X83467:H.sapiens PXMP1 gene, exon 1 (and joined CDS) /cds

- 37366_at Cluster Incl. AL049969:Homo sapiens mRNA; cDNA DKFZp564A072 (from clone
- 37655_at Cluster Incl. X75304:H.sapiens giantin mRNA /cds=(126,9905) /gb=X75304
- 37732_at Cluster Incl. AL049940:Homo sapiens mRNA; cDNA DKFZp564E1922 (from
- 5** clon
- 38485_at Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-128780
- 39557_at Cluster Incl. AI625844:ty65d07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 40184_at Cluster Incl. L37042:Homo sapiens casein kinase I alpha isoform (CSNK1A
- 40238_at Cluster Incl. AI674208:wc07f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 10** 40239_g_at Cluster Incl. AI674208:wc07f02.x1 Homo sapiens cDNA, 3 end /clone=IM
- 40623_at Cluster Incl. AI749193:at40e04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 41488_at Cluster Incl. AC002394:Human Chromosome 16 BAC clone CIT987SK-A-211C6
- /
- 33170_at Cluster Incl. AB023179:Homo sapiens mRNA for KIAA0962 protein, partial
- 15** 820_at U77604 /FEATURE= /DEFINITION=HSU77604 Homo sapiens microsomal glutathione
- 237_s_at M60483 /FEATURE=mRNA /DEFINITION=HUMPP2AA Human protein phosphatase 2A
- Metagene 37
- 20**
- 41718_g_at Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8
- 37631_at Cluster Incl. U14391:Human myosin-IC mRNA, complete cds /cds=(375,3704)
- 32164_at Cluster Incl. S79639:EXT1=putative tumour suppressor/hereditary multipl
- 35823_at Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mR
- 25** 36184_at Cluster Incl. L06419:Homo sapiens lysyl hydroxylase (PLOD) mRNA, comple
- 38087_s_at Cluster Incl. W72186:zd69b10.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 489_at U63329 /FEATURE=cds /DEFINITION=HSU63329 Human mutY homolog (hMYH) gene,
- Metagene 38
- 30**
- 32626_at Cluster Incl. M90516:Human glutamine-fructose-6-phosphate amidotransfer
- 34723_at Cluster Incl. U79270:Human clone 23707 mRNA, partial cds /cds=(0,460) /
- 35182_f_at Cluster Incl. W25874:14e9 Homo sapiens cDNA /gb=W25874 /gi=1306015 /u
- 33172_at Cluster Incl. T75292:yc89b05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
- 35** 33173_g_at Cluster Incl. T75292:yc89b05.r1 Homo sapiens cDNA, 5 end /clone=IMAG
- 1668_s_at L15409 /FEATURE= /DEFINITION=HUMHIPLIND Homo sapiens (clone g7)
- von Hi
- Metagene 39

- 32085_at Cluster Incl. AB023198:Homo sapiens mRNA for KIAA0981 protein, partial
 37619_at Cluster Incl. D42084:Human mRNA for KIAA0094 gene, partial cds /cds=(0,
 39380_at Cluster Incl. AB014597:Homo sapiens mRNA for KIAA0697 protein, partial
 5 39762_at Cluster Incl. AB007885:Homo sapiens KIAA0425 mRNA, complete cds /cds=(1
 33411_g_at Cluster Incl. S66213:integrin alpha 6B [human, mRNA Partial, 528 nt]
 34382_at Cluster Incl. AJ003112:Homo sapiens mRNA for doublecortin /cds=(415,149
 33103_s_at Cluster Incl. U37122:Human adducin gamma subunit mRNA, complete cds /
 1420_s_at D30655 /FEATURE= /DEFINITION=HUMELF4AII Homo sapiens mRNA for
 10 eukaryot
 1151_at Epstein-Barr Virus Small Rna-Associated Protein
- Metagene 40
- 15 37557_at Cluster Incl. U62531:Human AE2 anion exchanger (SLC4A2) mRNA, complete
 34372_at Cluster Incl. AB002310:Human mRNA for KIAA0312 gene, partial cds /cds=(
 36196_at Cluster Incl. U24183:Human phosphofructokinase (PFKM) mRNA, complete cd
 1709_g_at U07620 /FEATURE= /DEFINITION=HSU07620 Human MAP kinase mRNA,
 complete
- 20 Metagene 41
- 39055_at Cluster Incl. M32886:Human sorcin CP-22 mRNA, complete cds /cds=(12,608
 33378_at Cluster Incl. AB019494:Homo sapiens IDN3 mRNA, partial cds /cds=(706,75
 25 33870_at Cluster Incl. AB029005:Homo sapiens mRNA for KIAA1082 protein, partial
 35736_at Cluster Incl. AL050091:Homo sapiens mRNA; cDNA DKFZp586F1918 (from
 clon
 36935_at Cluster Incl. M23379:Human GTPase-activating protein ras p21 (RASA) mRN
 33164_at Cluster Incl. AJ132545:Homo sapiens mRNA for protein kinase /cds=(395,2
 30 507_s_at U43189 /FEATURE= /DEFINITION=HSU43189 Human Ets transcription factors
 N
- Metagene 42
- 35 31514_at Cluster Incl. AF034970:Homo sapiens docking protein (DOK-2) mRNA, compl
 35869_at Cluster Incl. AB020499:Homo sapiens BCG-regulated mRNA for MD-1 homolog
 36709_at Cluster Incl. Y00093:H.sapiens mRNA for leukocyte adhesion glycoprotein
 39239_at Cluster Incl. X13444:Human mRNA for CD8 beta-chain glycoprotein (CD8 be
 40008_at Cluster Incl. U46573:Human eotaxin precursor mRNA, complete cds /cds=(5

- 34663_at Cluster Incl. M28696:Human low-affinity IgG Fc receptor (beta-Fc-gamma-
 35633_at Cluster Incl. D87457:Human mRNA for KIAA0281 gene, complete cds /cds=(1
 36908_at Cluster Incl. M93221:Human macrophage mannose receptor (MRC1) gene /cds
 37976_at Cluster Incl. AL034397:Human DNA sequence from clone 159A1 on chromosom
 5 39778_at Cluster Incl. M55621:Human N-acetylglucosaminyltransferase I (GlcNAc-TI
 40081_at Cluster Incl. L26232:Human phospholipid transfer protein mRNA, complete
 32238_at Cluster Incl. AF001383:Homo sapiens amphiphysin II mRNA, complete cds /
 32826_at Cluster Incl. AJ133133:Homo sapiens mRNA for ecto-ATP diphosphohydrolas
 36103_at Cluster Incl. D90144:Homo sapiens gene for LD78 alpha precursor, comple
 10 36589_at Cluster Incl. X15414:Human mRNA for aldose reductase (EC 1.1.1.2) /cds=
 37398_at Cluster Incl. AA100961:zn40b06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 38404_at Cluster Incl. M55153:Human transglutaminase (TGase) mRNA, complete cds
 32550_r_at Cluster Incl. Y11525:H.sapiens mRNA for CCAAT/enhancer binding protei
 1780_at M19722 /FEATURE= /DEFINITION=HUMFGR Human fgr proto-oncogene encoded p55
 15 1786_at U08023 /FEATURE= /DEFINITION=HSU08023 Human cellular proto-oncogene (c-m
 1173_g_at Spermidine/Spermine N1-Acetyltransferase, Alt. Splice 2
 459_s_at U68485 /FEATURE= /DEFINITION=HSU68485 Homo sapiens bridging
 integrator
 268_at L34657 /FEATURE=mRNA /DEFINITION=HUMPECAM27 Homo sapiens
 20 platelet/endothe
 Metagene 43
 33527_at Cluster Incl. U39196:Human clone hGIRK1 G-protein coupled inwardly rect
 25 37511_at Cluster Incl. AB030506:Homo sapiens mRNA for B9, complete cds /cds=(158
 33244_at Cluster Incl. U07223:Human beta2-chimaerin mRNA, complete cds /cds=(444
 35227_at Cluster Incl. U72066:Homo sapiens CtBP interacting protein CtIP (CtIP)
 37983_at Cluster Incl. S77410:type 1 angiotensin II receptor [human, liver, mRNA
 41210_at Cluster Incl. M81057:Human procarboxypeptidase B mRNA, complete cds /cd
 30 40544_g_at Cluster Incl. L08424:Homo sapiens achaete scute homologous protein (A
 41543_at Cluster Incl. U34360:Human lymphoid nuclear protein (LAF-4) mRNA, compl
 346_s_at D13814 /FEATURE= /DEFINITION=HUMAGRT1B Homo sapiens mRNA for
 angiotensi
 35 Metagene 44
 34425_at Cluster Incl. AF031469:Homo sapiens MHC class I related protein 1 isofo
 34933_at Cluster Incl. AJ238381:Homo sapiens pax9 gene, exons 1-2 and joined CDS
 36694_at Cluster Incl. AF043472:Homo sapiens Shab-related delayed-rectifier K+ c

- 36080_at Cluster Incl. AB002332:Human mRNA for KIAA0334 gene, complete cds /cds=
 41741_at Cluster Incl. U28686:Human putative RNA binding protein RNPL mRNA, comp
 39162_at Cluster Incl. AA156987:z119b05.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 5** Metagene 45
- 38664_at Cluster Incl. AB009285:Homo sapiens BCNT mRNA, complete cds /cds=(109,1
 39331_at Cluster Incl. X79535:H.sapiens mRNA for beta tubulin, clone nuk_278 /cd
 34818_at Cluster Incl. X96381:H.sapiens erm gene, exon 2,3,4,5 (and joined CDS)
10 36960_at Cluster Incl. U89278:Human polyhomeotic 2 homolog (HPH2) mRNA, complete
 40207_g_at Cluster Incl. AI767675:wh38d11.x1 Homo sapiens cDNA, 3 end /clone=IM
 40567_at Cluster Incl. X01703:Human gene for alpha-tubulin (b alpha 1) /cds=(213
 483_g_at U59289 /FEATURE= /DEFINITION=HSU59289 Human H-cadherin mRNA,
 complete c
15 296_at Tubulin, Beta
 297_g_at Tubulin, Beta
- Metagene 46
- 20** 35375_at Cluster Incl. AJ011311:Homo sapiens mRNA for AP endonuclease XTH2, puta
 38156_at Cluster Incl. U78313:Human myogenic repressor I-mf (MDFI) mRNA, complet
 38594_i_at Cluster Incl. AB006622:Homo sapiens mRNA for KIAA0284 gene, partial c
 41047_at Cluster Incl. AI885170:wl90e10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41861_at Cluster Incl. AL050019:Homo sapiens mRNA; cDNA DKFZp564C186 (from
25 clone
 38686_at Cluster Incl. X71490:H.sapiens mRNA for vacuolar proton ATPase, subunit
 38998_g_at Cluster Incl. X96924:H.sapiens gene encoding mitochondrial citrate tr
 39347_at Cluster Incl. X97074:H.sapiens mRNS for clathrin-associated protein /cd
 33382_at Cluster Incl. M92449:Human LTR mRNA, 3 end of coding region and 3 fla
30 33424_at Cluster Incl. Y00281:Human mRNA for ribophorin I /cds=(137,1960) /gb=Y0
 34366_g_at Cluster Incl. AF042386:Homo sapiens cyclophilin-33B (CYP-33) mRNA, co
 35308_at Cluster Incl. D83200:Homo sapiens mRNA expressed in placenta /cds=UNKNO
 36653_g_at Cluster Incl. J03824:Human uroporphyrinogen III synthase mRNA, comple
 37335_at Cluster Incl. U41668:Human deoxyguanosine kinase mRNA, complete cds /cd
35 38830_at Cluster Incl. U66685:HSU66685 Homo sapiens cDNA /gb=U66685 /gi=1906570
 39516_at Cluster Incl. AI827793:wf33b11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39521_at Cluster Incl. U55054:Human K-Cl cotransporter (hKCC1) mRNA, complete cd
 39805_at Cluster Incl. AF070598:Homo sapiens clone 24410 ABC transporter mRNA, p
 39825_at Cluster Incl. L77567:Homo sapiens mitochondrial citrate transport prote

- 40171_at Cluster Incl. AF062739:Homo sapiens GSK-3 binding protein FRAT2 (FRAT2)
- 41332_at Cluster Incl. D38251:Homo sapiens mRNA for RPB5 (XAP4), complete cds /c
- 41551_at Cluster Incl. AW044624:wy78c04.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 32574_at Cluster Incl. X59960:H.sapiens mRNA for sphingomyelinase /cds=(122,2005
- 5** 33214_at Cluster Incl. Y11681:Homo sapiens mRNA for mitochondrial ribosomal prot
- 1879_at M14949 /FEATURE=cds /DEFINITION=HUMRASR2 Human R-ras gene, exons 2 throu
- 1333_f_at X02596 /FEATURE=cds /DEFINITION=HSBCRR Human mRNA for bcr
(breakpoint
- 905_at L76200 /FEATURE= /DEFINITION=HUMGUK1R Human guanylate kinase (GUK1)
- 10** mRNA,
- 537_f_atU07000 /FEATURE=cds#3 /DEFINITION=HSU07000 Human breakpoint cluster reg
- Metagene 47
- 15** 34256_at Cluster Incl. AB018356:Homo sapiens mRNA for GM3 synthase, complete cds
- 36994_at Cluster Incl. M62762:Human vacuolar H⁺ ATPase proton channel subunit mR
- Metagene 48
- 20** 36379_at Cluster Incl. AF085808:Homo sapiens uroplakin III mRNA, complete cds /c
- 32135_at Cluster Incl. U00968:Human SREBP-1 mRNA, complete cds /cds=(166,3609) /
- 37194_at Cluster Incl. M68891:Human GATA-binding protein (GATA2) mRNA, complete
- 1071_at M77810 /FEATURE= /DEFINITION=HUMGATA2A Human transcription factor GATA-2
- 1072_g_at M77810 /FEATURE= /DEFINITION=HUMGATA2A Human transcription factor
- 25** GATA
- 203_at M68891 /FEATURE= /DEFINITION=HUMGATA Human GATA-binding protein
(GATA2) m
- Metagene 49
- 30**
- 31722_at Cluster Incl. AL022326:dJ333H23.1.1 (60S Ribosomal Protein L3) /cds=(6,
- 31907_at Cluster Incl. D87735:Homo sapiens mRNA for ribosomal protein L14, compl
- 32432_f_at Cluster Incl. L25899:Human ribosomal protein L10 mRNA, complete cds /
- 33668_at Cluster Incl. AF037643:Homo sapiens 60S ribosomal protein L12 (RPL12) p
- 35** 35405_at Cluster Incl. X52520:Human mRNA for tyrosine aminotransferase (TAT) (EC
- 36894_at Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,84
- 39430_at Cluster Incl. AF082557:Homo sapiens TRF1-interacting ankyrin-related AD
- 32145_at Cluster Incl. X58141:Human mRNA for erythrocyte adducin alpha subunit /

	32254_at	Cluster Incl. AL050223:Homo sapiens mRNA; cDNA DKFZp586L1323 (from clon
	32259_at	Cluster Incl. AB002386:Human mRNA for KIAA0388 gene, complete cds /cds=
	35744_at	Cluster Incl. D50931:Human mRNA for KIAA0141 gene, complete cds /cds=(8
5	36587_at	Cluster Incl. Z11692:H.sapiens mRNA for elongation factor 2 /cds=(0,257
	36624_at	Cluster Incl. L33842:Homo sapiens (clone FFE-7) type II inosine monopho
	39110_at	Cluster Incl. X55733:H.sapiens initiation factor 4B cDNA /cds=(0,1835)
	39864_at	Cluster Incl. D78134:Homo sapiens mRNA for CIRP, complete cds /cds=(80,
	39866_at	Cluster Incl. AB028986:Homo sapiens mRNA for KIAA1063 protein, partial
10	39916_r_at	Cluster Incl. J02984:Human insulinoma rig-analog mRNA encoding DNA-bi
	1873_at D21089	/FEATURE= /DEFINITION=HUMXPCR Human mRNA for XP-C repair compleme
	1836_at D50310	/FEATURE= /DEFINITION=HUMCYI Human mRNA for cyclin I, complete cd
	1556_at U23946	/FEATURE= /DEFINITION=HSU23946 Human putative tumor suppressor (L
15	Metagene 50	
	34461_at	Cluster Incl. D67035:Homo sapiens mRNA for SCP-1, complete cds /cds=(17
	36809_at	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) prot
20	39993_at	Cluster Incl. D11466:Homo sapiens mRNA for PIG-A protein, complete cds
	36081_s_at	Cluster Incl. AB004848:Homo sapiens mRNA expressed in placenta, clone
	37047_at	Cluster Incl. AF002020:Homo sapiens Niemann-Pick C disease protein (NPC
	40253_at	Cluster Incl. AJ011123:Homo sapiens mRNA for phosphatidylinositol 4-kin
	980_at AF002020	/FEATURE= /DEFINITION=AF002020 Homo sapiens Niemann-Pick C disea
25	Metagene 51	
	41062_at	Cluster Incl. AA037278:zc52c04.r1 Homo sapiens cDNA, 5' end /clone=IMAG
	41672_at	Cluster Incl. AF007128:Homo sapiens clone 23870 mRNA sequence /cds=UNKN
30	32038_s_at	Cluster Incl. AI739308:wi30c12.x1 Homo sapiens cDNA, 3' end /clone=IM
	35695_at	Cluster Incl. U67615:Human beige protein homolog (chs) mRNA, complete c
	34341_at	Cluster Incl. U00238:Homo sapiens glutamine PRPP amidotransferase (GPAT
	792_s_at	X52611 /FEATURE=cds /DEFINITION=HSAP2 Human mRNA for transcription fact
35	Metagene 52	
	31935_s_at	Cluster Incl. U75968:Human clone C3 CHL1 protein (CHLR1) mRNA, altern
	35041_at	Cluster Incl. X53655:H.sapiens mRNA for NGF-2 /cds=(43,816) /gb=X53655

- 35853_at Cluster Incl. AL049654:Novel human mRNA similar to mouse gene PICK1 (TR
 37114_at Cluster Incl. L32832:Homo sapiens zinc finger homeodomain protein (ATBF
 41664_at Cluster Incl. AF026030:Homo sapiens putative mitochondrial inner membra
 41705_at Cluster Incl. U69198:U69198 Homo sapiens cDNA /clone=c-32h10 /gb=U69198
5 33713_at Cluster Incl. AJ005895:Homo sapiens mRNA for (JM3) preprotein transloca
 34224_at Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (B
 36891_at Cluster Incl. AL022237:bK1191B2.3.1 (PUTATIVE novel Acyl Transferase si
 37267_at Cluster Incl. Z50115:H.sapiens mRNA for thimet oligopeptidase (metallop
 38613_at Cluster Incl. U61837:Homo sapiens putative cyclin G1 interacting protei
10 39424_at Cluster Incl. U70321:Human herpesvirus entry mediator mRNA, complete cd
 39711_at Cluster Incl. J03075:Human 80K-H protein (kinase C substrate) mRNA, com
 40138_at Cluster Incl. U70735:Homo sapiens 34 kDa Mov34 homolog mRNA, complete c
 40452_at Cluster Incl. U83246:Homo sapiens copine I mRNA, complete cds /cds=(156
 33826_at Cluster Incl. AL120500:DKFZp761M078_s1 Homo sapiens cDNA, 3 end /clone
15 34318_at Cluster Incl. AJ005896:Homo sapiens mRNA for JM4 protein, complete CDS
 39832_at Cluster Incl. AL096723:Homo sapiens mRNA; cDNA DKFZp564H2023 (from
 clon
 39893_at Cluster Incl. AB010414:Homo sapiens mRNA for G-protein gamma 7, complet
 39918_at Cluster Incl. AF042379:Homo sapiens spindle pole body protein spc97 hom
20 40183_at Cluster Incl. AI660225:we68f05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41532_at Cluster Incl. Y09723:H.sapiens mRNA for Miz-1 protein /cds=(126,2537) /
 1795_g_at M92287 /FEATURE= /DEFINITION=HUMCYCD3A Homo sapiens cyclin D3
 (CCND3)
 1271_g_at L19067 /FEATURE= /DEFINITION=HUMNFKB65A Human NF-kappa-B
25 transcription
 1116_at M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD
 679_at J04990 /FEATURE=cds /DEFINITION=HUMCAPG Human cathepsin G gene, complete
 567_s_at M79463 /FEATURE= /DEFINITION=HUMPML2 Human PML-2 mRNA,
 complete CDS
30 214_at M97676 /FEATURE= /DEFINITION=HUMHOX7 Homo sapiens (region 7) homeobox pro
 Metagene 53
 41083_at Cluster Incl. AC006276:Homo sapiens chromosome 19, cosmid R28379 /cds=(
35 41084_at Cluster Incl. AI659108:tu08c09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41858_at Cluster Incl. AL049261:Homo sapiens mRNA; cDNA DKFZp564E053 (from
 clone
 33226_at Cluster Incl. AB020683:Homo sapiens mRNA for KIAA0876 protein, partial
 34255_at Cluster Incl. AF059202:Homo sapiens ACAT related gene product 1 mRNA, c

- 34707_at Cluster Incl. U91543:Homo sapiens zinc-finger helicase (hZFH) mRNA, com
 35160_at Cluster Incl. AF064491:Homo sapiens LIM homeobox protein cofactor (CLIM
 37931_at Cluster Incl. X05299:Human mRNA (~95%) for major centromere autoantigen
 37963_at Cluster Incl. X52151:Homo sapiens arylsulphatase A mRNA, complete cds /
5 38996_at Cluster Incl. U15655:Human ets domain protein ERF mRNA, complete cds /
 40149_at Cluster Incl. AL049924:Homo sapiens mRNA; cDNA DKFZp547G11110 (from
 clon
 32761_at Cluster Incl. AB002322:Human mRNA for KIAA0324 gene, partial cds /cds=(
 35292_at Cluster Incl. Z37166:H.sapiens BAT1 mRNA for nuclear RNA helicase (DEAD
10 36161_at Cluster Incl. M34175:Human beta adaptin mRNA, complete cds /cds=(177,29
 36200_at Cluster Incl. X69838:H.sapiens mRNA for G9a /cds=(47,3052) /gb=X69838 /
 37768_at Cluster Incl. M74905:Human 3-alkyladenine DNA glycosylase (HAAG) mRNA,
 39112_at Cluster Incl. Y07661:H.sapiens USF2 gene /cds=(0,1040) /gb=Y07661 /gi=1
 40225_at Cluster Incl. D88435:Homo sapiens mRNA for HsGAK, complete cds /cds=(0,
15 40955_at Cluster Incl. U79287:Human clone 23867 mRNA sequence /cds=UNKNOWN
 /gb=U
 41344_s_at Cluster Incl. M96684:H.sapiens Pur (pur-alpha) mRNA, complete cds /cd
 2052_g_at M31767 /FEATURE=mRNA /DEFINITION=HUMDNAMET Human O6-
 methylguanine-DNA
20 1000_at X60188 /FEATURE=mRNA /DEFINITION=HSERK1 Human ERK1 mRNA for protein
 seri
 453_at U66616 /FEATURE= /DEFINITION=HSU66616 Human SWI/SNF complex 170 KDa
 subun
 319_g_at D64142 /FEATURE=mRNA /DEFINITION=D64142 Human mRNA for histone
25 H1x, com
 197_at U29656 /FEATURE= /DEFINITION=HSU29656 Human DR-nm23 mRNA, complete cds
 Metagene 54
30 35861_at Cluster Incl. AA018440:ze50a07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 38701_at Cluster Incl. AJ000519:Homo sapiens mRNA for ubiquitin-conjugating enzy
 39348_at Cluster Incl. X99209:H.sapiens mRNA for arginine methyltransferase /cds
 41600_at Cluster Incl. U59435:Human cell cycle protein p38-2G4 homolog (hG4-1) m
35 Metagene 55
 33594_at Cluster Incl. AB017788:Homo sapiens hdkk-4 mRNA, complete cds /cds=(0,6
 32380_at Cluster Incl. Z34974:H.sapiens mRNA for plakophilin (partial) /cds=(252
 36798_g_at Cluster Incl. J04168:Human leukosialin mRNA, complete cds /cds=(95,12

- 35262_at Cluster Incl. AF022229:Homo sapiens translation initiation factor 6 (eI
 37307_at Cluster Incl. X04828:Human mRNA for G(i) protein alpha-subunit (adenyla
 1294_at L13852 /FEATURE= /DEFINITION=HUME1URP Homo sapiens ubiquitin-activating
 1014_at U60325 /FEATURE= /DEFINITION=HSU60325 Human DNA polymerase gamma mRNA,
 5 n
 210_at M95678 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-
- Metagene 56
- 10 40762_g_at Cluster Incl. AA705628:zf40a01.s1 Homo sapiens cDNA, 3 end /clone=37
 33371_s_at Cluster Incl. U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, c
 35742_at Cluster Incl. U95740:Human Chromosome 16 BAC clone CIT987SK-A-362G6 /cd
 40244_s_at Cluster Incl. AI743654:wg41d01.x1 Homo sapiens cDNA, 3 end /clone=IM
- 15 Metagene 57
- 34091_s_at Cluster Incl. Z19554:H.sapiens vimentin gene /cds=(122,1522) /gb=Z195
 37842_at Cluster Incl. AF054589:Homo sapiens HIC protein mRNA, complete cds /cds
 40297_at Cluster Incl. AC005053:Homo sapiens BAC clone RG041D11 from 7q21 /cds=(
 20 41388_at Cluster Incl. AF017418:Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA
 41401_at Cluster Incl. U57646:Homo sapiens cysteine and glycine-rich protein 2 (
 34246_at Cluster Incl. AA418437:zv92d11.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 35698_at Cluster Incl. Y00318:Human mRNA for complement control protein factor I
 36009_at Cluster Incl. AF091092:Homo sapiens clone 683 unknown mRNA, complete se
 25 36899_at Cluster Incl. M97287:Human MAR/SAR DNA binding protein (SATB1) mRNA,
 co
 39038_at Cluster Incl. AF093118:Homo sapiens UP50 mRNA, complete cds /cds=(168,1
 39070_at Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete
 39409_at Cluster Incl. M14058:Human complement C1r mRNA, complete cds /cds=(63,2
 30 39775_at Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54
 40071_at Cluster Incl. U03688:Human dioxin-inducible cytochrome P450 (CYP1B1) mR
 40496_at Cluster Incl. J04080:Human complement component C1r mRNA, complete cds
 32249_at Cluster Incl. M65292:Human factor H homologue mRNA, complete cds /cds=(
 32851_at Cluster Incl. AF036956:Homo sapiens neuroblastoma apoptosis-related RNA
 35 33867_s_at Cluster Incl. X77494:H.sapiens MSSP-2 mRNA /cds=(231,1400) /gb=X77494
 33876_at Cluster Incl. AL050107:Homo sapiens mRNA; cDNA DKFZp586I1419 (from clon
 36686_at Cluster Incl. U07919:Human aldehyde dehydrogenase 6 mRNA, complete cds
 36943_r_at Cluster Incl. U81992:Homo sapiens C2H2 zinc finger protein PLAGL1 (PL
 37043_at Cluster Incl. AL021154:dJ150O5.2 (Inhibitor of DNA binding 3 (dominant

- 37319_at Cluster Incl. M35878:Human insulin-like growth factor-binding protein-3
- 39098_at Cluster Incl. X52896:H.sapiens RNA for dermal fibroblast elastin /cds=U
- 39114_at Cluster Incl. AB022718:Homo sapiens mRNA for DEPP (decidual protein ind
- 41246_at Cluster Incl. AI743134:wg87f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 5 1586_at M35878 /FEATURE=expanded_cds /DEFINITION=HUMIBP3 Human insulin-like grow
- 859_at U03688 /FEATURE= /DEFINITION=HSU03688 Human dioxin-inducible cytochrome P
- Metagene 58
- 10 32459_at Cluster Incl. U66088:Human sodium iodide symporter mRNA, complete cds /
- 34147_g_at Cluster Incl. AB019529:Homo sapiens mRNA for OGG1 protein type 2c, pa
- 35124_at Cluster Incl. M62982:Human arachidonate 12-lipoxygenase mRNA, complete
- 33950_g_at Cluster Incl. AF011406:Homo sapiens corticotropin releasing hormone r
- 34485_r_at Cluster Incl. M21868:Human polymorphic epithelial mucin core protein
- 15 35967_at Cluster Incl. M69238:Human aryl hydrocarbon receptor nuclear translocat
- 37779_at Cluster Incl. Y08134:H.sapiens mRNA for ASM-like phosphodiesterase 3b /
- 38936_at Cluster Incl. M16652:Human pancreatic elastase IIA mRNA, complete cds /
- 39667_at Cluster Incl. AF083898:Homo sapiens RNA-binding protein Nova-2 mRNA, co
- 32100_r_at Cluster Incl. U06088:Human N-acetylgalactosamine 6-sulphatase (GALNS)
- 20 34240_s_at Cluster Incl. AL049786:Novel human gene mapping to chromosome 13 /cds=
- 40836_s_at Cluster Incl. W26677:11f7 Homo sapiens cDNA /gb=W26677 /gi=1305788 /u
- 41726_at Cluster Incl. Z35307:H.sapiens mRNA for endothelin-converting-enzyme 1
- 33828_at Cluster Incl. AF035262:Homo sapiens BAF57 (BAF57) gene, complete cds /c
- 39198_s_at Cluster Incl. W27763:37c8 Homo sapiens cDNA /gb=W27763 /gi=1307711 /u
- 25 39854_r_at Cluster Incl. AF055000:Homo sapiens clone 24519 unknown mRNA, partial
- 39855_at Cluster Incl. AC005787:Homo sapiens chromosome 19, cosmid R33374 /cds=(
- 39908_at Cluster Incl. AF069735:Homo sapiens PCAF associated factor 65 alpha mRN
- 40169_at Cluster Incl. AF057140:Homo sapiens cargo selection protein TIP47 (TIP4
- 40539_at Cluster Incl. U42391:Human myosin-LXb mRNA, complete cds /cds=(0,6068)
- 30 41301_at Cluster Incl. W28608:49b1 Homo sapiens cDNA /gb=W28608 /gi=1308556 /ug=
- 41324_g_at Cluster Incl. U90917:Human clone 23641 mRNA sequence /cds=UNKNOWN /gb
- 2090_i_at H12458 /FEATURE= /DEFINITION=H12458 yj12d03.s1 Soares placenta Nb2HP
- H
- 2079_s_at M13970 /FEATURE=mRNA /DEFINITION=HUMGFI21 Human insulin-like
- 35 growth fa
- 2038_g_at M13995 /FEATURE=mRNA /DEFINITION=HUMBCL2B Human B-cell
- leukemia/lympho
- 1827_s_at M13929 /FEATURE=mRNA /DEFINITION=HUMMYCPOA Human c-myc-P64
- mRNA, initi

- 1724_at S75174 /FEATURE= /DEFINITION=S75174 E2F-4=transcription factor [human, N
 1220_g_at X15949 /FEATURE=cds /DEFINITION=HSIRF2 Human mRNA for interferon
 regul
 1035_g_at U14394 /FEATURE= /DEFINITION=HSU14394 Human tissue inhibitor of metall
 5 598_at M60299 /FEATURE=cds /DEFINITION=HUMCOLII Human alpha-1 collagen type II g
 438_at X07767 /FEATURE=cds /DEFINITION=HSPKA Human mRNA for cAMP-dependent
 prote
 179_at U38980 /FEATURE= /DEFINITION=U38980 Human PMS2 related (hPMSR6) mRNA, co
 166_at U48405 /FEATURE=cds /DEFINITION=HSU48405 Human G protein coupled receptor
 10
 Metagene 59
 31463_s_at Cluster Incl. AL022097:Homo sapiens DNA sequence from PAC 256G22 on c
 31952_at Cluster Incl. X69391:H.sapiens mRNA for ribosomal protein L6 /cds=(26,8
 15 33674_at Cluster Incl. Z49148:H.sapiens mRNA for ribosomal protein L29 /cds=(29,
 35119_at Cluster Incl. X56932:H.sapiens mRNA for 23 kD highly basic protein /cds
 32330_at Cluster Incl. X06617:Human mRNA for ribosomal protein S11 /cds=(15,491)
 35987_g_at Cluster Incl. AL050395:Homo sapiens mRNA; cDNA DKFZp586D1020 (from cl
 35988_i_at Cluster Incl. AI417075:tg78e09.x1 Homo sapiens cDNA, 3 end /clone=IM
 20 39077_at Cluster Incl. U41843:Human Dr1-associated corepressor (DRAP1) mRNA, com
 34317_g_at Cluster Incl. W52024:zd13a03.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 39830_at Cluster Incl. AA044823:zk72a10.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 1817_at D89667 /FEATURE= /DEFINITION=D89667 Homo sapiens mRNA for c-myc binding
 25 Metagene 60
 37838_at Cluster Incl. M31315:Human coagulation factor XII (Hageman) mRNA, 3 en
 39303_at Cluster Incl. Y14153:Homo sapiens mRNA for beta-transducin repeat conta
 33334_at Cluster Incl. X84194:H.sapiens mRNA for acylphosphatase, erythrocyte (C
 30 41195_at Cluster Incl. U49957:Human LIM protein (LPP) mRNA, partial cds /cds=(24
 41230_at Cluster Incl. U71087:Human MAP kinase kinase MEK5b mRNA, complete cds /
 41746_at Cluster Incl. Z83840:Human DNA sequence from clone 216E10 on chromosome
 Metagene 61
 35
 36779_at Cluster Incl. X90908:H.sapiens mRNA for I-15P (I-BABP) protein /cds=(12
 32091_at Cluster Incl. AB007915:Homo sapiens mRNA for KIAA0446 protein, complete
 34771_at Cluster Incl. AF035959:Homo sapiens type-2 phosphatidic acid phosphatas

- 38986_at Cluster Incl. Z49835:H.sapiens mRNA for protein disulfide isomerase /cd
 40794_at Cluster Incl. X05332:Human mRNA for prostate specific antigen /cds=(43,
 36122_at Cluster Incl. X59417:H.sapiens PROS-27 mRNA /cds=(62,802) /gb=X59417 /g
 1514_g_at Antigen, Prostate Specific, Alt. Splice Form 3
- 5** 1296_at D83542 /FEATURE= /DEFINITION=HUMC15A Homo sapiens mRNA for cadherin-15,
- Metagene 62
- 35907_at Cluster Incl. Z36714:H.sapiens mRNA for cyclin F /cds=(43,2403) /gb=Z36
10 41060_at Cluster Incl. M74093:Human cyclin mRNA /cds=UNKNOWN /gb=M74093
 /gi=8066
 41439_at Cluster Incl. AJ001381:Homo sapiens incomplete cDNA for a mutated allele
 41650_at Cluster Incl. U63810:Homo sapiens WD40 protein Ciao 1 mRNA, complete cd
 33770_at Cluster Incl. AF009225:Homo sapiens Ikb kinase alpha subunit (IKK alpha
15 36046_at Cluster Incl. AL050144:Homo sapiens mRNA; cDNA DKFZp586C1620 (from
 clon
 37552_at Cluster Incl. U33632:Human two P-domain K+ channel TWIK-1 mRNA, complet
 37636_at Cluster Incl. D86969:Human mRNA for KIAA0215 gene, complete cds /cds=(2
 41128_at Cluster Incl. AF070537:Homo sapiens clone 24606 mRNA sequence /cds=UNKN
20 34829_at Cluster Incl. U59151:Human Cbf5p homolog (CBF5) mRNA, complete cds /cds
 35256_at Cluster Incl. AL096737:Homo sapiens mRNA; cDNA DKFZp434F152 (from
 clone
 38094_at Cluster Incl. M65028:Human hnRNP type A/B protein mRNA, complete cds /c
 38789_at Cluster Incl. L12711:Homo sapiens transketolase (tk) mRNA, complete cds
25 39826_f_at Cluster Incl. W29115:56e8 Homo sapiens cDNA /gb=W29115 /gi=1309081 /u
 40891_f_at Cluster Incl. X92896:H.sapiens mRNA for ITBA2 protein /cds=(10,327) /
 32529_at Cluster Incl. X69910:H.sapiens p63 mRNA for transmembrane protein /cds=
- Metagene 63
- 30**
- 32004_s_at Cluster Incl. W32483:zc67e07.r1 Homo sapiens cDNA, 5' end /clone=IMAG
 34415_at Cluster Incl. Z22536:Homo sapiens ALK-4 mRNA, complete CDS /cds=(0,1517
 36231_at Cluster Incl. AC002073:Human PAC clone DJ515N1 from 22q11.2-q22 /cds=(0
 33230_at Cluster Incl. AJ131186:Homo sapiens mRNA for nuclear matrix protein NMP
35 33794_g_at Cluster Incl. U19345:Homo sapiens AR1 (TCF20) mRNA, partial cds /cds=
 34197_at Cluster Incl. X80907:H.sapiens mRNA for p85 beta subunit of phosphatidy
 39011_at Cluster Incl. X99906:Homo sapiens mRNA for alpha endosulfine /cds=(125,
 39694_at Cluster Incl. W27517:31h6 Homo sapiens cDNA /gb=W27517 /gi=1307321 /ug=
 40100_at Cluster Incl. U72206:Human guanine nucleotide regulatory factor (LFP40)

- 40847_at Cluster Incl. AB018293:Homo sapiens mRNA for KIAA0750 protein, complete
 32811_at Cluster Incl. X98507:H.sapiens mRNA for myosin-I beta /cds=(65,3151) /g
 32836_at Cluster Incl. U56417:Human lysophosphatidic acid acyltransferase-alpha
 35798_at Cluster Incl. W25936:15b5 Homo sapiens cDNA /gb=W25936 /gi=1306059 /ug=
5 36977_at Cluster Incl. U39412:Homo sapiens alpha SNAP mRNA, complete cds /cds=(6
 32556_at Cluster Incl. X64044:H.sapiens mmRNA for large subunit of splicing fact
 1813_at Epidermal Growth Factor Receptor-Related Protein
 1726_at Dna Polymerase, Epsilon, Catalytic Subunit
 845_at U16031 /FEATURE= /DEFINITION=HSU16031 Human transcription factor IL-4 Sta
10 552_at U02570 /FEATURE= /DEFINITION=HSU02570 Human CDC42 GTPase-activating prote
 493_at U29171 /FEATURE= /DEFINITION=HSU29171 Human casein kinase I delta mRNA, c
 435_g_at X03473 /FEATURE=cds /DEFINITION=HSHIS10G Human gene for histone
 H1(0)
 388_at X80907 /FEATURE= /DEFINITION=HSPHOSINK H.sapiens mRNA for p85 beta subuni
15
 Metagene 64

 32117_at Cluster Incl. U51698:HSU51698 Homo sapiens cDNA /gb=U51698 /gi=1255268
 36498_at Cluster Incl. AI936759:wp69b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
20 41220_at Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete
 34858_at Cluster Incl. D79998:Human mRNA for KIAA0176 gene, partial cds /cds=(0,
 36121_at Cluster Incl. AB028988:Homo sapiens mRNA for KIAA1065 protein, complete
 36202_at Cluster Incl. S76965:protein kinase inhibitor [human, neuroblastoma cel
 1532_g_at U50535 /FEATURE= /DEFINITION=HSU50535 Human BRCA2 region, mRNA
25 sequenc
 355_s_at D38037 /FEATURE= /DEFINITION=HUMOTK4 Human mRNA for FK506-
 binding prote

 Metagene 65
30
 37860_at Cluster Incl. AL049942:Homo sapiens mRNA; cDNA DKFZp564F1422 (from
 clon
 38167_at Cluster Incl. AB020704:Homo sapiens mRNA for KIAA0897 protein, partial
 39583_at Cluster Incl. AF030435:Homo sapiens glioma amplified on chromosome 1 pr
35 40395_at Cluster Incl. AB007932:Homo sapiens mRNA for KIAA0463 protein, partial
 41099_at Cluster Incl. X84740:H.sapiens mRNA for DNA ligase III /cds=(333,3101)
 34276_at Cluster Incl. AB023197:Homo sapiens mRNA for KIAA0980 protein, partial
 40777_at Cluster Incl. X87838:H.sapiens mRNA for beta-catenin /cds=(214,2559) /g

Metagene 66

- 32993_s_at Cluster Incl. U70824:Human BLu protein (BLu) mRNA, complete cds /cds=
 32317_s_at Cluster Incl. U34804:Human thermostable phenol sulfotransferase (STP2
5 37437_at Cluster Incl. AB011162:Homo sapiens mRNA for KIAA0590 protein, complete
 39631_at Cluster Incl. U52100:Human XMP mRNA, complete cds /cds=(63,566) /gb=U52
 40325_at Cluster Incl. AB014460:Homo sapiens TSC2, NTHL1/NTH1 and
 SLC9A3R2/E3KAR
 41115_s_at Cluster Incl. AB018277:Homo sapiens mRNA for KIAA0734 protein, partia
10 41603_at Cluster Incl. U02609:Human transducin-like protein mRNA, complete cds /
 31804_f_at Cluster Incl. X78283:H.sapiens mRNA for aryl sulfotransferase (ST1A3)
 33269_at Cluster Incl. AB003723:Homo sapiens mRNA for GPII, complete cds /cds=(1
 34260_at Cluster Incl. AB014583:Homo sapiens mRNA for KIAA0683 protein, complete
 37982_at Cluster Incl. Z25821:H.sapiens gene for mitochondrial dodecenoyl-CoA de
15 32858_at Cluster Incl. AI341565:qq94g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 34841_at Cluster Incl. AC002544:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-
 35768_at Cluster Incl. AB014561:Homo sapiens mRNA for KIAA0661 protein, complete
 38798_s_at Cluster Incl. AI741833:wg29e04.x1 Homo sapiens cDNA, 3 end /clone=IM
 38813_at Cluster Incl. X75621:Homo sapiens TSC2 mRNA for tuberin /cds=(18,5441)
20 39184_at Cluster Incl. AI857469:wl57f04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39867_at Cluster Incl. S75463:P43=mitochondrial elongation factor homolog [human
 40956_at Cluster Incl. X90857:H.sapiens mRNA for -14 gene, containing globin reg
 1468_at U12595 /FEATURE= /DEFINITION=HSU12595 Human tumor necrosis factor type 1
 815_at U70987 /FEATURE= /DEFINITION=HSU70987 Human GAP binding protein p62dok (D
25 198_g_at U29656 /FEATURE= /DEFINITION=HSU29656 Human DR-nm23 mRNA,
 complete cds

Metagene 67

- 30** 31583_at Cluster Incl. X67247:H.sapiens rpS8 gene for ribosomal protein S8 /cds=
 31955_at Cluster Incl. X65923:H.sapiens fau mRNA /cds=(56,457) /gb=X65923 /gi=31
 34646_at Cluster Incl. Z25749:H.sapiens gene for ribosomal protein S7 /cds=(81,6
 39660_at Cluster Incl. AI309115:qo71a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40756_at Cluster Incl. AF081280:Homo sapiens nucleoplasmin-3 (NPM3) mRNA, comple
35 35635_at Cluster Incl. AL080202:Homo sapiens mRNA; cDNA DKFZp434F172 (from
 clone
 36027_at Cluster Incl. AA418779:zv98d05.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 38713_at Cluster Incl. Z99716:bK250D10.1 (sterol regulatory element binding tran
 39029_at Cluster Incl. U11861:Human G10 homolog (edg-2) mRNA, complete cds /cds=

- 40866_at Cluster Incl. AJ001258:Homo sapiens mRNA for NIPSNAP1 protein /cds=(254
 41235_at Cluster Incl. AL022312:dJ1104E15.2 (activating transcription factor 4 (
 41765_at Cluster Incl. AI541285:pec1.2-4.D10.r Homo sapiens cDNA, 5 end /clone_
 37730_at Cluster Incl. U22055:Human 100 kDa coactivator mRNA, complete cds /cds=
5 39120_at Cluster Incl. AA224832:nc33b06.s1 Homo sapiens cDNA /clone=IMAGE-100990
 1488_at L77886 /FEATURE= /DEFINITION=HUMPTPC Human protein tyrosine phosphatase
 1351_at U07695 /FEATURE= /DEFINITION=HSU07695 Human tyrosine kinase (HTK) mRNA,
 326_i_at Ribosomal Protein S20
- 10** Metagene 68
- 31599_f_at Cluster Incl. U10691:Human MAGE-6 antigen (MAGE6) gene, complete cds
 34575_f_at Cluster Incl. U10689:Human MAGE-5a antigen (MAGE5a) gene, complete cd
 33517_f_at Cluster Incl. U03735:Human MAGE-3 antigen (MAGE-3) gene, complete cds
15 33518_f_at Cluster Incl. L18920:Human MAGE-2 gene exons 1-4, complete cds /cds=(
 36284_at Cluster Incl. Y12642:H.sapiens E48 gene /cds=(24,410) /gb=Y12642 /gi=27
 37160_at Cluster Incl. M19888:Human small proline rich protein (spr1) mRNA, clon
 37473_at Cluster Incl. AF061812:Homo sapiens keratin 16 (KRT16A) mRNA, complete
 38489_at Cluster Incl. M60047:Human heparin binding protein (HBp17) mRNA, comple
20 40309_at Cluster Incl. X66839:H.sapiens MaTu MN mRNA for p54/58N protein /cds=(4
 41469_at Cluster Incl. L10343:Humalaifin gene, complete cds /cds=(516,869) /gb=
 39015_f_at Cluster Incl. L42611:Homo sapiens keratin 6 isoform K6e (KRT6E) mRNA,
 39016_r_at Cluster Incl. L42611:Homo sapiens keratin 6 isoform K6e (KRT6E) mRNA,
 35315_at Cluster Incl. X02544:Human mRNA for alpha1-acid glycoprotein (orosomuco
25 36100_at Cluster Incl. AF022375:Homo sapiens vascular endothelial growth factor
 36933_at Cluster Incl. D87953:Human mRNA for RTP, complete cds /cds=(122,1306) /
 1953_at AF024710 /FEATURE= /DEFINITION=AF024710 Homo sapiens vascular endothelia
 1549_s_at U19557 /FEATURE= /DEFINITION=HSU19557 Human squamous cell carcinoma
 an
30 601_s_at M28439 /FEATURE=cds /DEFINITION=HUMKER16A8 Human keratin type 16
 gene,
- Metagene 69
- 35** 36391_at Cluster Incl. AF048730:Homo sapiens cyclin T1 mRNA, complete cds /cds=(
 35436_at Cluster Incl. L06147:Human (clone SY11) golgin-95 mRNA, complete cds /c
 37508_f_at Cluster Incl. AA675900:g02504r Homo sapiens cDNA, 5 end /clone=g0250
 40645_at Cluster Incl. L33801:Human protein kinase mRNA, complete cds /cds=(39,1
 40725_at Cluster Incl. AF047438:Homo sapiens GOS28/P28 protein mRNA, complete cd

- 34273_at Cluster Incl. AI267373:aq64c09.x1 Homo sapiens cDNA /clone=IMAGE-203569
 35240_at Cluster Incl. W28983:54f11 Homo sapiens cDNA /gb=W28983 /gi=1308931 /ug
 37947_at Cluster Incl. D26362:Human mRNA for KIAA0043 gene, complete cds /cds=(1
 41185_f_at Cluster Incl. AI971724:wr07a04.x1 Homo sapiens cDNA, 3 end /clone=IM
 5 32154_at Cluster Incl. M36711:Human sequence-specific DNA-binding protein (AP-2)
 32800_at Cluster Incl. U66306:Human retinoid X receptor alpha mRNA, 3 UTR, parti
 36210_g_at Cluster Incl. S78771:NAT=CpG island-associated gene [human, mRNA, 174
 39844_at Cluster Incl. AI806379:wf27b10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41591_at Cluster Incl. AI652978:wb42a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 10 32509_at Cluster Incl. AI307607:tb15h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 1602_at L33881 /FEATURE= /DEFINITION=HUMPKCI Human protein kinase C iota isoform
 1253_at L33801 /FEATURE= /DEFINITION=HUMGLSYKIN Human protein kinase mRNA,
 compl
 1017_at U73737 /FEATURE=mRNA /DEFINITION=HUMMSH06 Human hMSH6 gene, exons 6-
 15 10 a
- Metagene 70
- 31505_at Cluster Incl. Z28407:H.sapiens mRNA for ribosomal protein L8 /cds=(43,8
 20 31708_at Cluster Incl. L05095:Homo sapiens ribosomal protein L30 mRNA, complete
 34472_at Cluster Incl. AB012911:Homo sapiens mRNA for Frizzled-6, complete cds /
 39953_i_at Cluster Incl. AB014528:Homo sapiens mRNA for KIAA0628 protein, comple
 40353_at Cluster Incl. AL049962:Homo sapiens mRNA; cDNA DKFZp564P0823 (from
 clon
 25 41604_at Cluster Incl. U79297:Human clone 23589 mRNA sequence /cds=UNKNOWN
 /gb=U
 32697_at Cluster Incl. AF042729:Homo sapiens lithium-sensitive myo-inositol mono
 33761_s_at Cluster Incl. AB007962:Homo sapiens mRNA, chromosome 1 specific trans
 34743_at Cluster Incl. D63481:Human mRNA for KIAA0147 gene, partial cds /cds=(0,
 30 36858_at Cluster Incl. D25218:Human mRNA for KIAA0112 gene, partial cds /cds=(0,
 37640_at Cluster Incl. M31642:Human hypoxanthine phosphoribosyltransferase (HPRT
 37948_at Cluster Incl. J05682:Human subunit C of V-ATPase (vat C) mRNA, 3 end /
 38283_at Cluster Incl. AB007619:Homo sapiens mRNA for EBAG9, complete cds /cds=(
 38306_at Cluster Incl. AA477576:zu44b03.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 35 39035_at Cluster Incl. AF006010:Human progesterin induced protein (DD5) mRNA, comp
 39036_g_at Cluster Incl. AF006010:Human progesterin induced protein (DD5) mRNA, co
 32173_at Cluster Incl. X95384:Homo sapiens mRNA for translational inhibitor prot
 32255_i_at Cluster Incl. U40705:Homo sapiens telomeric repeat binding factor (TR
 33368_at Cluster Incl. X76040:H.sapiens mRNA for Lon protease-like protein /cds=

	33877_s_at	Cluster Incl. AB028990:Homo sapiens mRNA for KIAA1067 protein, partia
	35819_at	Cluster Incl. X06994:Human mRNA for cytochrome c1 /cds=(8,985) /gb=X069
	35839_at	Cluster Incl. D78130:Homo sapiens mRNA for squalene epoxidase, complete
	36145_at	Cluster Incl. U51586:Human siah binding protein 1 (SiahBP1) mRNA, parti
5	37673_at	Cluster Incl. X96586:H.sapiens mRNA for FAN protein /cds=(12,2765) /gb=
	38114_at	Cluster Incl. D38551:Human mRNA for KIAA0078 gene, complete cds /cds=(1
	38472_at	Cluster Incl. D63477:Human mRNA for KIAA0143 gene, partial cds /cds=(0,
	40200_at	Cluster Incl. M64673:Human heat shock factor 1 (TCF5) mRNA, complete cd
	41503_at	Cluster Incl. AB020661:Homo sapiens mRNA for KIAA0854 protein, complete
10	1160_at J04444	/FEATURE=cds /DEFINITION=HUMCYC1A Human cytochrome c-1 gene, comp
	160043_at	X66087 /FEATURE=cds /DEFINITION=HSAMYB2 H.sapiens a-myb mRNA
	/NOTE=rep	
	Metagene 71	
15		
	31382_f_at	Cluster Incl. AF016492:Homo sapiens UDP-glucuronosyltransferase 2B mR
	33068_f_at	Cluster Incl. U08854:Human UDP glucuronosyltransferase precursor (UGT
	34084_at	Cluster Incl. Z28339:H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-red
	35599_at	Cluster Incl. X62250:H.sapiens mRNA for liver glycine methyltransferase
20	34050_at	Cluster Incl. AC003034:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-
	37430_at	Cluster Incl. U78294:Homo sapiens 15S-lipoxygenase mRNA, complete cds /
	39248_at	Cluster Incl. N74607:za55a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	39249_at	Cluster Incl. AB001325:Human AQP3 gene for aquaporine 3 (water channel)
	41377_f_at	Cluster Incl. J05428:Human 3,4-catechol estrogen UDP-glucuronosyltran
25	41399_at	Cluster Incl. AB029034:Homo sapiens mRNA for KIAA1111 protein, partial
	41648_at	Cluster Incl. X78706:H.sapiens mRNA for carnitine acetyltransferase /cd
	31841_at	Cluster Incl. M94151:Human cadherin-associated protein-related (cap-r)
	33332_at	Cluster Incl. Z93241:dJ222E13.1a.1 (C-terminal part of novel protein dJ
	33699_at	Cluster Incl. M18667:Human pepsinogen C gene /cds=(73,1230) /gb=M18667
30	35721_at	Cluster Incl. M38180:Human 3-beta-hydroxysteroid dehydrogenase/delta-5-
	37276_at	Cluster Incl. U51903:Human RasGAP-related protein (IQGAP2) mRNA, comple
	37540_at	Cluster Incl. X69089:H.sapiens mRNA for skeletal muscle 165kD protein /
	38642_at	Cluster Incl. Y10183:H.sapiens mRNA for MEMD protein /cds=(0,1748) /gb=
	40415_at	Cluster Incl. X14813:Human liver mRNA for 3-oxoacyl-CoA thiolase /cds=(
35	33421_s_at	Cluster Incl. AB016247:Homo sapiens mRNA for sterol-C5-desaturase, co
	35345_at	Cluster Incl. X83618:H.sapiens mRNA for 3-hydroxy-3-methylglutaryl coen
	40201_at	Cluster Incl. M76180:Human aromatic amino acid decarboxylase (ddc) mRNA
	1647_at U51903	/FEATURE= /DEFINITION=HSU51903 Human RasGAP-related protein (IQGA
	1348_s_at	S79219 /FEATURE= /DEFINITION=S79219 metastasis-associated gene [human,

928_at L02785 /FEATURE= /DEFINITION=HUMDRA Homo sapiens colon mucosa-associated

217_at S39329 /FEATURE= /DEFINITION=S39329 glandular kallikrein-1 {alternatively

Metagene 72

5

37111_g_at Cluster Incl. AB012229:Homo sapiens gene for fructose-6-phosphate,2-k

41864_at Cluster Incl. AF052181:Homo sapiens clone 24790 mRNA sequence /cds=UNKN

34398_at Cluster Incl. D86956:Human mRNA for KIAA0201 gene, complete cds /cds=(3

10 Metagene 73

37882_at Cluster Incl. X63468:H.sapiens mRNA for transcription factor TFIIIE alph

38161_at Cluster Incl. Y09022:H.sapiens mRNA for Not56-like protein /cds=(31,134

37920_at Cluster Incl. U70370:Human hindlimb expressed homeobox protein backfoot

15 40414_at Cluster Incl. X59303:Human G7a mRNA for valyl-tRNA synthetase /cds=(219

41732_at Cluster Incl. AA310786:EST181572 Homo sapiens cDNA, 5 end /clone=ATCC-

32203_at Cluster Incl. AA160708:zo72c02.r1 Homo sapiens cDNA, 5 end /clone=IMAG

32848_at Cluster Incl. AF020736:Homo sapiens ATPase homolog mRNA, complete cds /

36178_at Cluster Incl. U23143:Human mitochondrial serine hydroxymethyltransferas

20 38808_at Cluster Incl. D64154:Human mRNA for Mr 110,000 antigen, complete cds /c

33215_g_at Cluster Incl. Y11681:Homo sapiens mRNA for mitochondrial ribosomal pr

Metagene 74

25 38498_at Cluster Incl. Z99916:Human DNA sequence from clone 221G9 on chromosome

40332_at Cluster Incl. AF109134:Homo sapiens 7-60 mRNA, complete cds /cds=(205,2

36028_at Cluster Incl. U45285:Human specific 116-kDa vacuolar proton pump subuni

36036_at Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /cds

36834_at Cluster Incl. AL080058:Homo sapiens mRNA; cDNA DKFZp564G202 (from

30 clone

32533_s_at Cluster Incl. AF054825:Homo sapiens VAMP5 mRNA, complete cds /cds=(57

1003_s_at X68149 /FEATURE=cds /DEFINITION=HSBLR1A Homo sapiens BLR1 gene for
Bur

35 Metagene 75

31510_s_at Cluster Incl. Z48950:H.sapiens hH3.3B gene for histone H3.3 /cds=(10,

31932_f_at Cluster Incl. M90357:Human basic transcription factor 3a (BTF3a) gene

32655_s_at Cluster Incl. X87613:H.sapiens mRNA for skeletal muscle abundant prot

- 38252_s_at Cluster Incl. U84007:Human glycogen debranching enzyme isoform 1 (AGL
38695_at Cluster Incl. AA203303:zx55b01.r1 Homo sapiens cDNA, 5' end /clone=IMAG
39435_at Cluster Incl. D45333:HUMHG7879 Homo sapiens cDNA /gb=D45333
/gi=1136736
- 5** 40815_g_at Cluster Incl. L40586:Homo sapiens iduronate-2-sulphatase (IDS) mRNA,
41155_at Cluster Incl. U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=(4
32776_at Cluster Incl. M35416:Human GTP-binding protein (RALB) mRNA, complete cd
35808_at Cluster Incl. AL031681:dJ862K6.2.2 (splicing factor, arginine/serine-ri
37292_at Cluster Incl. D83785:Human mRNA for KIAA0200 gene, complete cds /cds=(2
- 10** 38431_at Cluster Incl. U09759:Human protein kinase (JNK2) mRNA, complete cds /cd
39517_at Cluster Incl. AF035313:Homo sapiens clone 23851 mRNA sequence /cds=UNKN
40966_at Cluster Incl. AF099989:Homo sapiens Ste-20 related kinase SPAK mRNA, co
41547_at Cluster Incl. AF047472:Homo sapiens spleen mitotic checkpoint BUB3 (BUB
2085_s_at D14705 /FEATURE= /DEFINITION=HUMALPHAC Human mRNA for alpha-
- 15** catenin, c
2069_s_at L23805 /FEATURE= /DEFINITION=HUMCATENIN Human alpha1(E)-catenin
mRNA,
1675_at M23379 /FEATURE= /DEFINITION=HUMGAPA Human GTPase-activating protein ras
1467_at U12535 /FEATURE= /DEFINITION=HSU12535 Human epidermal growth factor rece
- 20** 1238_at U09759 /FEATURE= /DEFINITION=HSU09759 Human protein kinase (JNK2) mRNA,
376_at AB000220 /FEATURE= /DEFINITION=AB000220 Homo sapiens mRNA for semaphorin
324_f_at Transcription Factor Btf3b
- Metagene 76
- 25**
- 33636_at Cluster Incl. U87459:Human autoimmunogenic cancer/testis antigen NY-ESO
39234_at Cluster Incl. AL050131:Homo sapiens mRNA; cDNA DKFZp586I111 (from clone
34280_at Cluster Incl. Y09765:Homo sapiens mRNA for putative GABA receptor epsil
37281_at Cluster Incl. D87071:Human mRNA for KIAA0233 gene, complete cds /cds=(2
- 30** 37977_at Cluster Incl. AI138834:qe04b02.x1 Homo sapiens cDNA, 3' end /clone=IMAG
41189_at Cluster Incl. Y09392:H.sapiens mRNA for WSL-LR, WSL-S1 and WSL-S2 prote
37351_at Cluster Incl. X90858:H.sapiens mRNA for uridine phosphorylase /cds=(352
37652_at Cluster Incl. AB002328:Human mRNA for KIAA0330 gene, partial cds /cds=(
38735_at Cluster Incl. AB011085:Homo sapiens mRNA for KIAA0513 protein, complete
- 35** 39891_at Cluster Incl. AI246730:qk40b01.x1 Homo sapiens cDNA, 3' end /clone=IMAG
576_at M93718 /FEATURE= /DEFINITION=HUMNIOXSYN Human nitric oxide synthase
mRNA,
545_g_at S76638 /FEATURE= /DEFINITION=S76638 p50-NF-kappa B homolog [human,
peri

Metagene 77

- 34462_at Cluster Incl. U38254:Human amiloride sensitive sodium channel delta sub
- 5 38177_at Cluster Incl. AJ001015:Homo sapiens mRNA encoding RAMP2 /cds=(68,595) /
- 33277_at Cluster Incl. AB028996:Homo sapiens mRNA for KIAA1073 protein, complete
- 34690_at Cluster Incl. U66616:Human SWI/SNF complex 170 KDa subunit (BAF170) mRN
- 40047_at Cluster Incl. AF077599:Homo sapiens hypothetical SBBI03 protein mRNA, c
- 33180_at Cluster Incl. U68111:Human protein phosphatase inhibitor 2 (PPP1R2) gen
- 10 1496_at M34668 /FEATURE= /DEFINITION=HUMPTPAAA Human protein tyrosine phosphatas
- 111_at Y08200 /FEATURE= /DEFINITION=HSRABGTRA Homo sapiens mRNA for rab
- geranylg

Metagene 78

- 15 32378_at Cluster Incl. M26252:Human TCB gene encoding cytosolic thyroid hormone-
- 39214_at Cluster Incl. U52111:plexin related protein /cds=(0,1418) /gb=U52111 /g
- 38324_at Cluster Incl. AD000684:Homo sapiens DNA from chromosome 19-cosmid R3087
- 40872_at Cluster Incl. T57872:yb19b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
- 20 41724_at Cluster Incl. X81817:H.sapiens BAP31 mRNA /cds=(73,813) /gb=X81817 /gi=
- 33856_at Cluster Incl. Y13374:Homo sapiens mRNA for putatively prenylated protei
- 34880_at Cluster Incl. AC002115:Human DNA from overlapping chromosome 19 cosmids
- 35274_at Cluster Incl. Y12226:H.sapiens mRNA for gamma-adaptin /cds=(28,2505) /g
- 35769_at Cluster Incl. AJ011001:Homo sapiens mRNA for TM7XN1 protein /cds=(316,2
- 25 36138_at Cluster Incl. X04106:Human mRNA for calcium dependent protease (small s
- 39088_at Cluster Incl. Y18007:Homo sapiens mRNA for putative seven transmembrane
- 39122_at Cluster Incl. K03515:Human neuroleukin mRNA, complete cds /cds=(15,1691
- 32566_at Cluster Incl. AA165701:zo75g08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 323_at Serine Kinase Psk-H1
- 30 160037_at Z48482 /FEATURE=cds /DEFINITION=HSMMPM2 H.sapiens mRNA for
- membrane-ty

Metagene 79

- 35 32444_at Cluster Incl. X69392:H.sapiens mRNA for ribosomal protein L26 /cds=(6,4
- 41696_at Cluster Incl. AI620381:tu94d05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 34230_r_at Cluster Incl. D84454:Human mRNA for UDP-galactose translocator, compl
- 36986_at Cluster Incl. AL031295:Human DNA sequence from clone 886K2 on chromosom

Metagene 80

- 31575_f_at Cluster Incl. M14087:Human HL14 gene encoding beta-galactoside-bindin
 35512_at Cluster Incl. AC005764:Homo sapiens chromosome 19, cosmid R31343 /cds=(
5 34674_at Cluster Incl. X58079:Human mRNA for S100 alpha protein /cds=(113,397) /
 39329_at Cluster Incl. X15804:Human mRNA for alpha-actinin /cds=(198,2876) /gb=X
 32182_at Cluster Incl. AB023182:Homo sapiens mRNA for KIAA0965 protein, partial

Metagene 81

10

- 37877_at Cluster Incl. AL050269:Homo sapiens mRNA; cDNA DKFZp564C103 (from
 clone
 39569_at Cluster Incl. U72849:untitled /cds=(98,6199) /gb=U72849 /gi=4097997 /ug
 39643_at Cluster Incl. U94703:Homo sapiens mitochondrial DNA polymerase accessor
15 40758_at Cluster Incl. X81788:Homo sapiens ICT1 (alias DS-1) mRNA /cds=(2,622) /
 34695_at Cluster Incl. AI816724:wj43c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 35630_at Cluster Incl. X87342:H.sapiens mRNA for human giant larvae homolog /cds
 35710_s_at Cluster Incl. U95006:Human D9 splice variant A mRNA, complete cds /cd
 38260_at Cluster Incl. AL050306:Human DNA sequence from clone 475B7 on chromosom
20 40451_at Cluster Incl. AL080203:Homo sapiens mRNA; cDNA DKFZp434F222 (from
 clone
 40465_at Cluster Incl. AF026402:Homo sapiens U5 snRNP 100 kD protein mRNA, compl
 32757_at Cluster Incl. U84720:Homo sapiens mRNA export protein (RAE1) mRNA, comp
 33904_at Cluster Incl. AB000714:Homo sapiens hRVP1 mRNA for RVP1, complete cds /
25 34885_at Cluster Incl. AJ002308:Homo sapiens mRNA for synaptogyrin 2 /cds=(29,70
 36602_at Cluster Incl. D21064:Human mRNA for KIAA0123 gene, partial cds /cds=(0,
 37766_s_at Cluster Incl. AF035309:Homo sapiens clone 23598 mRNA, complete cds /c
 1746_s_at Tumor Necrosis Factor Receptor 2 Associated Protein Trap3
 956_at Tubulin, Beta 2

30

Metagene 82

- 39966_at Cluster Incl. AF059274:Homo sapiens neuroglycan C mRNA, complete cds /c
 31885_at Cluster Incl. M64572:Human protein tyrosine phosphatase mRNA, complete
35 34213_at Cluster Incl. AB020676:Homo sapiens mRNA for KIAA0869 protein, partial
 40537_at Cluster Incl. AB018284:Homo sapiens mRNA for KIAA0741 protein, complete

Metagene 83

- 34563_at Cluster Incl. D26361:Human mRNA for KIAA0042 gene, complete cds /cds=(4
 38933_at Cluster Incl. AL021366:cICK0721Q.3 (Kinesin related protein) /cds=(163,
 39677_at Cluster Incl. D80008:Human mRNA for KIAA0186 gene, complete cds /cds=(9
 40690_at Cluster Incl. X54942:H.sapiens ckshs2 mRNA for Cks1 protein homologue /
5 40726_at Cluster Incl. U37426:Human kinesin-like spindle protein HKSP (HKSP) mRN
 41403_at Cluster Incl. AI032612:ow17e07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32120_at Cluster Incl. AF063308:Homo sapiens coiled-coil related protein DEEPEST
 34736_at Cluster Incl. M25753:Human cyclin B mRNA, 3 end /cds=UNKNOWN
 /gb=M2575
- 10** 35699_at Cluster Incl. AF053306:Homo sapiens mitotic checkpoint kinase Mad3L (MA
 35995_at Cluster Incl. AF067656:Homo sapiens ZW10 interactor Zwint mRNA, complet
 36813_at Cluster Incl. U96131:Homo sapiens HPV16 E1 protein binding protein mRNA
 36839_at Cluster Incl. U77949:Human Cdc6-related protein (HsCDC6) mRNA, complete
 37985_at Cluster Incl. L37747:Homo sapiens lamin B1 gene /cds=(340,2100) /gb=L37
- 15** 38675_at Cluster Incl. AI087268:oz77e01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40117_at Cluster Incl. D84557:Homo sapiens mRNA for HsMcm6, complete cds /cds=(6
 40145_at Cluster Incl. AI375913:tc14c08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40407_at Cluster Incl. U28386:Human nuclear localization sequence receptor hSRP1
 37302_at Cluster Incl. U30872:Human mitotin mRNA, complete cds /cds=(72,9413) /g
- 20** 37686_s_at Cluster Incl. Y09008:H.sapiens mRNA for uracil-DNA glycosylase /cds=(
 38116_at Cluster Incl. D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(6
 38399_at Cluster Incl. AL034428:Human DNA sequence from clone 705D16 on chromoso
 38456_s_at Cluster Incl. AL049650:dJ734P14.2.2 (snRNP (small nuclear ribonucleop
 39109_at Cluster Incl. AB024704:Homo sapiens mRNA for fls353, complete cds /cds=
- 25** 41278_at Cluster Incl. AF041474:Homo sapiens BAF53a (BAF53a) mRNA, complete cds
 2003_s_at U28946 /FEATURE= /DEFINITION=HSU28946 Human G/T mismatch binding
 prote
- 1945_at M25753 /FEATURE=mRNA /DEFINITION=HUMCYCB Human cyclin B mRNA, 3 end
 1884_s_at M15796 /FEATURE= /DEFINITION=HUMCYL Human cyclin protein gene,
30 complet
- 1833_at M68520 /FEATURE= /DEFINITION=HUMCDC2A Human cdc2-related protein kinase
 1803_at X05360 /FEATURE=cds /DEFINITION=HSCDC2 Human CDC2 gene involved in cell
 1651_at U73379 /FEATURE= /DEFINITION=HSU73379 Human cyclin-selective ubiquitin c
 904_s_at LA7276 /FEATURE=UTR#1 /DEFINITION=HUMTOPATR Homo sapiens (cell
35 line HL-
- 527_at U14518 /FEATURE= /DEFINITION=HSU14518 Human centromere protein-A (CENP-A)
 419_at X65550 /FEATURE=exon#15 /DEFINITION=HSMKI67 H.sapiens mki67a mRNA (long t
 349_g_at D14678 /FEATURE= /DEFINITION=HUMMHCB Human mRNA for kinesin-
 related pro

	151_s_at	V00599 /FEATURE=mRNA /DEFINITION=HSTUB2 Human mRNA fragment
	encoding be	
	Metagene 84	
5		
	39288_at	Cluster Incl. AI951798:wx37f11.x1 Homo sapiens cDNA, 3' end /clone=IMAG
	39579_at	Cluster Incl. U89916:Homo sapiens claudin-10 (CLDN10) mRNA, complete cd
	35202_at	Cluster Incl. AF025654:Homo sapiens mRNA capping enzyme (HCE) mRNA, com
10	41725_at	Cluster Incl. U89896:Homo sapiens casein kinase I gamma 2 mRNA, complet
	33362_at	Cluster Incl. AF094521:Homo sapiens MSE55-related protein (UB1) mRNA, c
	34297_at	Cluster Incl. U87460:Human putative endothelin receptor type B-like pro
	39143_at	Cluster Incl. U08015:Human NF-ATc mRNA, complete cds /cds=(239,2389) /g
	1327_s_at	U67156 /FEATURE= /DEFINITION=HSU67156 Human mitogen-activated kinase
15	k	
	Metagene 85	
	31671_at	Cluster Incl. D82351:Human retropseudogene MSSP-1 DNA, complete cds /cd
20	33255_at	Cluster Incl. M97856:Homo sapiens histone-binding protein mRNA, complet
	35977_at	Cluster Incl. AB020315:Homo sapiens Dickkopf-1 (hdkk-1) gene /cds=(0,80
	35309_at	Cluster Incl. U20428:Human SNC19 mRNA sequence /cds=UNKNOWN
	/gb=U20428	
	36639_at	Cluster Incl. AF067853:Homo sapiens adenylosuccinate lyase (ADSL) mRNA,
25	754_s_at	D87002 /FEATURE=cds#1 /DEFINITION=D87002 Homo sapiens
	immunoglobulin la	
	Metagene 86	
30	34110_g_at	Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial
	33252_at	Cluster Incl. D38073:Human mRNA for hRlf beta subunit (p102 protein), c
	36069_at	Cluster Incl. AB007925:Homo sapiens mRNA for KIAA0456 protein, partial
	38987_at	Cluster Incl. AF052183:Homo sapiens clone 24804 mRNA sequence /cds=UNKN
	36607_at	Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=
35		
	Metagene 87	
	41205_at	Cluster Incl. U84404:Human E6-associated protein E6-AP/ubiquitin-protei
	33149_at	Cluster Incl. U73524:Human putative ATP/GTP-binding protein (HEAB) mRNA

Metagene 88

- 5 40614_at Cluster Incl. X75342:H.sapiens SHB mRNA /cds=(310,2100) /gb=X75342 /gi=
 40964_at Cluster Incl. Z46376:H.sapiens HK2 mRNA for hexokinase II /cds=(1490,42
 1257_s_at L42379 /FEATURE=mRNA /DEFINITION=HUMBPGF Homo sapiens bone-
 derived gro

Metagene 89

- 10 36692_at Cluster Incl. AF052099:Homo sapiens clone 23632 mRNA sequence /cds=UNKN
 37423_at Cluster Incl. U30246:Human bumetanide-sensitive Na-K-Cl cotransporter (
 38687_at Cluster Incl. AL050051:Homo sapiens mRNA; cDNA DKFZp566D193 (from
 clone
 15 39328_at Cluster Incl. M11058:Human 3-hydroxy-3-methylglutaryl coenzyme A reduct
 39691_at Cluster Incl. AB007960:chromosome 1 specific transcript KIAA0491 /cds=U
 40868_at Cluster Incl. AA442799:zv69b10.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 34848_at Cluster Incl. X69141:H.sapiens mRNA for squalene synthase /cds=(91,1344

20 Metagene 90

- 35922_at Cluster Incl. Y08982:H.sapiens mRNA for synaptonemal complex lateral el
 39951_at Cluster Incl. L20826:Human I-plastin mRNA, complete cds /cds=(97,1986)
 37959_at Cluster Incl. D63876:Human mRNA for KIAA0154 gene, partial cds /cds=(0,
 25 36951_at Cluster Incl. U39400:Human NOF1 mRNA, complete cds /cds=(13,513) /gb=U3
 38792_at Cluster Incl. AD001528:Homo sapiens spermidine aminopropyltransferase m
 1399_at L34587 /FEATURE= /DEFINITION=HUMRPIE Homo sapiens RNA polymerase II elon
 1361_at U40705 /FEATURE= /DEFINITION=HSU40705 Homo sapiens telomeric repeat bind
 948_s_at D63861 /FEATURE=expanded_cds /DEFINITION=D63861 Homo sapiens DNA
 30 for cy

Metagene 91

- 35 31496_g_at Cluster Incl. D63789:Homo sapiens DNA for SCM-1beta precursor, comple
 35132_at Cluster Incl. X98411:H.sapiens mRNA for myosin-IE /cds=(0,2348) /gb=X98
 32297_s_at Cluster Incl. AJ001684:Homo sapiens NKG2C gene /cds=(45,740) /gb=AJ00
 32370_at Cluster Incl. M57888:Human (clone lambda B34) cytotoxic T-lymphocyte-as
 34914_at Cluster Incl. U94778:Human PEST phosphatase interacting protein homolog
 34927_at Cluster Incl. M28826:Human thymocyte antigen CD1b mRNA, complete cds /c

	36314_at	Cluster Incl. U04806:Human FLT3/FLK2 ligand mRNA, complete cds /cds=(92
	37100_at	Cluster Incl. AJ008112:Homo sapiens mRNA for C17orf1 protein /cds=(39,1
	37121_at	Cluster Incl. S69115:granulocyte colony-stimulating factor induced gene
	38578_at	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA
5	38893_at	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosom
	38894_g_at	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromos
	39649_at	Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X7881
	41654_at	Cluster Incl. X02994:Human mRNA for adenosine deaminase (adenosine amin
	31901_at	Cluster Incl. AF044253:Homo sapiens potassium channel beta 2 subunit (H
10	33813_at	Cluster Incl. AI813532:wj83a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35149_at	Cluster Incl. AI865431:wk11h09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	36030_at	Cluster Incl. AL080214:Homo sapiens mRNA; cDNA DKFZp586I2223 (from clon
	36062_at	Cluster Incl. AF062075:Homo sapiens leupaxin mRNA, complete cds /cds=(9
	36493_at	Cluster Incl. M33552:Human lymphocyte-specific protein 1 (LSP1) mRNA, c
15	36902_at	Cluster Incl. X61587:H.sapiens rhoG mRNA for GTPase /cds=(129,704) /gb=
	37536_at	Cluster Incl. Z11697:Homo sapiens mRNA for HB15 /cds=(10,627) /gb=Z1169
	37541_at	Cluster Incl. U25956:Human P-selectin glycoprotein ligand (SELPLG) gene
	38276_at	Cluster Incl. U91616:Human I kappa B epsilon (IkBe) mRNA, complete cds
	39049_at	Cluster Incl. AJ243937:Homo sapiens mRNA for G18.1a and G18.1b proteins
20	39119_s_at	Cluster Incl. AA631972:fmfc39 Homo sapiens cDNA /clone=CR7-5 /gb=AA63
	41522_at	Cluster Incl. Z93096:Human DNA sequence from BAC 390B3 on chromosome 22
	33106_at	Cluster Incl. U22662:Human nuclear orphan receptor LXR-alpha mRNA, comp
	2019_s_at	M68892 /FEATURE= /DEFINITION=HUMINTB7 Human integrin beta-7 subunit mR
25	1583_at	M32315 /FEATURE= /DEFINITION=HUMNFR Human tumor necrosis factor receptor
	1326_at	U60519 /FEATURE= /DEFINITION=HSU60519 Human apoptotic cysteine protease
	1056_s_at	M90391 /FEATURE= /DEFINITION=HUMCHEMA Homo sapiens putative IL-16 prot
	512_at	U22662 /FEATURE= /DEFINITION=HSU22662 Human nuclear orphan receptor LXR-a
30	Metagene 92	
	36333_at	Cluster Incl. X57958:H.sapiens mRNA for ribosomal protein L7 /cds=(22,7
	38393_at	Cluster Incl. D87434:Human mRNA for KIAA0247 gene, complete cds /cds=(2
35	193_at	U21858 /FEATURE= /DEFINITION=HSU21858 Human transcriptional activation fa
	Metagene 93	
	36310_at	Cluster Incl. X86570:Homo sapiens mRNA for acidic hair keratin 1 /cds=(

- 36799_at Cluster Incl. L37882:Human frizzled gene product mRNA, complete cds /cd
 33782_r_at Cluster Incl. AA587372:nn82f03.s1 Homo sapiens cDNA, 3 end /clone=IM
 39406_at Cluster Incl. U50330:Human procollagen C-proteinase (pCP-2) mRNA, compl
 35776_at Cluster Incl. AF064243:Homo sapiens intersectin short form mRNA, comple
5 36652_at Cluster Incl. J03824:Human uroporphyrinogen III synthase mRNA, complete
 39542_at Cluster Incl. AF059611:Homo sapiens nuclear matrix protein NRP/B (NRPB)
 1242_at U15655 /FEATURE= /DEFINITION=HSU15655 Human ets domain protein ERF mRNA,
 628_at L37882 /FEATURE= /DEFINITION=HUMFRIZ Human frizzled gene product mRNA, co
 160033_s_at NM_006297 /FEATURE=mRNA /DEFINITION=Homo sapiens X-ray repair
10 comple
- Metagene 94
- 31740_s_at Cluster Incl. AB008913:Homo sapiens mRNA for Pax-4, complete cds /cds
15 33583_r_at Cluster Incl. AA523313:ni41h09.s1 Homo sapiens cDNA, 3 end /clone=IM
 39395_at Cluster Incl. AA704137:ag47g01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 39700_at Cluster Incl. AI961929:wt39g02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32189_g_at Cluster Incl. M96980:Homo sapiens myelin transcription factor 1 (MTF1
 41293_at Cluster Incl. AI123710:oo16h01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
20 41340_at Cluster Incl. AA827795:od08a05.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 160020_at Z48481 /FEATURE=cds /DEFINITION=HSMMPM1 H.sapiens mRNA for
 membrane-ty
- Metagene 95
- 25**
- 32134_at Cluster Incl. AL050162:Homo sapiens mRNA; cDNA DKFZp586B2022 (from
 clon
 34739_at Cluster Incl. W26023:18c3 Homo sapiens cDNA /gb=W26023 /gi=1306308 /ug=
 35166_at Cluster Incl. D87343:Homo sapiens mRNA for DCRA, complete cds /cds=(239
30 36463_at Cluster Incl. AB020680:Homo sapiens mRNA for KIAA0873 protein, partial
 37991_at Cluster Incl. L38961:Human putative transmembrane protein precursor (B5
 39773_at Cluster Incl. W28235:43h8 Homo sapiens cDNA /gb=W28235 /gi=1308183 /ug=
 39784_at Cluster Incl. U26032:Human translation initiation factor eIF-2alpha mRN
 40865_at Cluster Incl. U51166:Human G/T mismatch-specific thymine DNA glycosylas
35 41122_at Cluster Incl. AB011173:Homo sapiens mRNA for KIAA0601 protein, partial
 32171_at Cluster Incl. AL080102:Homo sapiens mRNA; cDNA DKFZp564N1916 (from
 clon
 32857_at Cluster Incl. L13858:Human guanine nucleotide exchange factor mRNA, com
 35340_at Cluster Incl. AI819948:wj88e11.x1 Homo sapiens cDNA, 3 end /clone=IMAG

- 35838_at Cluster Incl. U90919:Human clones 23667 and 23775 zinc finger protein m
 37651_at Cluster Incl. D31888:Human mRNA for KIAA0071 gene, partial cds /cds=(0,
 38840_s_at Cluster Incl. L10678:Human profilin II mRNA, complete cds /cds=(13,43
 763_at AB001106 /FEATURE= /DEFINITION=AB001106 Homo sapiens mRNA for glia matura
- 5**
- Metagene 96
- 32969_r_at Cluster Incl. Y12661:H.sapiens vgf gene /cds=(212,2062) /gb=Y12661 /g
 39624_at Cluster Incl. D89078:Homo sapiens mRNA for leukotriene b4 receptor, com
10 40020_at Cluster Incl. AB011536:Homo sapiens mRNA for MEGF2, partial cds /cds=(0
 40862_i_at Cluster Incl. X15334:Human gene for creatine kinase B (EC 2.7.3.2) /c
 40863_r_at Cluster Incl. X15334:Human gene for creatine kinase B (EC 2.7.3.2) /c
 2046_at M21536 /FEATURE= /DEFINITION=HUMERG12 Human erg protein (ets-related gen
- 15**
- Metagene 97
- 37863_at Cluster Incl. J04076:Human early growth response 2 protein (EGR2) mRNA,
 38299_at Cluster Incl. X04430:Human IFN-beta 2a mRNA for interferon-beta-2 /cds=
 40448_at Cluster Incl. M92843:H.sapiens zinc finger transcriptional regulator mR
20 32786_at Cluster Incl. X51345:Human jun-B mRNA for JUN-B protein /cds=(253,1296)
 33439_at Cluster Incl. D15050:Human mRNA for transcription factor AREB6, complet
 36097_at Cluster Incl. M62831:Human transcription factor ETR101 mRNA, complete c
 36669_at Cluster Incl. L49169:Human G0S3 mRNA, complete cds /cds=(593,1609) /gb=
 36979_at Cluster Incl. M20681:Human glucose transporter-like protein-III (GLUT3)
25 37701_at Cluster Incl. L13463:Human helix-loop-helix basic phosphoprotein (G0S8)
 38772_at Cluster Incl. Y11307:H.sapiens CYR61 mRNA /cds=(223,1368) /gb=Y11307 /g
 32583_at Cluster Incl. J04111:Human c-jun proto oncogene (JUN), complete cds, cl
 33146_at Cluster Incl. L08246:Human myeloid cell differentiation protein (MCL1)
 2094_s_at K00650 /FEATURE=cds /DEFINITION=HUMFOS Human fos proto-oncogene (c-
30 fos
 1915_s_at V01512 /FEATURE=mRNA#1 /DEFINITION=HSCFOS Human cellular
 oncogene c-fos
 1916_s_at V01512 /FEATURE=mRNA#2 /DEFINITION=HSCFOS Human cellular
 oncogene c-fos
- 35**
- 1895_at J04111 /FEATURE=exon#1 /DEFINITION=HUMJUNA Human c-jun proto oncogene (J
 1776_at L24564 /FEATURE= /DEFINITION=HUMRAD Human Rad mRNA, complete cds
 1005_at X68277 /FEATURE=cds /DEFINITION=HSCL100 H.sapiens CL 100 mRNA for protei
 789_at X52541 /FEATURE=cds /DEFINITION=HSEGR1 Human mRNA for early growth respon
 277_at L08246 /FEATURE= /DEFINITION=HUMMCL1X Human myeloid cell differentiation

- 279_at L13740 /FEATURE= /DEFINITION=HUMTR3A Human TR3 orphan receptor mRNA, comp
- 280_g_at L13740 /FEATURE= /DEFINITION=HUMTR3A Human TR3 orphan receptor mRNA, co
- 5 190_at U12767 /FEATURE= /DEFINITION=HSU12767 Human mitogen induced nuclear orpha
- Metagene 98
- 10 31597_r_at Cluster Incl. L36055:Human 4E-binding protein 1 mRNA, complete cds /c
- 33642_s_at Cluster Incl. U17986:Human GABA/noradrenaline transporter mRNA, compl
- 35438_at Cluster Incl. X87852:H.sapiens mRNA for SEX gene /cds=(184,5799) /gb=X8
- 38965_at Cluster Incl. M55172:Human large aggregating cartilage proteoglycan cor
- 39207_r_at Cluster Incl. X17406:Human mRNA for cartilage specific proteoglycan /
- 35620_at Cluster Incl. AF043250:Homo sapiens mitochondrial outer membrane protei
- 15 39076_s_at Cluster Incl. AI991040:wu36b05.x1 Homo sapiens cDNA, 3 end /clone=IM
- 40195_at Cluster Incl. X14850:Human H2A.X mRNA encoding histone H2A.X /cds=(73,5
- 40619_at Cluster Incl. M91670:Human ubiquitin carrier protein (E2-EPF) mRNA, com
- 2023_g_at M77198 /FEATURE= /DEFINITION=HUMRPKB Human rac protein kinase beta mRN
- 20 1781_at M25269 /FEATURE= /DEFINITION=HUMELK1A Homo sapiens tyrosine kinase (ELK1
- 1590_s_at J00277 /FEATURE=cds /DEFINITION=HUMRASH Human (genomic clones lambda-[
- 1132_s_at L12060 /FEATURE=mRNA /DEFINITION=HUMRARG7A Homo sapiens retinoic acid
- 25 893_at M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier protein (E2
- 894_g_at M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier protein (
- 163_at U46461 /FEATURE= /DEFINITION=HSU46461 Human dishevelled homolog (DVL) mRN
- 30 Metagene 99
- 35221_at Cluster Incl. X91648:H.sapiens mRNA for pur alpha extended 3untranslate
- 38612_at Cluster Incl. M69023:Human globin gene /cds=UNKNOWN /gb=M69023
- 135 /gi=1831
- 38705_at Cluster Incl. AI310002:qo77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 39046_at Cluster Incl. AL049324:Homo sapiens mRNA; cDNA DKFZp564D246 (from clone
- 39431_at Cluster Incl. AJ132583:Homo sapiens mRNA for puromycin sensitive aminop

	39734_at	Cluster Incl. U10117:Human endothelial-monocyte activating polypeptide
	40063_at	Cluster Incl. U22897:Homo sapiens nuclear domain 10 protein (ndp52) mRN
	40797_at	Cluster Incl. AF009615:Homo sapiens ADAM10 (ADAM10) mRNA, complete cds
	41153_f_at	Cluster Incl. AF102803:untitled /cds=(2,2722) /gb=AF102803 /gi=409276
5	41156_g_at	Cluster Incl. U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=
	41196_at	Cluster Incl. L38951:Homo sapiens importin beta subunit mRNA, complete
	41768_at	Cluster Incl. M33336:Human cAMP-dependent protein kinase type I-alpha s
	32777_at	Cluster Incl. Y12478:H.sapiens mRNA for CHD5 protein /cds=(42,566) /gb=
	32778_at	Cluster Incl. D26070:Human mRNA for type 1 inositol 1,4,5-trisphosphate
10	32854_at	Cluster Incl. AB014596:Homo sapiens mRNA for KIAA0696 protein, partial
	35767_at	Cluster Incl. AI565760:tn20b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35845_at	Cluster Incl. AJ131245:Homo sapiens mRNA for Sec24 protein (Sec24B isof
	36975_at	Cluster Incl. W26659:34d2 Homo sapiens cDNA /gb=W26659 /gi=1307502 /ug=
	37007_at	Cluster Incl. U49188:Human placenta (Diff33) mRNA, complete cds /cds=(1
15	37363_at	Cluster Incl. AB007889:Homo sapiens KIAA0429 mRNA, complete cds /cds=(2
	37707_i_at	Cluster Incl. M81118:Human alcohol dehydrogenase chi polypeptide (ADH
	38070_at	Cluster Incl. AL080234:Homo sapiens mRNA; cDNA DKFZp586L081 (from clone
	38374_at	Cluster Incl. AF050110:Homo sapiens TGFb inducible early protein and ea
20	39160_at	Cluster Incl. D90086:Human pyruvate dehydrogenase (EC 1.2.4.1) beta sub
	39174_at	Cluster Incl. X77548:H. sapiens cDNA for RFG /cds=(76,1920) /gb=X77548
	39814_s_at	Cluster Incl. AI052724:oz27a12.x1 Homo sapiens cDNA, 3 end /clone=IM
	40203_at	Cluster Incl. AJ012375:Homo sapiens mRNA for SUI1 protein translation i
	41257_at	Cluster Incl. D16217:Human mRNA for calpastatin, complete cds /cds=(162
25	41277_at	Cluster Incl. AW021542:df25a06.y1 Homo sapiens cDNA, 5 end /clone=IMAG
	377_g_at	AB000220 /FEATURE= /DEFINITION=AB000220 Homo sapiens mRNA for semaphori
	224_at	S81439 /FEATURE= /DEFINITION=S81439 EGR alpha=early growth response gene
30	Metagene 100	
	35377_at	Cluster Incl. AL080159:Homo sapiens mRNA; cDNA DKFZp434M154 (from clone
	38203_at	Cluster Incl. U69883:Human calcium-activated potassium channel hSK1 (SK
35	37226_at	Cluster Incl. U15172:Homo sapiens BCL2/adenovirus E1B 19kD-interacting
	37576_at	Cluster Incl. U52969:Human PEP19 (PCP4) mRNA, complete cds /cds=(81,269
	Metagene 101	

31805_at	Cluster Incl. M64347:Human novel growth factor receptor mRNA, 3 cds /cd
37921_at	Cluster Incl. U61849:Human neuronal pentraxin 1 (NPTX1) mRNA, complete
Metagene 102	
5	
35585_at	Cluster Incl. X15675:Human pTR7 mRNA for repetitive sequence /cds=UNKNO
36417_s_at	Cluster Incl. AF035295:Homo sapiens clone 23623 mRNA, partial cds /cd
33487_at	Cluster Incl. D31628:Human gene for 4-hydroxyphenylpyruvic acid dioxyge
36691_at	Cluster Incl. X82224:H.sapiens mRNA for glutamine transaminase K./cds=(
10	39681_at Cluster Incl. AF060568:Homo sapiens promyelocytic leukemia zinc finger
33308_at	Cluster Incl. M15182:Human beta-glucuronidase mRNA, complete cds /cds=(
33708_at	Cluster Incl. AF045584:Homo sapiens PB39 mRNA, complete cds /cds=(76,17
37203_at	Cluster Incl. L07765:Human carboxylesterase mRNA, complete cds /cds=(67
39054_at	Cluster Incl. X08020:Human mRNA for glutathione S-transferase subunit 4
15	40501_s_at Cluster Incl. X73114:H.sapiens mRNA for slow MyBP-C /cds=(81,3452) /g
40503_at	Cluster Incl. X66276:H.sapiens mRNA for skeletal muscle C-protein /cds=
35771_at	Cluster Incl. AF049460:Homo sapiens nuclear DEAF-1 related transcriptio
35834_at	Cluster Incl. X59766:H.sapiens mRNA for Zn-alpha2-glycoprotein /cds=(10
1290_g_at	L02321 /FEATURE= /DEFINITION=HUMGSTM5 Human glutathione S-
20	transferase
556_s_at	M96233 /FEATURE=expanded_cds /DEFINITION=HUMGSTM4A Human
glutathione tr	
Metagene 103	
25	
34637_f_at	Cluster Incl. M12963:Human class I alcohol dehydrogenase (ADH1) alpha
36247_f_at	Cluster Incl. M12272:Homo sapiens alcohol dehydrogenase class I gamma
37122_at	Cluster Incl. AB005293:Homo sapiens mRNA for perilipin, complete cds /c
40657_r_at	Cluster Incl. H15814:yl28b07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
30	40658_r_at Cluster Incl. D45371:Human apM1 mRNA for GS3109 (novel adipose specif
35730_at	Cluster Incl. X03350:Human mRNA for alcohol dehydrogenase beta-1-subuni
38326_at	Cluster Incl. M69199:Human G0S2 protein gene, complete cds /cds=(160,47
41209_at	Cluster Incl. M15856:Human lipoprotein lipase mRNA, complete cds /cds=U
33902_at	Cluster Incl. L34041:Homo sapiens L-glycerol-3-phosphate-NAD oxidoreduc
35	37394_at Cluster Incl. J03507:Human complement protein component C7 mRNA, comple
37399_at	Cluster Incl. D17793:Human mRNA for KIAA0119 gene, complete cds /cds=(5
38430_at	Cluster Incl. AA128249:zl29d09.r1 Homo sapiens cDNA, 5 end /clone=IMAG
40282_s_at	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete
32542_at	Cluster Incl. AF063002:Homo sapiens LIM protein SLIMMER mRNA, complete

- 32552_at Cluster Incl. X00129:Human mRNA for retinol binding protein (RBP) /cds=
770_at D00632 /FEATURE= /DEFINITION=HUMGSHPXA Homo sapiens mRNA for glutathione
- Metagene 104
- 5**
- 33629_at Cluster Incl. AJ001982:Homo sapiens WWp2-like mRNA complete cds /cds=UN
36217_at Cluster Incl. Z35102:H.sapiens mRNA for Ndr protein kinase /cds=(595,19
40362_at Cluster Incl. X61498:H.sapiens mRNA for NF-kB subunit /cds=(163,2964) /
41404_at Cluster Incl. AJ010119:Homo sapiens mRNA for Ribosomal protein kinase B
10 41717_at Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (B
38661_at Cluster Incl. X75315:H.sapiens seb4B mRNA /cds=(0,693) /gb=X75315 /gi=4
40470_at Cluster Incl. D10523:Human mRNA for 2-oxoglutarate dehydrogenase; compl
40789_at Cluster Incl. U54645:Human adenylate kinase 2B (adk2b) gene, complete c
41168_at Cluster Incl. AF029750:Homo sapiens tapasin (NGS-17) mRNA, complete cds
15 35807_at Cluster Incl. M21186:Human neutrophil cytochrome b light chain p22 phag
39829_at Cluster Incl. AB016811:Homo sapiens mRNA for ADP ribosylation factor-li
2065_s_at L22473 /FEATURE= /DEFINITION=HUMBAXA Human Bax alpha mRNA,
complete cd
1997_s_at U19599 /FEATURE= /DEFINITION=HSU19599 Human (BAX delta) mRNA,
20 complete
1462_s_at M80397 /FEATURE= /DEFINITION=HUMDNAPOLC Human DNA polymerase
delta cat
794_at X62055 /FEATURE=cds /DEFINITION=HSPTP1C H.sapiens PTP1C mRNA for protein-
771_s_at D00749 /FEATURE=cds /DEFINITION=HUMCD7G3 Human T cell surface
25 antigen C
570_at M83221 /FEATURE= /DEFINITION=HUMIRELA Homo sapiens I-Rel mRNA, complete
c
544_at S76638 /FEATURE= /DEFINITION=S76638 p50-NF-kappa B homolog [human, periph
- 30** Metagene 105
- 39697_at Cluster Incl. U26726:Human 11-beta-hydroxysteroid dehydrogenase type 2
40147_at Cluster Incl. U18009:Human chromosome 17q21 mRNA clone LF113 /cds=(0,93
36126_at Cluster Incl. U18919:Human chromosome 17q12-21 mRNA, clone pOV-2, parti
35 36127_g_at Cluster Incl. U18919:Human chromosome 17q12-21 mRNA, clone pOV-2, par
40199_at Cluster Incl. M97676:Homo sapiens (region 7) homeobox protein (HOX7) mR
1162_g_at Guanine Nucleotide-Binding Protein Hsr1

Metagene 106

	41429_at	Cluster Incl. M65254:Protein phosphatase 2A 65 kDa regulatory subunit-b
	35997_g_at	Cluster Incl. X98261:H.sapiens mRNA for M-phase phosphoprotein, mpp5
	33908_at	Cluster Incl. X04366:Human mRNA for calcium activated neutral protease
5	Metagene 107	
	31684_at	Cluster Incl. M62896:Human lipocortin (LIP) 2 pseudogene mRNA, complete
	35039_at	Cluster Incl. D87466:Human mRNA for KIAA0276 gene, partial cds /cds=(0,
10	32051_at	Cluster Incl. AJ224875:Homo sapiens mRNA for putative glucosyltransfera
	36872_at	Cluster Incl. AL120559:DKFZp761B219_r1 Homo sapiens cDNA, 5 end /clone
	38967_at	Cluster Incl. AF054175:Homo sapiens mitochondrial proteolipid 68MP homo
	38981_at	Cluster Incl. AA203354:zx58b07.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	39391_at	Cluster Incl. AF052135:Homo sapiens clone 23625 mRNA sequence /cds=UNKN
15	39699_at	Cluster Incl. D28476:Human mRNA for KIAA0045 gene, complete cds /cds=(1
	41139_at	Cluster Incl. W26633:34b1 Homo sapiens cDNA /gb=W26633 /gi=1307476 /ug=
	41750_at	Cluster Incl. D49489:Human mRNA for protein disulfide isomerase-related
	32855_at	Cluster Incl. L00352:Human low density lipoprotein receptor gene /cds=(
	33389_at	Cluster Incl. U23942:Human lanosterol 14-demethylase cytochrome P450 (C
20	33420_g_at	Cluster Incl. U83857:Human Aac11 (aac11) mRNA, complete cds /cds=(77,
	33854_at	Cluster Incl. AA877795:nr10g08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	33875_at	Cluster Incl. AI547262:PN001_AH_H03.r Homo sapiens cDNA, 5 end /clone_
	34329_at	Cluster Incl. N25547:yx76e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	34370_at	Cluster Incl. X81198:H.sapiens mRNA (clone p5) for archain /cds=(78,149
25	35303_at	Cluster Incl. U96876:Homo sapiens insulin induced protein 1 (INSIG1) ge
	35805_at	Cluster Incl. AA447263:zw93f01.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	37037_at	Cluster Incl. M24486:Human prolyl 4-hydroxylase alpha subunit mRNA, com
	37696_at	Cluster Incl. L06328:Human voltage-dependent anion channel isoform 2 (V
	37697_s_at	Cluster Incl. L08666:Homo sapiens porin (por) mRNA, complete cds and
30	37736_at,	Cluster Incl. D13892:Human mRNA for carboxyl methyltransferase, complet
	37751_at	Cluster Incl. D87444:Human mRNA for KIAA0255 gene, complete cds /cds=(3
	38403_at	Cluster Incl. X77196:H.sapiens mRNA for lysosome-associated membrane pr
	38811_at	Cluster Incl. D82348:Homo sapiens mRNA for 5-aminoimidazole-4-carboxami
	39169_at	Cluster Incl. AF054184:Homo sapiens Sec61 gamma mRNA, complete cds /cds
35	40556_at	Cluster Incl. D42073:Human mRNA for reticulocalbin, complete cds /cds=(
	40901_at	Cluster Incl. U17989:Homo sapiens nuclear autoantigen GS2NA mRNA, compl
	41242_at	Cluster Incl. AB011004:Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosa
	32539_at	Cluster Incl. U51205:Human COP9 homolog (HCOP9) mRNA, complete cds /cds

- 1940_at M54968 /FEATURE= /DEFINITION=HUMKRASM Human K-ras oncogene protein mRNA,
- 949_s_at D78275 /FEATURE= /DEFINITION=D78275 Homo sapiens mRNA for proteasome su
- 5** 575_s_at M93036 /FEATURE=mRNA /DEFINITION=HUMGA7A08 Human (clone 21726) carcinom
- 549_at S80343 /FEATURE= /DEFINITION=S80343 ArgRS=arginyl-tRNA synthetase [human,
- 379_at AB006679 /FEATURE= /DEFINITION=AB006679 Homo sapiens mRNA for ATP binding
- 10** Metagene 108
- 34075_at Cluster Incl. AJ001019:Homo sapiens mRNA for RNF3A (DONG1) ring finger
- 41667_s_at Cluster Incl. AJ006068:Homo sapiens mRNA for dTDP-D-glucose 4,6-dehyd
- 31849_at Cluster Incl. AB011136:Homo sapiens mRNA for KIAA0564 protein, partial
- 15** 32144_at Cluster Incl. AL050135:Homo sapiens mRNA; cDNA DKFZp586K091 (from clone
- 41170_at Cluster Incl. AB014563:Homo sapiens mRNA for KIAA0663 protein, complete
- 41215_s_at Cluster Incl. D13891:Human mRNA for Id-2H, complete cds /cds=(96,500)
- 33885_at Cluster Incl. AB020714:Homo sapiens mRNA for KIAA0907 protein, complete
- 20** 34804_at Cluster Incl. AL049246:Homo sapiens mRNA; cDNA DKFZp564C053 (from clone
- 34813_at Cluster Incl. AL079283:Homo sapiens mRNA full-length insert cDNA clone
- 38105_at Cluster Incl. W26521:32g11 Homo sapiens cDNA /gb=W26521 /gi=1307382 /ug
- 38383_at Cluster Incl. U73338:Human methionine synthase mRNA, complete cds /cds=
- 25** 40946_at Cluster Incl. AI023044:ow65c01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- Metagene 109
- 31499_s_at Cluster Incl. X16863:Human Fc-gamma RIIB-1 cDNA for Fc-gamma receptor
- 30** 31593_at Cluster Incl. Z70200:H.sapiens gene for U5 snRNP-specific 200kD protein
- 33646_g_at Cluster Incl. X61094:H.sapiens RNA for GM2-activator protein (clone p
- 34172_s_at Cluster Incl. M99578:Human lymphocyte surface protein exons 1-5, comp
- 35402_at Cluster Incl. AF068868:Homo sapiens TNFR-related death receptor-6 (DR6)
- 35474_s_at Cluster Incl. Y15915:Homo sapiens mRNA for chimaeric transcript of co
- 35** 36770_at Cluster Incl. U18671:Human Stat2 gene, complete cds /cds=(57,2612) /gb=
- 37528_at Cluster Incl. U03109:Human aspartyl beta-hydroxylase mRNA, complete cds
- 39254_at Cluster Incl. AL050011:Homo sapiens mRNA; cDNA DKFZp564G013 (from clone
- 40696_at Cluster Incl. U50062:Homo sapiens RIP protein kinase mRNA, complete cds

- 32098_at Cluster Incl. M20777:Homo sapiens, alpha-2 (VI) collagen /cds=UNKNOWN /
- 34747_at Cluster Incl. X83535:H.sapiens mRNA for membrane-type matrix metallopro
- 40823_s_at Cluster Incl. U85430:Human transcription factor NFATx4 mRNA, complete
- 32146_s_at Cluster Incl. L07261:Human alpha adducin mRNA, partial cds including
- 5 35287_at Cluster Incl. AF046888:Homo sapiens proliferation inducing ligand APRIL
- 35339_at Cluster Incl. AI743606:wg51f08.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 37674_at Cluster Incl. Y00451:Human mRNA for 5-aminolevulinate synthase /cds=(83
- 38022_s_at Cluster Incl. Z54367:H.sapiens gene for plectin /cds=(0,14054) /gb=Z5
- 41291_at Cluster Incl. AC004528:Homo sapiens chromosome 19, cosmid R32184 /cds=(
- 10 41350_at Cluster Incl. M20776:Homo sapiens, alpha-1 (VI) collagen /cds=UNKNOWN /
- 41552_g_at Cluster Incl. AW044624:wy78c04.x1 Homo sapiens cDNA, 3' end /clone=IM
- 1984_s_at X69549 /FEATURE=cds /DEFINITION=HSRHO2 H.sapiens mRNA for rho
- GDP-diss
- 1986_at X74594 /FEATURE=cds /DEFINITION=HSRB2P130 H.sapiens mRNA for Rb2/p130 pr
- 15 1844_s_at L05624 /FEATURE= /DEFINITION=HUMMKK Homo sapiens MAP kinase
- kinase mRN
- 1856_at X75042 /FEATURE=cds /DEFINITION=HSRNAREL H.sapiens rel proto-oncogene mR
- 1794_at M92287 /FEATURE= /DEFINITION=HUMCYCD3A Homo sapiens cyclin D3 (CCND3)
- mR
- 20 1703_g_at S75174 /FEATURE= /DEFINITION=S75174 E2F-4=transcription factor [human,
- 1710_s_at U07804 /FEATURE= /DEFINITION=HSU07804 Human DNA topoisomerase I
- mRNA,
- 1457_at M64174 /FEATURE= /DEFINITION=HUMPTKJAK1 Human protein-tyrosine kinase (J
- 1321_s_at U43916 /FEATURE= /DEFINITION=HSU43916 Human tumor-associated
- 25 membrane
- 1267_at M55284 /FEATURE= /DEFINITION=HUMPKCL Human protein kinase C-L (PRKCL)
- mR
- 1189_at X85753 /FEATURE= /DEFINITION=HSCDK8 Homo sapiens mRNA for CDK8 protein k
- 1146_at Cd4 Antigen
- 30 1130_at L11284 /FEATURE= /DEFINITION=HUMMEK1NF Homosapiens ERK activator kinase
- 1045_s_at U33838 /FEATURE= /DEFINITION=HSU33838 Human NF-kappa-B p65delta3
- mRNA,
- 953_g_at Fk506-Binding Protein, Alt. Splice 2
- 957_at Arrestin, Beta 2
- 35 476_s_at U50079 /FEATURE= /DEFINITION=HSU50079 Human histone deacetylase HD1
- mRN
- 422_s_at X66867 /FEATURE=cds#2 /DEFINITION=HSMAXG H.sapiens max gene
- 201_s_at S82297 /FEATURE= /DEFINITION=S82297 beta 2-microglobulin {11bp deleted

- 160044_g_at NM_001098 /FEATURE=mRNA /DEFINITION=Homo sapiens aconitase 2, mitochondrion
- Metagene 110
- 5**
- 39219_at Cluster Incl. U20240:Human C/EBP gamma mRNA, complete cds /cds=(250,702
- 39230_at Cluster Incl. AL022318:bK150C2.2 (Phorbolin 3) /cds=(29,1177) /gb=AL022
- 40041_at Cluster Incl. AF017790:Homo sapiens retinoblastoma-associated protein H
- 40347_at Cluster Incl. AA913812:ol39a08.s1 Homo sapiens cDNA, 3' end /clone=IMAG
- 10** 40348_s_at Cluster Incl. W25866:14c12 Homo sapiens cDNA /gb=W25866 /gi=1305989 /
- 41632_at Cluster Incl. D38550:Human mRNA for KIAA0075 gene, partial cds /cds=(0,
- 32069_at Cluster Incl. AB014515:Homo sapiens mRNA for KIAA0615 protein, complete
- 34755_at Cluster Incl. AJ236876:Homo sapiens mRNA for poly(ADP-ribose) polymerase
- 35249_at Cluster Incl. AF091433:Homo sapiens cyclin E2 mRNA, complete cds /cds=(
- 15** 36863_at Cluster Incl. AF032862:Homo sapiens intracellular hyaluronic acid binding
- 36898_r_at Cluster Incl. X74331:H.sapiens mRNA for DNA primase (subunit p58) /cd
- 37174_at Cluster Incl. D14660:Human mRNA for KIAA0104 gene, complete cds /cds=(3
- 37971_at Cluster Incl. AL050089:Homo sapiens mRNA; cDNA DKFZp586E0518 (from
- clon
- 20** 32222_at Cluster Incl. AA152202:zl06a03.s1 Homo sapiens cDNA, 3' end /clone=IMAG
- 32767_at Cluster Incl. M74558:Human SIL mRNA, complete cds /cds=(380,4243) /gb=M
- 37305_at Cluster Incl. U61145:Human enhancer of zeste homolog 2 (EZH2) mRNA, com
- 37337_at Cluster Incl. AI803447:tc39g04.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 37758_s_at Cluster Incl. W28479:47d8 Homo sapiens cDNA /gb=W28479 /gi=1308427 /u
- 25** 38065_at Cluster Incl. X62534:H.sapiens HMG-2 mRNA /cds=(214,843) /gb=X62534 /gi
- 39092_at Cluster Incl. AW007731:wt68d11.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 40532_at Cluster Incl. U75285:Homo sapiens apoptosis inhibitor survivin gene, co
- 32617_at Cluster Incl. W74442:zd75e09.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-
- 1809_at AB003698 /FEATURE= /DEFINITION=AB003698 Homo sapiens mRNA for Cdc7-relat
- 30** 1782_s_at M31303 /FEATURE=mRNA /DEFINITION=HUMOP18A Human oncoprotein 18 (Op18)
- 1544_at U39817 /FEATURE= /DEFINITION=HSU39817 Human Bloom syndrome protein (BL
- 1265_g_at M25393 /FEATURE= /DEFINITION=HUMPTPASE Human protein tyrosine phosphatase
- 35** 1055_g_at M87339 /FEATURE= /DEFINITION=HUMACT1A Human replication factor C, 37-kDa
- 572_at M86699 /FEATURE= /DEFINITION=HUMTTK Human kinase (TTK) mRNA, complete cds

Metagene 111

	31737_at	Cluster Incl. J00068:Human adult skeletal muscle alpha-actin mRNA /cds=
	35042_at	Cluster Incl. L12398:Homo sapiens dopamine D4 receptor (DRD4) mRNA (D4.
5	32313_at	Cluster Incl. M12125:Human fibroblast muscle-type tropomyosin mRNA, com
	35917_at	Cluster Incl. W26631:34a8 Homo sapiens cDNA /gb=W26631 /gi=1307474 /ug=
	37147_at	Cluster Incl. AF020044:Homo sapiens lymphocyte secreted C-type lectin p
	41013_at	Cluster Incl. AL080114:Homo sapiens mRNA; cDNA DKFZp586M2022 (from
	clon	
10	31856_at	Cluster Incl. Z24680:H.sapiens garp gene mRNA, complete CDS /cds=(94,20
	32138_at	Cluster Incl. L07807:Human dynamin mRNA, alternative exons and complete
	34216_at	Cluster Incl. AA478904:zv20c05.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	35146_at	Cluster Incl. AB007836:Homo sapiens mRNA for Hic-5, partial cds /cds=(0
	35219_at	Cluster Incl. AL050202:Homo sapiens mRNA; cDNA DKFZp586E2023 (from
15	clon	
	36452_at	Cluster Incl. AB028952:Homo sapiens mRNA for KIAA1029 protein, complete
	36524_at	Cluster Incl. AB029035:Homo sapiens mRNA for KIAA1112 protein, partial
	38338_at	Cluster Incl. AI201108:qf69g07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	38351_at	Cluster Incl. AL050154:Homo sapiens mRNA; cDNA DKFZp586L0120 (from
20	clon	
	38636_at	Cluster Incl. AB003184:Homo sapiens mRNA for ISLR, complete cds /cds=(9
	39330_s_at	Cluster Incl. M95178:Human non-muscle alpha-actinin mRNA, complete cd
	32749_s_at	Cluster Incl. AL050396:Homo sapiens mRNA; cDNA DKFZp586K1720 (from cl
	32845_at	Cluster Incl. M85289:Human heparan sulfate proteoglycan (HSPG2) mRNA, c
25	33900_at	Cluster Incl. U76702:Homo sapiens follistatin-related protein FLRG (FLR
	33903_at	Cluster Incl. AB007144:Homo sapiens mRNA for ZIP-kinase, complete cds /
	34320_at	Cluster Incl. AL050224:Homo sapiens mRNA; cDNA DKFZp586L2123 (from
	clon	
	34802_at	Cluster Incl. X15882:Human mRNA for collagen VI alpha-2 C-terminal glob
30	35347_at	Cluster Incl. AF093119:Homo sapiens UPH1 (UPH1) mRNA, complete cds /cds
	35740_at	Cluster Incl. AL050138:Homo sapiens mRNA; cDNA DKFZp586M121 (from
	clon	
	36931_at	Cluster Incl. M95787:Human 22kDa smooth muscle protein (SM22) mRNA, com
	36993_at	Cluster Incl. M33210:Human colony stimulating factor 1 receptor (CSF1R)
35	37005_at	Cluster Incl. D28124:Human mRNA for unknown product, complete cds /cds=
	37028_at	Cluster Incl. U83981:Homo sapiens apoptosis associated protein (GADD34)
	37032_at	Cluster Incl. U08021:Human nicotinamide N-methyltransferase (NNMT) mRNA
	37375_at	Cluster Incl. AB014538:Homo sapiens mRNA for KIAA0638 protein, partial
	37408_at	Cluster Incl. AB014609:Homo sapiens mRNA for KIAA0709 protein, complete

- 39145_at Cluster Incl. J02854:Human 20-kDa myosin light chain (MLC-2) mRNA, comp
1771_s_at J03278 /FEATURE= /DEFINITION=HUMPDGFRA Human platelet-derived
growth f
- 5** Metagene 112
- 32905_s_at Cluster Incl. M30038:Human tryptase mRNA, complete cds /cds=(17,844)
35960_at Cluster Incl. AF031416:Homo sapiens Ikb kinase beta subunit mRNA, compl
41442_at Cluster Incl. AB010419:Homo sapiens mRNA for MTG8-related protein MTG16
- 10** 33321_r_at Cluster Incl. M33494:Homo sapiens tryptase-I gene, complete cds /cds=
38845_at Cluster Incl. R89044:ym99b08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
41484_r_at Cluster Incl. X56681:Human junD mRNA /cds=(174,1217) /gb=X56681 /gi=3
1337_s_at X06614 /FEATURE=cds /DEFINITION=HSRRA Human mRNA for receptor of
retin
- 15** 411_i_atX57351 /FEATURE=cds /DEFINITION=HS18D Human 1-8D gene from interferon-i
160041_at X79568 /FEATURE=cds /DEFINITION=HSBDP1 H.sapiens BDP1 mRNA for
protein
- Metagene 113
- 20**
- 39578_at Cluster Incl. W27191:23e6 Homo sapiens cDNA /gb=W27191 /gi=1306707 /ug=
40314_at Cluster Incl. AJ002309:Homo sapiens mRNA for synaptogyrin 3 /cds=(17,67
35242_at Cluster Incl. X66362:H.sapiens mRNA PCTAIRE-3 for serine/threonine prot
- 25** Metagene 114
- 32965_f_at Cluster Incl. W28645:52e8 Homo sapiens cDNA /gb=W28645 /gi=1308800 /u
39788_at Cluster Incl. X81889:H.sapiens mRNA for p0071 protein /cds=(141,3776) /
40422_at Cluster Incl. X16302:Human mRNA for insulin-like growth factor binding
- 30** 40861_at Cluster Incl. D14812:Human mRNA for KIAA0026 gene, complete cds /cds=(3
37030_at Cluster Incl. AB020694:Homo sapiens mRNA for KIAA0887 protein, partial
38067_at Cluster Incl. D86957:Human mRNA for KIAA0202 gene, partial cds /cds=(0,
1893_s_at Estrogen Receptor
1741_s_at S37730 /FEATURE=cds /DEFINITION=S37712S4 insulin-like growth factor bi
- 35** 1142_at Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 1
- Metagene 115
- 32647_at Cluster Incl. AF060902:Homo sapiens vesicle soluble NSF attachment prot

- 40515_at Cluster Incl. AF035280:Homo sapiens clone 23689 mRNA, complete cds /cds
 32801_at Cluster Incl. AB002315:Human mRNA for KIAA0317 gene, complete cds /cds=
 1154_at J02645 /FEATURE=mRNA /DEFINITION=HUMEIF2A Human translational initiation
- 5** Metagene 116
- 38505_at Cluster Incl. AL050151:Homo sapiens mRNA; cDNA DKFZp586J0720 (from clon
 38932_at Cluster Incl. M29580:Human zinc-finger protein 7 (ZFP7) mRNA, complete
 32059_at Cluster Incl. U79282:Human clone 23801 mRNA sequence /cds=UNKNOWN
10 /gb=U
 32142_at Cluster Incl. U26424:Human Ste20-like kinase (MST2) mRNA, complete cds
 33241_at Cluster Incl. AB014526:Homo sapiens mRNA for KIAA0626 protein, complete
 34192_at Cluster Incl. AB011104:Homo sapiens mRNA for KIAA0532 protein, partial
 38341_at Cluster Incl. AL079286:Homo sapiens mRNA full length insert cDNA clone
15 39427_at Cluster Incl. T79616:yd71e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 39706_at Cluster Incl. AB014536:Homo sapiens mRNA for KIAA0636 protein, complete
 40129_at Cluster Incl. U47077:Human DNA-dependent protein kinase catalytic subun
 32221_at Cluster Incl. AL050361:Homo sapiens mRNA; cDNA DKFZp564H0223 (from
 clon
20 32248_at Cluster Incl. AL045811:DKFZp434H166_r1 Homo sapiens cDNA, 5 end /clone
 34314_at Cluster Incl. X59543:Human mRNA for M1 subunit of ribonucleotide reduct
 34840_at Cluster Incl. AI700633:we38g03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 35290_at Cluster Incl. AL050081:Homo sapiens mRNA; cDNA DKFZp566J2146 (from clon
 36117_at Cluster Incl. L13616:Human focal adhesion kinase (FAK) mRNA, complete c
25 37698_at Cluster Incl. X97335:H.sapiens mRNA for kinase A anchor protein /cds=(1
 40198_at Cluster Incl. L06132:Human voltage-dependent anion channel isoform 1 (V
 32561_at Cluster Incl. D63480:Human mRNA for KIAA0146 gene, partial cds /cds=(0,
 32595_at Cluster Incl. U07231:Homo sapiens G-rich sequence factor-1 (GRSF-1) mRN
 1250_at U47077 /FEATURE= /DEFINITION=HSU47077 Homo sapiens DNA-dependent protein
30 142_at U75308 /FEATURE= /DEFINITION=HSU75308 Human TBP-associated factor (hTAFII
- Metagene 117
- 34223_at Cluster Incl. M59818:Human granulocyte colony-stimulating factor recept
35 41721_at Cluster Incl. AA658877:nt84c12.s1 Homo sapiens cDNA /clone=IMAGE-120520
 35360_at Cluster Incl. Y17711:Homo sapiens mRNA for atopy related autoantigen CA
 1317_at X70040 /FEATURE=cds /DEFINITION=HSRON H.sapiens RON mRNA for tyrosine ki
 596_s_at M59820 /FEATURE=mRNA /DEFINITION=HUMGCSFR3 Human granulocyte
 colony-sti

Metagene 118

- 31527_at Cluster Incl. X17206:Human mRNA for LLRep3 /cds=(240,905) /gb=X17206 /g
- 5** 33002_at Cluster Incl. AF047487:Homo sapiens Nck-2 (NCK2) mRNA, complete cds /cd
- 33468_at Cluster Incl. Z26317:H.sapiens mRNA for desmoglein 2 /cds=(11,3364) /gb
- 34478_at Cluster Incl. X79780:H.sapiens YPT3 mRNA /cds=(6,662) /gb=X79780 /gi=76
- 38219_at Cluster Incl. D10656:Human mRNA for CRK-II, complete cds /cds=(105,1019
- 39281_at Cluster Incl. AB002378:Human mRNA for KIAA0380 gene, complete cds /cds=
- 10** 41633_at Cluster Incl. AL050283:Homo sapiens mRNA; cDNA DKFZp586K0919 (from
clon
- 34691_f_at Cluster Incl. AF006087:Homo sapiens Arp2/3 protein complex subunit p2
- 34742_at Cluster Incl. Z23115:H.sapiens bcl-xL mRNA /cds=(134,835) /gb=Z23115 /g
- 35155_at Cluster Incl. AC005306:Homo sapiens chromosome 19, cosmid R27216 /cds=(
- 15** 39708_at Cluster Incl. L29277:Homo sapiens DNA-binding protein (APRF) mRNA, comp
- 40439_at Cluster Incl. AF047469:Homo sapiens arsenite translocating ATPase (ASNA
- 40514_at Cluster Incl. AF091085:Homo sapiens clone 638 unknown mRNA, complete se
- 40845_at Cluster Incl. U10324:Human nuclear factor NF90 mRNA, complete cds /cds=
- 34374_g_at Cluster Incl. Z97054:Human DNA sequence from PAC 339A18 on chromosome
- 20** 35806_at Cluster Incl. W26854:17b4 Homo sapiens cDNA /gb=W26854 /gi=1306217 /ug=
- 35812_at Cluster Incl. AJ133769:Homo sapiens mRNA for nuclear transport receptor
- 36151_at Cluster Incl. U60644:Human HU-K4 mRNA, complete cds /cds=(487,1800) /gb
- 36180_s_at Cluster Incl. X75346:H.sapiens mRNA for MAP kinase activated protein
- 38757_at Cluster Incl. U41745:Human PDGF associated protein mRNA, complete cds /
- 25** 39537_at Cluster Incl. X98248:H.sapiens mRNA for sortilin /cds=(21,2522) /gb=X98
- 41550_at Cluster Incl. AF091071:Homo sapiens clone 192 Rer1 mRNA, complete cds /
- 2067_f_at L22475 /FEATURE= /DEFINITION=HUMBAXG Human Bax gamma mRNA,
complete cd
- 2049_s_at M29039 /FEATURE=cds /DEFINITION=HUMJUNCAA Human transactivator
- 30** (jun-B)
- 2016_s_at M64241 /FEATURE= /DEFINITION=HUMQM Human Wilm s tumor-related
protein
- 1906_at Ras Inhibitor Inf
- 1826_at M12174 /FEATURE= /DEFINITION=HUMRHOA Human ras-related rho mRNA (clone 6
- 35** 1747_at AD000092 /FEATURE=cds#2 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro
- 1750_at AD000092 /FEATURE=cds#5 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro
- 1752_at AD000092 /FEATURE=cds#6 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro
- 1753_s_at AD000092 /FEATURE=cds#7 /DEFINITION=CH19HHR23 Homo sapiens DNA
from ch

- 1764_s_at D85131 /FEATURE= /DEFINITION=D85131 Homo sapiens mRNA for Myc-associat
- 918_at Atp-Binding Cassette Protein
- 835_at U41745 /FEATURE= /DEFINITION=HSU41745 Human PDGF associated protein mRNA,
- 5 612_s_at M19650 /FEATURE= /DEFINITION=HUMCNPDEA Human 2,3 -cyclic nucleotide 3
- 518_at U07132 /FEATURE= /DEFINITION=HSU07132 Human steroid hormone receptor Ner-
- 434_at X03473 /FEATURE=cds /DEFINITION=HSHIS10G Human gene for histone H1(0)
- 392_g_at X89416 /FEATURE=cds /DEFINITION=HSRNAPPP5 H.sapiens mRNA for
- 10 protein ph
- 146_at U81802 /FEATURE= /DEFINITION=HSU81802 Human PtdIns 4-kinase (PI4Kb) mRNA,
- 108_g_at Z95624 /FEATURE=cds /DEFINITION=HSU237H1 Human DNA sequence from cosmid
- 15 Metagene 119
- 38208_at Cluster Incl. AB021981:Homo sapiens mRNA for UDP-N-acetylglucosamine tr
- 37623_at Cluster Incl. X75918:H.sapiens mRNA for NOT /cds=(317,2113) /gb=X75918
- 39730_at Cluster Incl. X16416:Human c-abl mRNA encoding p150 protein /cds=(147,3
- 20 40281_at Cluster Incl. D63878:Human mRNA for KIAA0158 gene, complete cds /cds=(2
- 1635_at U07563 /FEATURE=Poly_A_Site#1 /DEFINITION=HSABLGR3 Human proto-oncogene
- 1636_g_at U07563 /FEATURE=Poly_A_Site#1 /DEFINITION=HSABLGR3 Human proto-oncogen
- 547_s_at S77154 /FEATURE= /DEFINITION=S77154 TINUR= NGFI-B/nur77 beta-type
- 25 trans
- Metagene 120
- 31477_at Cluster Incl. L08044:Human intestinal trefoil factor mRNA, complete cds
- 30 36432_at Cluster Incl. AL079298:Homo sapiens mRNA full length insert cDNA clone
- 37141_at Cluster Incl. U39840:Human hepatocyte nuclear factor-3 alpha (HNF-3 alp
- 32079_at Cluster Incl. AB014539:Homo sapiens mRNA for KIAA0639 protein, partial
- 33232_at Cluster Incl. AI017574:ou23f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 33730_at Cluster Incl. AF095448:Homo sapiens putative G protein-coupled receptor
- 35 35148_at Cluster Incl. AC005954:Homo sapiens chromosome 19, cosmid R28784 /cds=(
- 35676_at Cluster Incl. AF006386:Homo sapiens axonemal dynein light chain (hp28)
- 37897_s_at Cluster Incl. AI985964:wr79d08.x1 Homo sapiens cDNA, 3 end /clone=IM
- 38630_at Cluster Incl. AL080192:Homo sapiens mRNA; cDNA DKFZp434B102 (from clone

	39755_at	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome
	39756_g_at	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromoso
	40079_at	Cluster Incl. AA156240:zl50c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	40800_at	Cluster Incl. AI590869:tw88g03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
5	41126_at	Cluster Incl. AA978353:oq40b07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	32787_at	Cluster Incl. M34309:Human epidermal growth factor receptor (HER3) mRNA
	34775_at	Cluster Incl. AF065388:Homo sapiens tetraspan NET-1 mRNA, complete cds
	34862_at	Cluster Incl. AA005018:zh96a09.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	35371_at	Cluster Incl. M83822:Human beige-like protein (BGL) mRNA, partial cds /
10	35822_at	Cluster Incl. L15702:Human complement factor B mRNA, complete cds /cds=
	38390_at	Cluster Incl. Z34975:H.sapiens LDLC mRNA /cds=(95,2311) /gb=Z34975 /gi=
	38394_at	Cluster Incl. D42047:Human mRNA for KIAA0089 gene, partial cds /cds=(0,
	38459_g_at	Cluster Incl. L39945:Human cytochrome b5 (CYB5) gene /cds=(120,548) /
	38783_at	Cluster Incl. J05581:Human polymorphic epithelial mucin (PEM) mRNA, com
15	38784_g_at	Cluster Incl. J05581:Human polymorphic epithelial mucin (PEM) mRNA, c
	38785_at	Cluster Incl. X52228:Human mRNA for secreted epithelial tumour mucin an
	38827_at	Cluster Incl. AF038451:Homo sapiens secreted cement gland protein XAG-2
	40602_at	Cluster Incl. AF052178:Homo sapiens clone 24523 mRNA sequence /cds=UNKN
	41271_at	Cluster Incl. Y18483:Homo sapiens mRNA for SLC7A8 protein /cds=(730,233
20	41826_at	Cluster Incl. W28287:47f12 Homo sapiens cDNA /gb=W28287 /gi=1308442 /ug
	2011_s_at	U34584 /FEATURE= /DEFINITION=HSU34584 Human Bcl-2 interacting killer (
	1577_at	M23263 /FEATURE= /DEFINITION=HUMARB Human androgen receptor mRNA,
		comple
	1578_g_at	M23263 /FEATURE= /DEFINITION=HUMARB Human androgen receptor
25		mRNA, comp
	1585_at	M34309 /FEATURE= /DEFINITION=HUMHER3A Human epidermal growth factor rece
	1083_s_at	M35093 /FEATURE=cds /DEFINITION=HUMETMAGA Human secreted
		epithelial tu
	1020_s_at	U85611 /FEATURE= /DEFINITION=HSU85611 Human DNA-PK interaction
30		protein
	927_s_at	J05582 /FEATURE=mRNA /DEFINITION=HUMPANMU Human pancreatic
		mucin mRNA,
	700_s_at	Mucin 1, Epithelial, Alt. Splice 9
	573_at	M86826 /FEATURE= /DEFINITION=HUMIGFACID Human IGF binding protein
35		complex
		Metagene 121
	35941_f_at	Cluster Incl. U91329:Human kinesin-like motor protein KIF1C mRNA, com

35978_at Cluster Incl. AF009242:Homo sapiens proline-rich Gla protein 1 (PRGP1)
 41491_s_at Cluster Incl. AB028944:Homo sapiens mRNA for KIAA1021 protein, partia
 136_at U65402 /FEATURE=cds /DEFINITION=HSU65402 Human seven transmembrane G-coup

5 Metagene 122

31364_i_at Cluster Incl. W27762:37c6 Homo sapiens cDNA /gb=W27762 /gi=1307710 /u
 35379_at Cluster Incl. X54412:Human mRNA for alpha1(IX) collagen (long form) /cd
 38921_at Cluster Incl. U86078:Homo sapiens calmodulin-stimulated phosphodiesterase
 10 39512_s_at Cluster Incl. AA457029:aa38b10.s1 Homo sapiens cDNA, 3 end /clone=IM
 707_s_at Mucin 6, Gastric
 648_at L37112 /FEATURE=mRNA /DEFINITION=HUMVVR Homo sapiens vasopressin V3
 recep

15 Metagene 123

31350_at Cluster Incl. AC004597:Homo sapiens chromosome 19, cosmid F20722 /cds=(
 31391_at Cluster Incl. AF040723:Homo sapiens neuroan1 mRNA, complete cds /cds=(1
 31681_at Cluster Incl. X57282:H.sapiens mRNA for soluble erythropoietin receptor
 20 31991_at Cluster Incl. AL049430:Homo sapiens mRNA; cDNA DKFZp586H201 (from
 clone
 32007_at Cluster Incl. W29045:55e12 Homo sapiens cDNA /gb=W29045 /gi=1309002 /ug
 32407_f_at Cluster Incl. U92818:Homo sapiens c33.28 unnamed HERV-H protein mRNA,
 34604_at Cluster Incl. L05568:Human Na⁺/Cl⁻ dependent serotonin transporter mRNA
 25 34634_s_at Cluster Incl. U68487:Human 5-hydroxytryptamine7 receptor isoform b mR
 34636_at Cluster Incl. M23892:Human 15-lipoxygenase mRNA, complete cds /cds=(3,1
 35536_at Cluster Incl. AB011176:Homo sapiens mRNA for KIAA0604 protein, complete
 32271_at Cluster Incl. X16707:Human fra-1 mRNA /cds=(34,849) /gb=X16707 /gi=3146
 32915_at Cluster Incl. AL109730:Homo sapiens mRNA full length insert cDNA clone
 30 33470_at Cluster Incl. AF052177:Homo sapiens clone 24510 mRNA sequence /cds=UNKN
 33568_at Cluster Incl. U48861:Human beta 4 nicotinic acetylcholine receptor subu
 34457_at Cluster Incl. U76010:Human putative zinc transporter ZnT-3 (ZnT-3) mRNA
 34906_g_at Cluster Incl. AA977136:oq24f02.s1 Homo sapiens cDNA, 3 end /clone=IM
 35485_at Cluster Incl. X80818:H.sapiens mRNA for metabotropic glutamate receptor
 35 35939_s_at Cluster Incl. L20433:Human octamer binding transcription factor 1 (OT
 36222_at Cluster Incl. AJ012008:Homo sapiens genes encoding RNCC protein, DDAH p
 36242_at Cluster Incl. M21539:Human small proline rich protein (sprII) mRNA, clo
 36285_at Cluster Incl. U07364:Human inwardly rectifying potassium channel mRNA,
 38507_at Cluster Incl. X16867:Human mRNA for cytochrome P-450IID (clone pMP34) /

- 38858_at Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) m
- 38942_r_at Cluster Incl. W28610:49b12 Homo sapiens cDNA /gb=W28610 /gi=1308558 /
- 40643_at Cluster Incl. M34480:Human platelet glycoprotein IIb (GPIIb) mRNA, comp
- 41036_at Cluster Incl. AL022314:dJ1170K4.1 (novel protein similar to KIAA0176 an
- 5 31829_r_at Cluster Incl. AF027515:Homo sapiens trans-golgi network glycoprotein
- 32710_at Cluster Incl. X83127:H.sapiens mRNA for voltage gated potassium channel
- 33712_at Cluster Incl. N63574:yy63f05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
- 34704_r_at Cluster Incl. AA151971:zo30b03.r1 Homo sapiens cDNA, 5 end /clone=IM
- 35996_at Cluster Incl. X98261:H.sapiens mRNA for M-phase phosphoprotein, mpp5 /c
- 10 37270_at Cluster Incl. AF007876:Homo sapiens Na,K-ATPase beta 2 subunit gene, co
- 39051_at Cluster Incl. U31767:Human neuronatin alpha and neuronatin beta genes,
- 32815_at Cluster Incl. AI687419:tp95h03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 35756_at Cluster Incl. AF089816:Homo sapiens RGS-GAIP interacting protein GIPC m
- 39469_s_at Cluster Incl. W25905:14g5 Homo sapiens cDNA /gb=W25905 /gi=1306028 /u
- 15 41361_at Cluster Incl. W28148:43f2 Homo sapiens cDNA /gb=W28148 /gi=1308159 /ug=
- 32560_s_at Cluster Incl. W30959:zc65h10.r1 Homo sapiens cDNA, 5 end /clone=IMAG
- 1937_at Retinoblastoma 1
- 1662_r_at Antigen, Prostate Specific, Alt. Splice Form 2
- 1289_at L02321 /FEATURE= /DEFINITION=HUMGSTM5 Human glutathione S-transferase (G
- 20 1032_at U11872 /FEATURE= /DEFINITION=HSU11872 Human interleukin-8 receptor type
- 732_f_at Mucin 3, Intestinal
- 666_at L20965 /FEATURE= /DEFINITION=HUMPDEA Human phosphodiesterase mRNA,
- comple
- 25 Metagene 124
- 40379_at Cluster Incl. J02625:Human cytochrome P-450j mRNA, complete cds /cds=(1
- 37274_at Cluster Incl. AF018631:untitled /cds=(35,1666) /gb=AF018631 /gi=2674074
- 39720_g_at Cluster Incl. X56777:H.sapiens mRNA for ZP3 gene /cds=(30,1148) /gb=X
- 30 40770_f_at Cluster Incl. AB017019:Homo sapiens mRNA for JKTBP2, complete cds /cd
- 32244_at Cluster Incl. AB018280:Homo sapiens mRNA for KIAA0737 protein, complete
- 38449_at Cluster Incl. W28931:56f3 Homo sapiens cDNA /gb=W28931 /gi=1309086 /ug=
- 33157_at Cluster Incl. M93119:Human zinc-finger DNA-binding motifs (IA-1) mRNA,
- 1667_s_at J02871 /FEATURE= /DEFINITION=HUMCP45IV Human lung cytochrome P450
- 35 (IV
- 416_s_at X61755 /FEATURE=mRNA /DEFINITION=HSHOX3D Human HOX3D gene for
- homeoprot
- 247_s_at M26856 /FEATURE=cds /DEFINITION=HUMCP21OH Human 21-hydroxylase
- B gene,

Metagene 125

- 32402_s_at Cluster Incl. Y10931:H.sapiens mRNA for symplekin /cds=(459,3887) /gb
- 5 35092_at Cluster Incl. AF032387:Homo sapiens snRNA activating protein complex 19
- 37101_at Cluster Incl. AL050008:Homo sapiens mRNA; cDNA DKFZp564A063 (from clone
- 39651_at Cluster Incl. AB006532:Homo sapiens RecQ4 mRNA for DNA helicase, comple
- 33225_at Cluster Incl. AI928387:wo96f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 10 35239_at Cluster Incl. X86810:Homo sapiens EDMD gene /cds=(110,874) /gb=X86810 /
- 35615_at Cluster Incl. D50914:Human mRNA for KIAA0124 gene, partial cds /cds=(0,
- 36862_at Cluster Incl. AB029038:Homo sapiens mRNA for KIAA1115 protein, complete
- 39068_at Cluster Incl. L76702:Homo sapiens protein phosphatase 2A B56-delta (PP2
- 40476_s_at Cluster Incl. U58198:Human interleukin enhancer binding factor 3 mRNA
- 15 32158_at Cluster Incl. U53174:Human cell cycle checkpoint control protein mRNA,
- 32825_at Cluster Incl. Y10805:H.sapiens mRNA for arginine methyltransferase, spl
- 35758_at Cluster Incl. AB024301:Homo sapiens mRNA for RuvB-like DNA helicase TIP
- 39158_at Cluster Incl. AB021663:Homo sapiens mRNA for leucine-zipper protein, co
- 40232_at Cluster Incl. U75370:Human mitochondrial RNA polymerase mRNA, nuclear g
- 20 33132_at Cluster Incl. U37012:Human cleavage and polyadenylation specificity fac

Metagene 126

- 32341_f_at Cluster Incl. U37230:Human ribosomal protein L23a mRNA, complete cds
- 25 41627_at Cluster Incl. D50645:Homo sapiens mRNA for SDF2, complete cds /cds=(39,
- 41659_at Cluster Incl. U46691:Human putative chromatin structure regulator (SUPT
- 37912_at Cluster Incl. X80200:H.sapiens MLN62 mRNA /cds=(85,1497) /gb=X80200 /gi
- 39783_at Cluster Incl. D43947:Human mRNA for KIAA0100 gene, complete cds /cds=(3
- 40107_at Cluster Incl. AF054987:Homo sapiens clone 23831 aldolase C mRNA, comple
- 30 32181_at Cluster Incl. M60922:Human surface antigen mRNA, complete cds /cds=(126
- 32791_at Cluster Incl. L19183:Human MAC30 mRNA, 3 end /cds=(0,569) /gb=L19183 /
- 34379_at Cluster Incl. AF082657:Homo sapiens Era GTPase A protein (HERA-A) mRNA,
- 36940_at Cluster Incl. D86970:Human mRNA for KIAA0216 gene, complete cds /cds=(4
- 36988_at Cluster Incl. M80783:Human B12 protein mRNA, complete cds /cds=(153,110
- 35 37700_at Cluster Incl. X92106:H.sapiens mRNA for bleomycin hydrolase /cds=(78,14
- 38107_at Cluster Incl. U40998:Human retinal protein (HRG4) mRNA, complete cds /c
- 41561_s_at Cluster Incl. AI651368:wb05d07.x1 Homo sapiens cDNA, 3 end /clone=IM

Metagene 127

	31508_at	Cluster Incl. S73591:brain-expressed HHCPA78 homolog [human, HL-60 acut
	37416_at	Cluster Incl. Z35227:H.sapiens TTF mRNA for small G protein /cds=(579,1
	37543_at	Cluster Incl. D25304:Human mRNA for KIAA0006 gene, partial cds /cds=(0,
5	39411_at	Cluster Incl. AL080156:Homo sapiens mRNA; cDNA DKFZp434J214 (from clone
	37294_at	Cluster Incl. X61123:Human BTG1 mRNA /cds=(308,823) /gb=X61123 /gi=2950
	1461_at	M69043 /FEATURE= /DEFINITION=HUMMAD3A Homo sapiens MAD-3 mRNA
	encoding I	
	160040_at	X52001 /FEATURE=cds /DEFINITION=HSET3AA H.sapiens endothelin 3
10	mRNA /N	
	Metagene 128	
	36305_at	Cluster Incl. M95167:Homo sapiens dopamine transporter (SLC6A3) mRNA, c
15	37836_at	Cluster Incl. AB023215:Homo sapiens mRNA for KIAA0998 protein, partial
	41865_at	Cluster Incl. AF052185:Homo sapiens clone 24418 mRNA sequence /cds=UNKN
	31842_at	Cluster Incl. AF038195:Homo sapiens clone 23661 unknown protein mRNA, c
	33300_at	Cluster Incl. AL031282:dJ283E3.3.1 (Cell Division Cycle 2-Like 2 (PITSL
	33760_at	Cluster Incl. AB017546:Homo sapiens Pex14 mRNA for peroxisomal membrane
20	34285_at	Cluster Incl. AB018338:Homo sapiens mRNA for KIAA0795 protein, partial
	35190_at	Cluster Incl. AL031447:dJ126A5.2.1 (novel protein) (isoform 1) /cds=(0,
	36458_at	Cluster Incl. AB023235:Homo sapiens mRNA for KIAA1018 protein, complete
	40139_at	Cluster Incl. U88966:Human protein rapamycin associated protein (FRAP2)
	32197_at	Cluster Incl. AF070548:Homo sapiens clone 24408 2-oxoglutarate carrier
25	33915_at	Cluster Incl. W22655:71B9 Homo sapiens cDNA /clone=(not-directional) /g
	35836_at	Cluster Incl. AB019408:Homo sapiens mRNA, expressed in fibroblasts of p
	36673_at	Cluster Incl. X76057:H.sapiens PMI1 mRNA for phosphomannose isomerase /
	Metagene 129	
30	34198_at	Cluster Incl. U12128:Human protein tyrosine phosphatase 1E (PTP1E) mRNA
	38978_at	Cluster Incl. AF013758:Homo sapiens polyadenylate binding protein-inter
	34332_at	Cluster Incl. D31766:Human mRNA for KIAA0060 gene, complete cds /cds=(4
	35745_f_at	Cluster Incl. X78136:H.sapiens hnRNP-E2 mRNA /cds=(22,1119) /gb=X7813
35	36611_at	Cluster Incl. U25849:Human red cell-type low molecular weight acid phos
	37681_i_at	Cluster Incl. AB018266:Homo sapiens mRNA for KIAA0723 protein, comple
	38016_at	Cluster Incl. M94630:Homo sapiens hnRNP-C like protein mRNA, complete c
	1629_s_at	Tyrosine Phosphatase 1, Non-Receptor, Alt. Splice 3

Metagene 130

- 37149_s_at Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (c
 40385_at Cluster Incl. U64197:Homo sapiens chemokine exodus-1 mRNA, complete cds
5 39341_at Cluster Incl. AJ001902:Homo sapiens mRNA for TRIP6 (thyroid receptor in
 40824_at Cluster Incl. AB018288:Homo sapiens mRNA for KIAA0745 protein, partial
 41140_at Cluster Incl. U05875:Human clone pSK1 interferon gamma receptor accesso
 41755_at Cluster Incl. AB023194:Homo sapiens mRNA for KIAA0977 protein, complete
 34892_at Cluster Incl. AF016266:Homo sapiens TRAIL receptor 2 mRNA, complete cds
10 1183_at D43767 /FEATURE= /DEFINITION=HUMAR Human mRNA for chemokine, complete cd

Metagene 131

- 38132_at Cluster Incl. M88338:Human serum constituent protein (MSE55) mRNA, comp
15 31831_at Cluster Incl. AI888563:wn33a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32073_at Cluster Incl. AB014577:Homo sapiens mRNA for KIAA0677 protein, complete
 32094_at Cluster Incl. AB017915:Homo sapiens mRNA for condroitin 6-sulfotransfe
 38641_at Cluster Incl. AJ133115:Homo sapiens mRNA for TSC-22-like protein /cds=(
 34780_at Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(
20 35336_at Cluster Incl. AL021707:Human DNA sequence from clone 508I15 on chromoso
 36618_g_at Cluster Incl. X77956:H.sapiens Id1 mRNA /cds=(35,499) /gb=X77956 /gi=
 36619_r_at Cluster Incl. S78825:Id1 (Id1-b)=transcription regulator helix-loop-h
 36958_at Cluster Incl. X95735:Homo sapiens mRNA for zyxin /cds=(71,1789) /gb=X95
 823_at U84487 /FEATURE= /DEFINITION=HSU84487 Human CX3C chemokine precursor,
25 mRN
 406_at X53587 /FEATURE=mRNA /DEFINITION=HSINTB4R Human mRNA for integrin beta 4

Metagene 132

- 30** 34645_at Cluster Incl. X55715:Human Hums3 mRNA for 40S ribosomal protein s3 /cds
 39297_at Cluster Incl. U38810:Human mab-21 cell fate-determining protein homolog
 36867_at Cluster Incl. W03846:za60a02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 39025_at Cluster Incl. AI557912:pro3.2-2.E07.r Homo sapiens cDNA, 5 end /clone_
 40111_g_at Cluster Incl. U49283:Human NAD⁺-specific isocitrate dehydrogenase bet
35 32744_at Cluster Incl. AI526078:DU3.2-7.G08.r Homo sapiens cDNA, 5 end /clone_e
 34866_at Cluster Incl. AF055029:Homo sapiens clone 24711 mRNA sequence /cds=UNKN
 35298_at Cluster Incl. U54558:Homo sapiens translation initiation factor eIF3 p6
 39173_at Cluster Incl. X56597:Human humFib mRNA for fibrillarin /cds=(59,1024) /
 1897_at L07594 /FEATURE= /DEFINITION=HUMTGFB3C Human transforming growth factor-

1625_at Insulin-Like Growth Factor Ib

Metagene 133

- 5** 38853_at Cluster Incl. X81892:H.sapiens mRNA for HE6 Tm7 receptor /cds=(72,3116)
 41476_at Cluster Incl. N36926:yy38e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 32696_at Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841
 /gi=35314
 39048_at Cluster Incl. U95299:Human Notch4 (hNotch4) mRNA, complete cds /cds=(90
10 41770_at Cluster Incl. AA420624:nc61c12.r1 Homo sapiens cDNA /clone=IMAGE-745750
 41771_g_at Cluster Incl. AA420624:nc61c12.r1 Homo sapiens cDNA /clone=IMAGE-7457
 41772_at Cluster Incl. M68840:Human monoamine oxidase A (MAOA) mRNA, complete cd
 33162_at Cluster Incl. X02160:Human mRNA for insulin receptor precursor /cds=(48

15 Metagene 134

- 33071_at Cluster Incl. Z98744:histone H2B /cds=(5,382) /gb=Z98744 /gi=3080457 /u
 35117_at Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromoso
 33961_at Cluster Incl. AL109666:Homo sapiens mRNA full length insert cDNA clone
20 34905_at Cluster Incl. AA977136:oaq24f02.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 35896_at Cluster Incl. D87002:Human (lambda) DNA for immunoglobulin light chain /c
 35913_at Cluster Incl. U88047:Homo sapiens DNA binding protein homolog (DRIL1) m
 37796_at Cluster Incl. AF053356:Homo sapiens chromosome 7q22 sequence /cds=(0,24
 38197_at Cluster Incl. M64934:Human kell blood group protein mRNA /cds=(123,2321
25 38518_at Cluster Incl. Y18004:Homo sapiens mRNA for SCML2 protein /cds=(91,2193)
 39586_at Cluster Incl. AF097935:Homo sapiens desmoglein 1 (DSG1) mRNA, complete
 39990_at Cluster Incl. U07559:Human ISL-1 (Islet-1) mRNA, complete cds /cds=(248
 40322_at Cluster Incl. D12763:Homo sapiens mRNA for ST2 protein /cds=(46,1032) /
 41863_at Cluster Incl. AF070623:Homo sapiens clone 24468 mRNA sequence /cds=UNKN
30 32062_at Cluster Incl. D25216:Human mRNA for KIAA0014 gene, complete cds /cds=(1
 36001_at Cluster Incl. Y18643:Homo sapiens mRNA for methyltransferase-like prote
 36546_r_at Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, comple
 36567_at Cluster Incl. W26700:11h4 Homo sapiens cDNA /gb=W26700 /gi=1305802 /ug=
 33450_at Cluster Incl. AB015906:Homo sapiens mRNA for actin-related protein, com
35 38044_at Cluster Incl. AF035283:Homo sapiens clone 23916 mRNA sequence /cds=UNKN
 40938_at Cluster Incl. Y13835:Homo sapiens mRNA for farnesylated-proteins conver
 41001_at Cluster Incl. AB023202:Homo sapiens mRNA for KIAA0985 protein, complete
 41262_at Cluster Incl. AL021707:Human DNA sequence from clone 508I15 on chromoso
 725_i_at Chorionic Somatomammotropin Hormone Cs-5

208_at M94151 /FEATURE= /DEFINITION=HUMCAPR Homo sapiens cadherin-associated pro

Metagene 135

- 5 39255_at Cluster Incl. X02750:Human liver mRNA for protein C /cds=(97,1482) /gb=
 40724_at Cluster Incl. Y14443:Homo sapiens mRNA for zinc finger protein /cds=(33
 37588_s_at Cluster Incl. U62317:Chromosome 22q13 BAC Clone CIT987SK-384D8 comple
 38710_at Cluster Incl. AL096714:Homo sapiens mRNA; cDNA DKFZp564E242 (from
 clone
 10 34864_at Cluster Incl. AF070638:Homo sapiens clone 24448 unknown mRNA, partial c
 37049_g_at Cluster Incl. U58970:Human putative outer mitochondrial membrane 34 k
 38398_at Cluster Incl. AB002356:Human mRNA for KIAA0358 gene, complete cds /cds=
 816_g_at U70987 /FEATURE= /DEFINITION=HSU70987 Human GAP binding protein
 p62dok

15

Metagene 136

- 32087_at Cluster Incl. M65217:Human heat shock factor 2 (HSF2) mRNA, complete cd
 33325_at Cluster Incl. W26667:11a1 Homo sapiens cDNA /gb=W26667 /gi=1305733 /ug=
 20 35139_at Cluster Incl. AL049341:Homo sapiens mRNA; cDNA DKFZp566A163 (from
 clone
 35707_at Cluster Incl. AI057614:oy31f04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39367_at Cluster Incl. AA522537:ni38e08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 40104_at Cluster Incl. D63780:Homo sapiens mRNA for YSK1, complete cds /cds=(114
 25 40973_at Cluster Incl. AI146846:qb92h04.x1 Homo sapiens cDNA, 3 end /clone=IMAG

Metagene 137

- 31438_s_at Cluster Incl. Z22971:H.sapiens mRNA for.M130 antigen extracellular va
 30 36372_at Cluster Incl. U51333:Human hexokinase III (HK3) mRNA, complete cds /cds
 36753_at Cluster Incl. AF072099:Homo sapiens immunoglobulin-like transcript 3 pr
 37148_at Cluster Incl. AF025533:Homo sapiens leucocyte immunoglobulin-like recep
 37823_at Cluster Incl. Y16645:Homo sapiens mRNA for monocyte chemotactic protein
 38222_at Cluster Incl. AF007893:Homo sapiens P2Y6 receptor pseudogene, complete
 35 41409_at Cluster Incl. AF044896:Homo sapiens ICB-1 mRNA, complete cds /cds=(128,
 32128_at Cluster Incl. Y13710:Homo sapiens mRNA for alternative activated macrop
 33731_at Cluster Incl. AJ130718:Homo sapiens mRNA for glycoprotein-associated am
 33802_at Cluster Incl. Z82244:bK286B10.2 (Heme Oxygenase 1 (HO-1, EC 1.14.99.3))
 36889_at Cluster Incl. M33195:Human Fc-epsilon-receptor gamma-chain mRNA, comple

- 37200_at Cluster Incl. J04162:Human leukocyte IgG receptor (Fc-gamma-R) mRNA, co
 37220_at Cluster Incl. M63835:Human IgG Fc receptor I gene /cds=(155,1279) /gb=M
 37233_at Cluster Incl. AF079167:untitled /cds=(61,882) /gb=AF079167 /gi=4050003
 38363_at Cluster Incl. W60864:zd27g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
5 39728_at Cluster Incl. J03909:Human gamma-interferon-inducible protein (IP-30) m
 41764_at Cluster Incl. AA976838:oq35c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 33374_at Cluster Incl. L09708:Human complement component 2 (C2) gene allele b /c
 33390_at Cluster Incl. AA203487:zx53d03.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 34378_at Cluster Incl. X97324:H.sapiens mRNA for adipophilin /cds=(0,1313) /gb=X
10 35820_at Cluster Incl. X62078:H.sapiens mRNA for GM2 activator protein /cds=UNKN
 36575_at Cluster Incl. S59049:BL34=B cell activation gene [human, mRNA, 1398 nt]
 36657_at Cluster Incl. AA883870:am26f01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 37391_at Cluster Incl. X12451:Human mRNA for pro-cathepsin L (major excreted pro
 38379_at Cluster Incl. X76534:H.sapiens NMB mRNA /cds=(91,1773) /gb=X76534 /gi=6
15 38796_at Cluster Incl. X03084:Human mRNA for C1q B-chain of complement system /c
 1021_at J00219 /FEATURE=mRNA /DEFINITION=HUMIFNG Human immune interferon (IFN-ga
 925_at J03909 /FEATURE= /DEFINITION=HUMIIP Human gamma-interferon-inducible prot
 608_at M12529 /FEATURE=mRNA /DEFINITION=HUMAPOE Human apolipoprotein E mRNA,
 com
20 495_at U31628 /FEATURE= /DEFINITION=HSU31628 Human interleukin-15 receptor alpha

Metagene 138

- 40663_at Cluster Incl. AF010233:Homo sapiens RalBP1-interacting protein (POB1) m
25 41365_at Cluster Incl. Y09788:H.sapiens MUC5B gene /cds=(0,2538) /gb=Y09788 /gi=
 33740_at Cluster Incl. AF023268:Homo sapiens clk2 kinase (CLK2), propin1, cotel1,
 35244_at Cluster Incl. AB007929:Homo sapiens mRNA for KIAA0460 protein, partial
 37584_at Cluster Incl. AJ007669:Homo sapiens mRNA for Fanconi anemia group G /cd
 39010_at Cluster Incl. AI658639:tu06g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
30 39445_at Cluster Incl. AF038661:Homo sapiens chromosome 1q21-1q23 beta-1,4-galac
 39735_at Cluster Incl. AF069987:Homo sapiens nitrilase 1 (NIT1) mRNA, complete c
 39800_s_at Cluster Incl. U68566:Human HS1 binding protein HAX-1 mRNA, nuclear ge
 40124_at Cluster Incl. Y18418:Homo sapiens mRNA for erythrocyte cytosolic protei
 33346_r_at Cluster Incl. M61764:Human gamma-tubulin mRNA, complete cds /cds=(24,
35 33873_at Cluster Incl. D43642:Human YL-1 mRNA for YL-1 protein (nuclear protein
 33909_at Cluster Incl. L35013:Human spliceosomal protein (SAP 49) gene, complete
 39149_at Cluster Incl. X99720:H.sapiens TPRC gene /cds=(212,1687) /gb=X99720 /gi=
 40210_at Cluster Incl. X75593:H.sapiens mRNA for rab 13 /cds=(139,750) /gb=X7559
 1637_at U09578 /FEATURE= /DEFINITION=HSU09578 Homo sapiens MAPKAP kinase (3pK) m

1343_s_at S66896 /FEATURE= /DEFINITION=S66896 squamous cell carcinoma antigen=se

Metagene 139

- 5** 38200_at Cluster Incl. U11690:Human faciogenital dysplasia (FGD1) mRNA, complete
 33806_at Cluster Incl. AF052106:Homo sapiens clone 23781 mRNA sequence /cds=UNKN
 35686_s_at Cluster Incl. Z24459:H.sapiens MTCP1 gene, exons 2A to 7 (and joined
 37554_at Cluster Incl. U62801:Human protease M mRNA, complete cds /cds=(245,979)
 37926_at Cluster Incl. D14520:Human mRNA for GC-Box binding protein BTEB2, compl
10 41234_at Cluster Incl. AI540318:tq34f03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 1674_at M15990 /FEATURE= /DEFINITION=HUMCYES1 Human c-yes-1 mRNA
 1518_at J04101 /FEATURE= /DEFINITION=HUMETS1A Human erythroblastosis virus oncog
 930_at L07590 /FEATURE= /DEFINITION=HUMPP2A130 Human protein phosphatase 2A 130
 633_s_at L40386 /FEATURE=mRNA /DEFINITION=HUMDP2M Human DP-2 mRNA,
15 complete cds
 622_at M28212 /FEATURE= /DEFINITION=HUMRAB6A Homo sapiens GTP-binding protein (R
 131_at X83928 /FEATURE=cds /DEFINITION=HSTAFII28 H.sapiens mRNA for transcriptio

Metagene 140

- 20**
 38863_at Cluster Incl. L07540:Human replication factor C, 36-kDa subunit mRNA, c
 32738_at Cluster Incl. AF050640:Homo sapiens NADH-ubiquinone oxidoreductase NDUF
 38679_g_at Cluster Incl. AA733050:zg79b05.s1 Homo sapiens cDNA, 3 end /clone=39
 39012_g_at Cluster Incl. X99906:Homo sapiens mRNA for alpha endosulfine /cds=(12
25 32799_at Cluster Incl. AF023268:Homo sapiens clk2 kinase (CLK2), propin1, cotel,
 36189_at Cluster Incl. U10323:Human nuclear factor NF45 mRNA, complete cds /cds=
 38014_at Cluster Incl. X79448:H.sapiens IFI-4 mRNA for type I protein /cds=(1165
 38089_at Cluster Incl. D63478:Human mRNA for KIAA0144 gene, complete cds /cds=(1
 41514_s_at Cluster Incl. W26628:34a4 Homo sapiens cDNA /gb=W26628 /gi=1307471 /u
30 41834_g_at Cluster Incl. AB016492:Homo sapiens hJTB gene, complete cds /cds=(464
 33154_at Cluster Incl. D26600:Human mRNA for proteasome subunit HsN3, complete c
 1860_at U58334 /FEATURE= /DEFINITION=HSU58334 Human Bcl2, p53 binding protein Bb
 1356_at U18321 /FEATURE= /DEFINITION=HSU18321 Human ionizing radiation resistanc
 1311_at D26600 /FEATURE= /DEFINITION=HUMPSH3 Human mRNA for proteasome subunit H
35 1287_at J03473 /FEATURE=mRNA /DEFINITION=HUMRISDAD Human poly(ADP-ribose)
 synthe
 421_at X66397 /FEATURE=cds /DEFINITION=HSTPRM H.sapiens tpr mRNA
 338_at AF005887 /FEATURE= /DEFINITION=AF005887 Homo sapiens ATF family member AT

Metagene 141

- 38582_at Cluster Incl. AI961220:wt15b04.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 39294_at Cluster Incl. X16155:Human mRNA for chicken ovalbumin upstream promoter
5 40099_at Cluster Incl. AB014551:Homo sapiens mRNA for KIAA0651 protein, complete
 38076_at Cluster Incl. X69907:H.sapiens gene for mitochondrial ATP synthase c subunit

Metagene 142

- 10** 34031_i_at Cluster Incl. U90268:Human Krit1 mRNA, complete cds /cds=(25,1614) /g
 35958_at Cluster Incl. AL050379:Homo sapiens mRNA; cDNA DKFZp586F1922 (from
 clon
 36234_at Cluster Incl. U79273:Human clone 23933 mRNA sequence /cds=UNKNOWN
 /gb=U
15 37507_i_at Cluster Incl. AA675900:g02504r Homo sapiens cDNA, 5' end /clone=g0250
 37869_at Cluster Incl. AB029004:Homo sapiens mRNA for KIAA1081 protein, partial
 38207_at Cluster Incl. AW006742:wr28g10.x1 Homo sapiens cDNA, 3' end /clone=IMAG,
 38224_at Cluster Incl. U71300:Human snRNA activating protein complex 50kD subunit
 31872_at Cluster Incl. X79201:H.sapiens mRNA for SYT /cds=(3,1178) /gb=X79201 /g
20 32124_at Cluster Incl. AL030996:dJ1189B24.4 (novel PUTATIVE protein similar to h
 34195_at Cluster Incl. AL121073:DKFZp762B235_r1 Homo sapiens cDNA, 5' end /clone
 34279_at Cluster Incl. AL050141:Homo sapiens mRNA; cDNA DKFZp586O031 (from
 clone
 35705_at Cluster Incl. D16815:Homo sapiens mRNA for EAR-1r, complete cds /cds=(3
25 37621_at Cluster Incl. M57230:Human membrane glycoprotein gp130 mRNA, complete c
 37946_at Cluster Incl. M60724:Human p70 ribosomal S6 kinase alpha-I mRNA, comple
 38614_s_at Cluster Incl. U77413:Human O-linked GlcNAc transferase mRNA, complete
 40060_r_at Cluster Incl. AF061258:Homo sapiens LIM protein mRNA, complete cds /c
 40101_g_at Cluster Incl. U72206:Human guanine nucleotide regulatory factor (LFP4
30 40495_at Cluster Incl. AA306076:EST177079 Homo sapiens cDNA, 5' end /clone=ATCC-
 33855_at Cluster Incl. M96995:Homo sapiens epidermal growth factor receptor-bind
 34890_at Cluster Incl. L09235:Human vacuolar ATPase (isoform VA68) mRNA, complet
 36962_at Cluster Incl. U24105:Homo sapiens coatamer protein (COPA) mRNA, complet
 39879_s_at Cluster Incl. H16917:ym39e02.r1 Homo sapiens cDNA, 5' end /clone=IMAG
35 1472_g_at U22376 /FEATURE=cds#1 /DEFINITION=HSU22376 Human (c-myc) gene,
 complet
 932_i_atL11672 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finger
 933_f_atL11672 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finger
 714_at Adenylyl Cyclase-Associated Protein 2

Metagene 143

- 34600_s_at Cluster Incl. U54644:Human tub homolog mRNA, complete cds /cds=(152,1
5 38564_at Cluster Incl. U40152:Human origin recognition complex 1 (HsORC1) mRNA,
41445_at Cluster Incl. X02812:Human mRNA for transforming growth factor-beta (TG
37969_at Cluster Incl. M59979:Human prostaglandin endoperoxide synthase mRNA, co
38468_at Cluster Incl. U65676:Human Hermansky-Pudlak syndrome protein (HPS) mRNA
39862_at Cluster Incl. AA528252:nh92c11.s1 Homo sapiens cDNA, 3 end /clone=IMAG
10 40241_at Cluster Incl. U09850:Human zinc finger protein (ZNF143) mRNA, complete
40636_at Cluster Incl. AI807620:wf49b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
40886_at Cluster Incl. L41498:Homo sapiens longation factor 1-alpha 1 (PTI-1) mR
1792_g_at M68520 /FEATURE= /DEFINITION=HUMCDC2A Human cdc2-related protein
kinas
15 713_at Helix-Loop-Helix Protein Delta Max, Alt. Splice 1

Metagene 144

- 41610_at Cluster Incl. AB011105:Homo sapiens mRNA for KIAA0533 protein, partial
20 41698_at Cluster Incl. AL031685:dJ963K23.4 (KIAA0939 (novel Sodium/hydrogen exch
35727_at Cluster Incl. AI249721:qj64d06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
37211_at Cluster Incl. M93107:Homo sapiens heart (R)-3-hydroxybutyrate dehydroge
34345_at Cluster Incl. AF026031:Homo sapiens putative mitochondrial outer membra
35765_at Cluster Incl. X91504:H.sapiens mRNA for ARP1 protein /cds=(11,616) /gb=
25 40635_at Cluster Incl. AF089750:Homo sapiens flotillin-1 mRNA, complete cds /cds
41258_at Cluster Incl. N29665:yw73e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
41812_s_at Cluster Incl. AB020713:Homo sapiens mRNA for KIAA0906 protein, partia

Metagene 145

- 30**
39304_g_at Cluster Incl. Y14153:Homo sapiens mRNA for beta-transducin repeat con
31862_at Cluster Incl. L20861:Homo sapiens proto-oncogene (Wnt-5a) mRNA, complet
32643_at Cluster Incl. L07956:Homo sapiens 1,4-alpha-glucan branching enzyme (HG
33264_at Cluster Incl. X89602:H.sapiens mRNA for rTS beta protein /cds=(17,1267)
35 33800_at Cluster Incl. AF036927:Homo sapiens adenylyl cyclase type IX mRNA, comp
36818_at Cluster Incl. AF052100:Homo sapiens clone 23645 mRNA sequence /cds=UNKN
37249_at Cluster Incl. AF079529:Homo sapiens cAMP-specific phosphodiesterase 8B
33386_at Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosome
35824_at Cluster Incl. AJ223321:Homo sapiens RP58 gene, complete CDS /cds=(523,2

	38115_at	Cluster Incl. AF055479:Homo sapiens lung cancer candidate FUS1 (FUS1) m
	38118_at	Cluster Incl. U73377:Human p66shc (SHC) mRNA, complete cds /cds=(194,19
	38385_at	Cluster Incl. S65738:actin depolymerizing factor [human, fetal brain, m
	40629_at	Cluster Incl. L19783:Human GPI-H mRNA, complete cds /cds=(60,626) /gb=L
5	32558_at	Cluster Incl. AB021868:Homo sapiens PIAS3 mRNA for protein inhibitor of
	1669_at L20861	/FEATURE= /DEFINITION=HUMWNT5A Homo sapiens proto-oncogene (Wnt-5
	1230_g_at	U78556 /FEATURE= /DEFINITION=HSU78556 Human cisplatin resistance assoc
	243_g_at	M64571 /FEATURE=mRNA /DEFINITION=HUMMAP4 Human microtubule-
	associated p	
10	Metagene 146	
	35061_at	Cluster Incl. AF030514:Homo sapiens interferon stimulated T-cell alpha
	34974_at	Cluster Incl. Y13323:Homo sapiens mRNA for disintegrin-protease /cds=(6
15	36776_at	Cluster Incl. X51985:Human LAG-3 mRNA for CD4-related protein involved
	36804_at	Cluster Incl. M34455:Human interferon-gamma-inducible indoleamine 2,3-d
	37126_at	Cluster Incl. M62800:Human 52-kD SS-A/Ro autoantigen mRNA, complete cds
	37137_at	Cluster Incl. M17016:Human serine protease-like protein mRNA, complete
	37145_at	Cluster Incl. M85276:Homo sapiens NKG5 gene, complete cds /cds=(128,565
20	37168_at	Cluster Incl. AB013924:Homo sapiens mRNA for TSC403 protein, complete c
	37420_i_at	Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex,
	37454_at	Cluster Incl. AJ001634:Homo sapiens mRNA for CC-chemokine MCP-4 /cds=(4
	38241_at	Cluster Incl. U90548:Human butyrophilin (BTF3) mRNA, complete cds /cds=
	39959_at	Cluster Incl. AL031983:dJ271M21.6 (Diubiquitin) /cds=(18,515) /gb=AL031
25	39988_at	Cluster Incl. M74447:Human PSF-2 mRNA, complete cds /cds=(96,2207) /gb=
	32700_at	Cluster Incl. M55543:Human guanylate binding protein isoform II (GBP-2)
	33304_at	Cluster Incl. U88964:Human HEM45 mRNA, complete cds /cds=(37,582) /gb=U
	36879_at	Cluster Incl. M63193:Human platelet-derived endothelial cell growth fac
	37219_at	Cluster Incl. X72755:H.sapiens Humig mRNA /cds=(39,416) /gb=X72755 /gi=
30	37944_at	Cluster Incl. U19523:Human GTP cyclohydrolase I mRNA, complete cds /cds
	38287_at	Cluster Incl. AA808961:nw16h03.s1 Homo sapiens cDNA /clone=IMAGE-124066
	39412_at	Cluster Incl. U09825:Human acid finger protein mRNA, complete cds /cds=
	40153_at	Cluster Incl. X57522:H.sapiens RING4 cDNA /cds=(30,2456) /gb=X57522 /gi
	41171_at	Cluster Incl. D45248:Human mRNA for proteasome activator hPA28 subunit
35	41184_s_at	Cluster Incl. X87344:H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LM
	41237_at	Cluster Incl. D32129:Human mRNA for HLA class-I (HLA-A26) heavy chain,
	32859_at	Cluster Incl. M97935:Homo sapiens transcription factor ISGF-3 mRNA, com
	33338_at	Cluster Incl. M97936:Human transcription factor ISGF-3 mRNA sequence /c
	33339_g_at	Cluster Incl. M97936:Human transcription factor ISGF-3 mRNA sequence

- 35735_at Cluster Incl. M55542:Human guanylate binding protein isoform I (GBP-2)
- 37383_f_at Cluster Incl. X58536:Human mRNA for HLA class I locus C heavy chain /
- 38121_at Cluster Incl. X59892:H.sapiens mRNA for IFN-inducible gamma2 protein /c
- 38759_at Cluster Incl. U97502:Homo sapiens butyrophilin (BT3.3) gene /cds=(73,22
- 5** 38760_f_at Cluster Incl. U90546:Human butyrophilin (BTF4) mRNA, complete cds /cd
- 40639_at Cluster Incl. AL021683:Homo sapiens cDNA homologous to Yeast SCO1 & SCO
- 1184_at D45248 /FEATURE= /DEFINITION=HUMHPA28A Human mRNA for proteasome
activa
- 669_s_at L05072 /FEATURE=expaned_cds /DEFINITION=HUMIFNRF1A Homo sapiens
- 10** interfe
- 431_at X02530 /FEATURE=cds /DEFINITION=HSINFGER Human mRNA for gamma-interferon
- 195_s_at U28014 /FEATURE= /DEFINITION=HSU28014 Human cysteine protease
(ICErel-I
- 15** Metagene 147
- 31609_s_at Cluster Incl. L33799:Human procollagen C-proteinase enhancer protein
- 31720_s_at Cluster Incl. M10905:Human cellular fibronectin mRNA /cds=(0,2383) /g
- 32465_at Cluster Incl. AF009801:Homo sapiens homeodomain protein (BAPX1) mRNA, c
- 20** 32488_at Cluster Incl. X14420:Human mRNA for pro-alpha-1 type 3 collagen /cds=(1
- 32305_at Cluster Incl. J03464:Human collagen alpha-2 type I mRNA, complete cds,
- 32306_g_at Cluster Incl. J03464:Human collagen alpha-2 type I mRNA, complete cds
- 32307_s_at Cluster Incl. V00503:Human mRNA encoding Pro-alpha-2 chain of type I
- 34494_at Cluster Incl. AJ003125:Homo sapiens mRNA for procollagen I-N proteinase
- 25** 37459_at Cluster Incl. X57527:Human COL8A1 mRNA for alpha 1(VIII) collagen /cds=
- 38566_at Cluster Incl. X60382:H.sapiens COL10A1 gene for collagen (alpha-1 type
- 39945_at Cluster Incl. U09278:Human fibroblast activation protein mRNA, complete
- 39973_at Cluster Incl. U47926:Human unknown protein B mRNA, complete cds /cds=(8
- 31897_at Cluster Incl. U53445:Human ovarian cancer downregulated myosin heavy ch
- 30** 36497_at Cluster Incl. W28438:47g10 Homo sapiens cDNA /gb=W28438 /gi=1308449 /ug
- 36811_at Cluster Incl. U24389:Human lysyl oxidase-like protein gene /cds=(446,21
- 36861_at Cluster Incl. AL049946:Homo sapiens mRNA; cDNA DKFZp564I1922 (from clon
- 37573_at Cluster Incl. AF007150:Homo sapiens clone 23767 and 23782 mRNA sequence
- 38637_at Cluster Incl. L16895:Human lysyl oxidase (LOX) gene, exon 7 /cds=(0,6)
- 35** 38722_at Cluster Incl. X15880:Human mRNA for collagen VI alpha-1 C-terminal glob
- 39069_at Cluster Incl. AF053944:Homo sapiens aortic carboxypeptidase-like protei
- 39407_at Cluster Incl. M22488:Human bone morphogenetic protein 1 (BMP-1) mRNA /c
- 39695_at Cluster Incl. M31516:Human decay-accelerating factor mRNA, complete cds
- 39710_at Cluster Incl. U30521:Human P311 HUM (3.1) mRNA, complete cds /cds=(202,

	39753_at	Cluster Incl. X06256:Human mRNA for integrin alpha 5 subunit /cds=(23,3
	40848_g_at	Cluster Incl. AB018293:Homo sapiens mRNA for KIAA0750 protein, comple
	33412_at	Cluster Incl. AI535946:vicpro2.D07.r Homo sapiens cDNA, 5 end /clone_e
	33910_at	Cluster Incl. AL049338:Homo sapiens mRNA; cDNA DKFZp564P116 (from
5	clone	
	34390_at	Cluster Incl. U90441:Human prolyl 4-hydroxylase alpha (II) subunit mRNA
	34778_at	Cluster Incl. AA418080:zv97h07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	35366_at	Cluster Incl. M30269:Human nidogen mRNA, complete cds /cds=(90,3833) /g
	35832_at	Cluster Incl. AB029000:Homo sapiens mRNA for KIAA1077 protein, partial
10	36149_at	Cluster Incl. D78014:Homo sapiens mRNA for dihydropyrimidinase related
	37671_at	Cluster Incl. S78569:laminin alpha 4 chain [human, fetal lung, mRNA, 62
	38077_at	Cluster Incl. X52022:H.sapiens RNA for type VI collagen alpha3 chain /c
	38111_at	Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate proteo
	38112_g_at	Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate prot
15	38126_at	Cluster Incl. J04599:Human hPGI mRNA encoding bone small proteoglycan I
	38420_at	Cluster Incl. Y14690:Homo sapiens mRNA for procollagen alpha 2(V) /cds=
	38442_at	Cluster Incl. U19718:Human microfibril-associated glycoprotein (MFAP2)
	38466_at	Cluster Incl. X82153:H.sapiens mRNA for cathepsin O /cds=(129,1118) /gb
	32535_at	Cluster Incl. X63556:H.sapiens mRNA for fibrillin /cds=(0,9010) /gb=X63
20	33127_at	Cluster Incl. U89942:Human lysyl oxidase-related protein (WS9-14) mRNA,
	1451_s_at	D13666 /FEATURE= /DEFINITION=HUMOSF2OS Homo sapiens osf-2 mRNA
		for ost
	1372_at	M31165 /FEATURE=mRNA /DEFINITION=HUMTSG6A Human tumor necrosis factor-in
	1385_at	M77349 /FEATURE= /DEFINITION=HUMTGFBIG Human transforming growth factor-
25	1233_s_at	M76125 /FEATURE= /DEFINITION=HUMTYRKINR Human tyrosine kinase
		receptor
	753_at	D86425 /FEATURE= /DEFINITION=D86425 Homo sapiens mRNA for osteonidogen, c
	718_at	D87258 /FEATURE= /DEFINITION=D87258 Homo sapiens mRNA for serin protease
	719_g_at	D87258 /FEATURE= /DEFINITION=D87258 Homo sapiens mRNA for serin
30	proteas	
	671_at	J03040 /FEATURE= /DEFINITION=HUMSPARC Human SPARC/osteonectin mRNA,
		compl
	658_at	L12350 /FEATURE=mRNA /DEFINITION=HUMTHRSPO Human thrombospondin 2
		(THBS2)
35	659_g_at	L12350 /FEATURE=mRNA /DEFINITION=HUMTHRSPO Human
		thrombospondin 2 (THBS
	311_s_at	Fibronectin, Alt. Splice 1
	212_at	M97639 /FEATURE= /DEFINITION=HUMROR2A Human transmembrane receptor (ror2)
	120_at	X68742 /FEATURE= /DEFINITION=HSINTASA H.sapiens mRNA for integrin, alpha

Metagene 148

- 36488_at Cluster Incl. AB011542:Homo sapiens mRNA for MEGF9, partial cds /cds=(0
- 5** 36508_at Cluster Incl. AF030186:Homo sapiens glypican-4 (GPC4) mRNA, complete cd
- 37930_at Cluster Incl. U11700:Human copper transporting ATPase mRNA, complete cd
- 33348_at Cluster Incl. M80627:Human HEB helix-loop-helix protein (HEB) mRNA, com
- 33405_at Cluster Incl. N90755:zb22c08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
- 36571_at Cluster Incl. X68060:H.sapiens topIIb mRNA for topoisomerase IIb /cds=(
- 10** 37669_s_at Cluster Incl. U16799:Human Na,K-ATPase beta-1 subunit mRNA, complete
- 38805_at Cluster Incl. X89750:H.sapiens mRNA for TGIF protein /cds=(311,1129) /g
- 38843_at Cluster Incl. AL079310:Novel human gene mapping to chromosome 22 /cds=(5
- 40621_at Cluster Incl. U63809:Homo sapiens prostate apoptosis response protein p
- 41329_at Cluster Incl. AI458463:tj99b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 15** 41841_at Cluster Incl. AF052138:Homo sapiens clone 23718 mRNA sequence /cds=UNKN
- 1846_at L78132 /FEATURE= /DEFINITION=HUMPCTA1A Human prostate carcinoma tumor an

Metagene 149

- 20** 38215_at Cluster Incl. U84894:Human 239AB mRNA, complete cds /cds=(114,1028) /gb
- 32089_at Cluster Incl. AF079363:Homo sapiens sperm flagellar protein Repro-SA-1
- 38688_at Cluster Incl. AB007930:Homo sapiens mRNA for KIAA0461 peroteine, partial
- 34835_at Cluster Incl. D87442:Human mRNA for KIAA0253 gene, partial cds /cds=(0,
- 36179_at Cluster Incl. U12779:Human MAP kinase activated protein kinase 2 mRNA,
- 25** 1908_at L16464 /FEATURE= /DEFINITION=HUMETSONC Human ETS oncogene (PEP1)
- mRNA, c
- 1554_f_at U22028 /FEATURE=expanded_cds /DEFINITION=HSU22028 Human
- cytochrome P45
- 1555_f_at U22029 /FEATURE= /DEFINITION=HSU22029 Human cytochrome P450
- 30** (CYP2A7) m
- 1523_g_at U43408 /FEATURE= /DEFINITION=HSU43408 Human tyrosine kinase (Tnk1)
- mRN
- 1517_at J02906 /FEATURE=mRNA /DEFINITION=HUMCYPIIF Human cytochrome P450IIF1
- pro
- 35** 1492_f_at M33317 /FEATURE=mRNA /DEFINITION=HUMCYIIA4A Human cytochrome
- P450IIA4
- 1494_f_at M33318 /FEATURE=mRNA /DEFINITION=HUMCPPIA3A Human cytochrome
- P450IIA3

	1338_s_at	X13930 /FEATURE=cds /DEFINITION=HSCYP2A4 Human CYP2A4 mRNA for P-450 I
	646_s_at	L29218 /FEATURE=mRNA /DEFINITION=HUMCLK2B Homo sapiens clk2 mRNA, compl
5	Metagene 150	
	31936_s_at	Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds /cds=
	34445_at	Cluster Incl. AB007940:Homo sapiens mRNA for KIAA0471 protein, complete
10	38164_at	Cluster Incl. U57629:Human retinitis pigmentosa GTPase regulator (RPGR)
	38892_at	Cluster Incl. D87077:Human mRNA for KIAA0240 gene, partial cds /cds=(0,
	41372_at	Cluster Incl. AB020638:Homo sapiens mRNA for KIAA0831 protein, complete
	41621_i_at	Cluster Incl. AA868898:ak55b08.s1 Homo sapiens cDNA, 3 end /clone=IM
	41665_at	Cluster Incl. AB020631:Homo sapiens mRNA for KIAA0824 protein, partial
15	41710_at	Cluster Incl. AL079277:Homo sapiens mRNA full length insert cDNA clone
	32119_at	Cluster Incl. AL049423:Homo sapiens mRNA; cDNA DKFZp586B211 (from clone
	36456_at	Cluster Incl. AL080063:Homo sapiens mRNA; cDNA DKFZp564I052 (from clone
	38674_at	Cluster Incl. AA115140:zl10d12.r1 Homo sapiens cDNA, 5 end /clone=IMAG
20	40109_at	Cluster Incl. J03161:Human serum response factor (SRF) mRNA, complete c
	40453_s_at	Cluster Incl. U30826:Human splicing factor SRp40-1 (SRp40) mRNA, comp
	40828_at	Cluster Incl. D63476:Human mRNA for KIAA0142 gene, complete cds /cds=(4
	41219_at	Cluster Incl. AL050376:Homo sapiens mRNA; cDNA DKFZp586J101 (from clone
	41784_at	Cluster Incl. AL080186:Homo sapiens mRNA; cDNA DKFZp564B0769 (from
25	clon	
	32172_at	Cluster Incl. AL096858:Novel human gene mapping to chromosome 1 /cds=(33
	32183_at	Cluster Incl. M74002:Human arginine-rich nuclear protein mRNA, complete
	32218_at	Cluster Incl. AF034176:AF034176 Homo sapiens cDNA /clone=ntcon5-contig
	32253_at	Cluster Incl. AB007927:Homo sapiens mRNA for KIAA0458 protein, complete
30	32833_at	Cluster Incl. M59287:Human protein kinase mRNA /cds=UNKNOWN
	/gb=M59287	
	33373_at	Cluster Incl. AL049951:Homo sapiens mRNA; cDNA DKFZp564O0122 (from clon
	33457_at	Cluster Incl. AB029028:Homo sapiens mRNA for KIAA1105 protein, partial
35	33839_at	Cluster Incl. D26350:Human mRNA for type 2 inositol 1,4,5-trisphosphate
	34355_at	Cluster Incl. AJ132917:Homo sapiens mRNA for methyl-CpG-binding protein
	35843_at	Cluster Incl. L40402:Homo sapiens (clone Zap2) mRNA fragment /cds=UNKNO
	36680_at	Cluster Incl. M24895:Homo sapiens alpha-amylase mRNA, complete cds /cds
	36991_at	Cluster Incl. L14076:Human pre-mRNA splicing factor SRp75 mRNA, complet

	37034_at	Cluster Incl. U73477:Human acidic nuclear phosphoprotein pp32 mRNA, com
	38072_at	Cluster Incl. AL031432:Human DNA sequence from clone 465N24 on chromoso
	39163_at	Cluster Incl. W27233:24b7 Homo sapiens cDNA /gb=W27233 /gi=1306749 /ug=
	39507_at	Cluster Incl. AL050366:Homo sapiens mRNA; cDNA DKFZp564A126 (from
5	clone	
	40576_f_at	Cluster Incl. D89678:Homo sapiens mRNA for A+U-rich element RNA bindi
	40961_at	Cluster Incl. X72889:H.sapiens hbrm mRNA /cds=(222,4982) /gb=X72889 /gi
	41338_at	Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41529_g_at	Cluster Incl. W72239:zd62h08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
10	41808_at	Cluster Incl. AF052102:Homo sapiens clone 23926 mRNA sequence /cds=UNKN
	292_s_at	Protein Kinase
	Metagene 151	
15	33090_at	Cluster Incl. AJ007292:Homo sapiens mRNA for ephrin-A2 /cds=(15,656) /g
	33601_at	Cluster Incl. AF052145:Homo sapiens clone 24400 mRNA sequence /cds=UNKN
	35113_at	Cluster Incl. X98332:H.sapiens mRNA for organic cation transporter, liv
	33492_at	Cluster Incl. AI624840:ts71g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35897_r_at	Cluster Incl. AB005297:Homo sapiens BAI 1 mRNA, complete cds /cds=(18
20	36252_at	Cluster Incl. U43030:Human cardiotrophin-1 (CTF1) mRNA, complete cds /c
	37095_r_at	Cluster Incl. M84562:Human formyl peptide receptor-like receptor (FPR
	37153_at	Cluster Incl. AB014573:Homo sapiens mRNA for KIAA0673 protein, partial
	39601_at	Cluster Incl. AF061836:Homo sapiens putative tumor suppressor protein (
	39655_at	Cluster Incl. M26901:Human renin gene /cds=(90,1301) /gb=M26901 /gi=488
25	40286_r_at	Cluster Incl. AL050370:Homo sapiens mRNA; cDNA DKFZp566C0546 (from cl
	40324_r_at	Cluster Incl. AF070585:Homo sapiens clone 24675 mRNA sequence /cds=UN
	40336_at	Cluster Incl. J03826:Human adrenodoxin reductase mRNA, complete cds /cd
	40694_at	Cluster Incl. X73502:H. Sapiens mRNA for cytokeratin 20 /cds=(0,1019) /
	40714_at	Cluster Incl. S82198:caldecrin=serum calcium-decreasing factor [human,
30	41095_at	Cluster Incl. X52221:H.sapiens ERCC2 gene, exons 1 & 2 (partial) /cds=U
	41426_at	Cluster Incl. U38864:Human zinc-finger protein C2H2-150 mRNA, complete
	32681_at	Cluster Incl. S68616:Na+/H+ exchanger NHE-1 isoform [human, heart, mRNA
	36038_r_at	Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /c
	36075_at	Cluster Incl. AL037167:DKFZp564P1564_s1 Homo sapiens cDNA, 3 end /clon
35	37278_at	Cluster Incl. X92762:H.sapiens mRNA for tafazzins protein /cds=(288,116
	37970_at	Cluster Incl. AB028989:Homo sapiens mRNA for KIAA1066 protein, partial
	38258_at	Cluster Incl. U79290:Human clone 23908 mRNA sequence /cds=UNKNOWN
	/gb=U	
	32202_at	Cluster Incl. U67322:Human HBV associated factor (XAP4) mRNA, complete

- 33432_at Cluster Incl. AI547308:PN001_AH_B03.r Homo sapiens cDNA, 5' end /clone_
 34351_at Cluster Incl. AL022394:dJ511B24.2 (1-Phosphatidylinositol-4,5-Bisphosph
 34854_at Cluster Incl. AC004382:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-
 35269_at Cluster Incl. AF093420:Homo sapiens Hsp70 binding protein HspBP1 mRNA,
5 38478_at Cluster Incl. U08377:Human homolog of Drosophila splicing regulator sup
 39508_at Cluster Incl. AI201607:qb81b03.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 39543_at Cluster Incl. AI077476:oz49b01.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 39816_g_at Cluster Incl. AA883101:am24d05.s1 Homo sapiens cDNA, 3' end /clone=IM
 39821_s_at Cluster Incl. N95168:zb55f11.s1 Homo sapiens cDNA, 3' end /clone=IMAG
10 40186_at Cluster Incl. Y08302:H.sapiens mRNA for MAP kinase phosphatase 4 /cds=(
 40264_g_at Cluster Incl. AF001891:Homo sapiens clone lambda MEN1 region unknown
 40609_at Cluster Incl. AI475497:tj92g12.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 40892_s_at Cluster Incl. N91508:za91e09.s1 Homo sapiens cDNA, 3' end /clone=IMAG
 847_at U17969 /FEATURE=exons#1-6 /DEFINITION=HSU17969 Human initiation factor eI
15 720_at D87673 /FEATURE= /DEFINITION=D87673 Homo sapiens mRNA for heat shock tran
 721_g_at D87673 /FEATURE= /DEFINITION=D87673 Homo sapiens mRNA for heat
 shock tr
 225_at M31328 /FEATURE=mRNA /DEFINITION=HUMGNBPB3 Human guanine nucleotide-
 bindi
20
 Metagene 152
 35912_at Cluster Incl. AJ010901:Homo sapiens MUC4 gene, 3' flanking region /cds=(
 33744_at Cluster Incl. AL080150:Homo sapiens mRNA; cDNA DKFZp434D174 (from
25 clone
 34708_at Cluster Incl. D88587:Homo sapiens mRNA for Hakata antigen, complete cds
 35626_at Cluster Incl. U30894:Human N-sulphoglucosamine sulphohydrolase mRNA, co
 39846_at Cluster Incl. AF071748:Homo sapiens cathepsin F (CATSF) mRNA, complete
 1047_s_at U37055 /FEATURE=mRNA /DEFINITION=HSU37055 Human hepatocyte
30 growth fact
 Metagene 153
 31673_s_at Cluster Incl. X65784:H.sapiens CAR gene /cds=(0,428) /gb=X65784 /gi=4
35 33633_at Cluster Incl. AF030335:Homo sapiens purinergic P2Y11 receptor (P2Y11) m
 35170_at Cluster Incl. AF044414:Homo sapiens alpha mannosidase 6A8B (6a8b) mRNA,
 36522_at Cluster Incl. AB014516:Homo sapiens mRNA for KIAA0616 protein, partial
 37189_at Cluster Incl. AL023553:dJ347H13.3 (phosphomannomutase 1 (PMMH-22, yeast
 37903_at Cluster Incl. L25665:Human GTP-binding protein (HSR1) mRNA, complete cd

	39326_at	Cluster Incl. Z71460:H.sapiens mRNA for vacuolar-type H(+)-ATPase 115 k
	39437_at	Cluster Incl. Z78324:HSZ78324 Homo sapiens cDNA /clone=2.45-(CEPH) /gb=
	33833_at	Cluster Incl. J05243:Human nonerythroid alpha-spectrin (SPTAN1) mRNA, c
	35852_at	Cluster Incl. AB014558:Homo sapiens mRNA for KIAA0658 protein, partial
5	36123_at	Cluster Incl. D87292:Homo sapiens mRNA for rhodanese, complete cds /cds
	36124_at	Cluster Incl. X59434:Human rohu mRNA for rhodanese /cds=(34,924) /gb=X5
	38063_at	Cluster Incl. U00952:Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containi
	38064_at	Cluster Incl. X79882:H.sapiens lrp mRNA /cds=(105,2795) /gb=X79882 /gi=
	39134_at	Cluster Incl. AJ006973:Homo sapiens mRNA for TOM1 protein /cds=(61,1539
10	40234_at	Cluster Incl. X96484:H.sapiens mRNA for DGCR6 protein /cds=(422,676) /g
	40960_at	Cluster Incl. D29805:Human mRNA for beta-1,4-galactosyltransferase, com
	41282_s_at	Cluster Incl. AA194159:zr37h01.r1 Homo sapiens cDNA, 5 end /clone=IM
	41596_s_at	Cluster Incl. U43572:Human alpha-N-acetylglucosaminidase (NAGLU) gene
	32610_at	Cluster Incl. X93510:H.sapiens mRNA for 37 kDa LIM domain protein /cds=
15	533_g_at	U17418 /FEATURE= /DEFINITION=HSU17418 Human parathyroid
	hormone/parathy	

Metagene 154

20	34565_at	Cluster Incl. X78416:H.sapiens alpha-s1-casein mRNA /cds=(49,606) /gb=X
	34596_at	Cluster Incl. M73628:Homo sapiens kappa-casein mRNA, complete cds /cds=
	36288_at	Cluster Incl. X81420:H.sapiens mRNA for hHKb1 protein /cds=(0,1279) /gb
	38551_at	Cluster Incl. U52112:neural cell adhesion molecule L1 /cds=(19,3792) /g
	41470_at	Cluster Incl. AF027208:Homo sapiens AC133 antigen mRNA, complete cds /c
25	41656_at	Cluster Incl. AF043325:Homo sapiens N-myristoyltransferase 2 mRNA, comp
	41669_at	Cluster Incl. D83776:Human mRNA for KIAA0191 gene, partial cds /cds=(0,
	31786_at	Cluster Incl. AF051321:Homo sapiens Sam68-like phosphotyrosine protein
	32107_at	Cluster Incl. AL050173:Homo sapiens mRNA; cDNA DKFZp586F0422 (from
	clon	
30	33331_at	Cluster Incl. U17077:Human BENE mRNA, partial cds /cds=(0,446) /gb=U170
	34720_at	Cluster Incl. U85193:Human nuclear factor I-B2 (NFIB2) mRNA, complete c
	36821_at	Cluster Incl. AL050367:Homo sapiens mRNA; cDNA DKFZp564A026 (from
	clone	
	37265_at	Cluster Incl. D87074:Human mRNA for KIAA0237 gene, complete cds /cds=(4
35	38249_at	Cluster Incl. Z97632:dJ196E23.1.1 (novel protein) (isoform 1) /cds=(155
	32827_at	Cluster Incl. AI365215:qz41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	34296_at	Cluster Incl. AF041210:Homo sapiens midline 1 fetal kidney isoform 3 (M
	36635_at	Cluster Incl. AB023173:Homo sapiens mRNA for KIAA0956 protein, partial
	38098_at	Cluster Incl. D80010:Human mRNA for KIAA0188 gene, partial cds /cds=(0,

	39903_at	Cluster Incl. AB012955:Homo sapiens mRNA for KIP2, complete cds /cds=(6
	41355_at	Cluster Incl. N95229:zb53g09.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-
	1740_g_at	M99487 /FEATURE= /DEFINITION=HUMPSM Human prostate-specific
	membrane a	
5	160031_at	X63629 /FEATURE=cds /DEFINITION=HSPCAD H.sapiens mRNA for p
	cadherin /	
	Metagene 155	
10	32363_at	Cluster Incl. AF059214:Homo sapiens cholesterol 25-hydroxylase mRNA, co
	41690_at	Cluster Incl. AL049471:Homo sapiens mRNA; cDNA DKFZp586N012 (from
	clone	
	32666_at	Cluster Incl. U19495:Human intercrine-alpha (HIRH) mRNA, complete cds /
	36917_at	Cluster Incl. Z26653:H.sapiens mRNA for laminin M chain (merosin) /cds=
15	37187_at	Cluster Incl. M36820:Human cytokine (GRO-beta) mRNA, complete cds /cds=
	37279_at	Cluster Incl. U10550:Human Gem GTPase (gem) mRNA, complete cds /cds=(21
	37532_at	Cluster Incl. M91432:Human medium-chain acyl-CoA dehydrogenase (MCAD) g
	37599_at	Cluster Incl. AF017060:untitled /cds=(298,4314) /gb=AF017060 /gi=234315
	37958_at	Cluster Incl. AL049257:Homo sapiens mRNA; cDNA DKFZp564E153 (from
20	clone	
	38717_at	Cluster Incl. AL050159:Homo sapiens mRNA; cDNA DKFZp586A0522 (from
	clon	
	38968_at	Cluster Incl. AB005047:Homo sapiens mRNA for SH3 binding protein, compl
	38972_at	Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKN
25	39066_at	Cluster Incl. L38486:Human microfibril-associated glycoprotein 4 (MFAP4
	40767_at	Cluster Incl. M59499:Human lipoprotein-associated coagulation inhibitor
	40775_at	Cluster Incl. AL021786:Human DNA sequence from PAC 696H22 on chromosome
	41123_s_at	Cluster Incl. L35594:Human autotaxin mRNA, complete cds /cds=(49,2796
	41124_r_at	Cluster Incl. L35594:Human autotaxin mRNA, complete cds /cds=(49,2796
30	32239_at	Cluster Incl. U69263:Human matrilin-2 precursor mRNA, partial cds /cds=
	33834_at	Cluster Incl. L36033:Human pre-B cell stimulating factor homologue (SDF
	34363_at	Cluster Incl. Z11793:H.sapiens mRNA for selenoprotein P /cds=(36,1181)
	34388_at	Cluster Incl. Y11710:H.sapiens mRNA for extracellular matrix protein co
	34853_at	Cluster Incl. AB007865:Homo sapiens KIAA0405 mRNA, complete cds /cds=(1
35	34877_at	Cluster Incl. AL039831:DKFZp434D1112_s1 Homo sapiens cDNA, 3' end /clon
	36119_at	Cluster Incl. AF070648:Homo sapiens clone 24651 mRNA sequence /cds=UNKN
	36606_at	Cluster Incl. X51405:Human mRNA for carboxypeptidase E (EC 3.4.17.10) /
	36627_at	Cluster Incl. X86693:H.sapiens mRNA for hevin like protein /cds=(322,23
	36690_at	Cluster Incl. M10901:Human glucocorticoid receptor alpha mRNA, complete

- 37015_at Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022)
- 38737_at Cluster Incl. X57025:Human IGF-I mRNA for insulin-like growth factor I
- 38767_at Cluster Incl. AF041037:Homo sapiens novel antagonist of FGF signaling (
- 38786_at Cluster Incl. AL079279:Homo sapiens mRNA full length insert cDNA clone
- 5 40202_at Cluster Incl. D31716:Human mRNA for GC box bindig protein, complete cds
- 40230_at Cluster Incl. U91903:Human Fritz mRNA, complete cds /cds=(69,1046) /gb=
- 40570_at Cluster Incl. AF032885:Homo sapiens forkhead protein (FKHR) mRNA, compl
- 40607_at Cluster Incl. U97105:Homo sapiens N2A3 mRNA, complete cds /cds=(1336,30
- 32538_at Cluster Incl. S95936:transferrin [human, liver, mRNA, 2347 nt] /cds=(79
- 10 32551_at Cluster Incl. U03877:Human extracellular protein (S1-5) mRNA, complete
- 32587_at Cluster Incl. U07802:Human Tis11d gene, complete cds /cds=(291,1739) /g
- 32612_at Cluster Incl. X04412:Human mRNA for plasma gelsolin /cds=(14,2362) /gb=
- 1975_s_at X03563 /FEATURE=cds /DEFINITION=HSIGF1G1 Human gene for insulin-like
g
- 15 1814_at D50683 /FEATURE= /DEFINITION=D50683 Homo sapiens mRNA for TGF-betaIIIR al
- 1501_at X57025 /FEATURE=mRNA /DEFINITION=HSIGFACI Human IGF-I mRNA for insulin-l
- 656_at L08488 /FEATURE= /DEFINITION=HUMINOS Human inositol polyphosphate 1-phosp
- 607_s_at M10321 /FEATURE=mRNA /DEFINITION=HUMVWFM Human von
Willebrand factor mR
- 20 Metagene 156
- 38223_at Cluster Incl. AB024057:Homo sapiens mRNA for vascular Rab-GAP/TBC-conta
- 40666_at Cluster Incl. AF039918:Homo sapiens CD39L4 (CD39L4) mRNA, complete cds
- 25 33710_at Cluster Incl. U72515:Human C3f mRNA, complete cds /cds=(117,1262) /gb=U
- 35643_at Cluster Incl. X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /g
- 36543_at Cluster Incl. J02931:Human placental tissue factor (two forms) mRNA, co
- 39033_at Cluster Incl. Z78368:HSZ78368 Homo sapiens cDNA /clone=3.142-(CEPH) /gb
- 40504_at Cluster Incl. AF001601:Homo sapiens paraoxonase (PON2) mRNA, complete c
- 30 41129_at Cluster Incl. D26067:Human mRNA for KIAA0033 gene, partial cds /cds=(0,
- 35279_at Cluster Incl. U33821:Human tax1-binding protein TXBP151 mRNA, complete
- 36596_r_at Cluster Incl. S68805:L-arginine-glycine amidinotransferase [human, ki
- 36688_at Cluster Incl. U11313:Human sterol carrier protein-X/sterol carrier prot
- 38079_at Cluster Incl. AL049367:Homo sapiens mRNA; cDNA DKFZp586B0918 (from
- 35 clon
- 39150_at Cluster Incl. U69559:U69559 Homo sapiens cDNA /clone=26077 /gb=U69559 /
- 1228_s_at U73682 /FEATURE= /DEFINITION=HSU73682 Human meningioma-expressed
antig
- 498_at U33821 /FEATURE= /DEFINITION=HSU33821 Homo sapiens tax1-binding protein T

291_s_at J04152 /FEATURE=mRNA /DEFINITION=HUMGA733A Human
gastrointestinal tumor

Metagene 157

5

39698_at Cluster Incl. U51712:HSU51712 Homo sapiens cDNA /gb=U51712 /gi=1255282
35361_at Cluster Incl. W28299:44h4 Homo sapiens cDNA /gb=W28299 /gi=1308247 /ug=
38791_at Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(1
1557_at U24152 /FEATURE= /DEFINITION=HSU24152 Human p21-activated protein kinase
10 1558_g_at U24152 /FEATURE= /DEFINITION=HSU24152 Human p21-activated protein
kina

Metagene 158

15 37780_at Cluster Incl. AB011131:Homo sapiens mRNA for KIAA0559 protein, partial
41049_at Cluster Incl. S62539:insulin receptor substrate-1 [human, skeletal musc
34759_at Cluster Incl. U68494:Human hbc647 mRNA sequence /cds=UNKNOWN
/gb=U68494
37197_s_at Cluster Incl. AL050006:Homo sapiens mRNA; cDNA DKFZp564A033 (from clo
20 38312_at Cluster Incl. AL050002:Homo sapiens mRNA; cDNA DKFZp564O222 (from
clone
33452_at Cluster Incl. M15518:Human tissue-type plasminogen activator (t-PA) mRNA
37027_at Cluster Incl. M80899:Human novel protein AHNAK mRNA, partial sequence /
32531_at Cluster Incl. X52947:Human mRNA for cardiac gap junction protein /cds=(
25 1529_at U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence
872_i_at S62539 /FEATURE= /DEFINITION=S62539 insulin receptor substrate-1 [human
851_s_at S62539 /FEATURE= /DEFINITION=S62539 insulin receptor substrate-1 [human

Metagene 159

30

37832_at Cluster Incl. AL080062:Homo sapiens mRNA; cDNA DKFZp564I122 (from clone
39598_at Cluster Incl. X04325:Human liver mRNA for gap junction protein /cds=(62
41376_i_at Cluster Incl. J05428:Human 3,4-catechol estrogen UDP-glucuronosyltran
31843_at Cluster Incl. AB020639:Homo sapiens mRNA for KIAA0832 protein, complete
35 40141_at Cluster Incl. AB014595:Homo sapiens mRNA for KIAA0695 protein, complete
35343_at Cluster Incl. M37400:Human cytosolic aspartate aminotransferase mRNA, c
35837_at Cluster Incl. AJ224677:Homo sapiens mRNA for scrapie responsive protein
36667_at Cluster Incl. U47025:Human fetal brain glycogen phosphorylase B mRNA, c
36978_at Cluster Incl. D38521:Human mRNA for KIAA0077 gene, partial cds /cds=(0,

Metagene 160

- 34082_at Cluster Incl. W28356:48e3 Homo sapiens cDNA /gb=W28356 /gi=1308511 /ug=
5 37491_at Cluster Incl. D90359:Human CCG1 mRNA /cds=(51,5669) /gb=D90359 /gi=5593
 38962_at Cluster Incl. AB002296:Human mRNA for KIAA0298 gene, complete cds /cds=
 41386_i_at Cluster Incl. AB002344:Human mRNA for KIAA0346 gene, partial cds /cds
 32064_at Cluster Incl. Y13467:Homo sapiens mRNA for RB18A protein /cds=(235,4935
 32125_at Cluster Incl. AA928996:oo27f06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
10 35198_at Cluster Incl. AF070596:Homo sapiens clone 24796 mRNA sequence /cds=UNKN
 36915_at Cluster Incl. AI810485:wb89b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 37935_at Cluster Incl. AF016369:Homo sapiens U4/U6 small nuclear ribonucleoprote
 39343_at Cluster Incl. AW026656:vv15c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40792_s_at Cluster Incl. AF091395:Homo sapiens Trio isoform mRNA, complete cds /
15 33377_at Cluster Incl. X03168:Human mRNA for S-protein /cds=(61,1497) /gb=X03168
 33381_at Cluster Incl. AF012108:Homo sapiens Amplified in Breast Cancer (AIB1) m
 34886_at Cluster Incl. L02320:Human radixin mRNA, complete cds /cds=(30,1781) /g
 35733_at Cluster Incl. AF006082:Homo sapiens actin-related protein Arp2 (ARP2) m
 36999_at Cluster Incl. S66431:RBP2=retinoblastoma binding protein 2 [human, Nalm
20 37012_at Cluster Incl. U03271:Human F-actin capping protein beta subunit mRNA, c
 37711_at Cluster Incl. S57212:hMEF2C=myocyte enhancer-binding factor 2 [human, s
 39518_at Cluster Incl. H97470:yw11b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 39540_at Cluster Incl. AF000561:Homo sapiens TTF-I interacting peptide 21 mRNA,
 40581_at Cluster Incl. U42390:Homo sapiens Trio mRNA, complete cds /cds=(66,8651
25 41260_at Cluster Incl. U59321:Human DEAD-box protein p72 (P72) mRNA, complete cd
 1818_at Ras-Like Protein Tc10
 1124_at L04731 /FEATURE= /DEFINITION=HUMTRLALL1 Homo sapiens translocation T(4:1
 960_g_at Guanine Nucleotide-Binding Protein G25k
 834_at U40462 /FEATURE= /DEFINITION=HSU40462 Human Ikaros/LyF-1 homolog (hIk-1)
30 199_s_at U33052 /FEATURE= /DEFINITION=HSU33052 Human lipid-activated, protein
 ki

Metagene 161

- 35** 36229_at Cluster Incl. U58917:Homo sapiens IL-17 receptor mRNA, complete cds /cd
 38997_at Cluster Incl. X96924:H.sapiens gene encoding mitochondrial citrate tran
 38790_at Cluster Incl. L25879:Homo sapiens p53/HEH epoxide hydrolase (EPHX) mRNA
 39159_at Cluster Incl. X99656:H.sapiens mRNA for protein containing SH3 domain,
 40222_s_at Cluster Incl. AI677689:wd33c06.x1 Homo sapiens cDNA, 3 end /clone=IM

Metagene 162

- 38242_at Cluster Incl. AF068180:Homo sapiens B cell linker protein BLNK mRNA, al
5 37610_at Cluster Incl. AI765280:wi73a08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40054_at Cluster Incl. D43949:Human mRNA for KIAA0082 gene, partial cds /cds=(0,
 35777_at Cluster Incl. AB000468:Homo sapiens mRNA for zinc finger protein, compl
 36932_at Cluster Incl. D13636:Human mRNA for KIAA0011 gene, complete cds /cds=(3
 38369_at Cluster Incl. U70451:Human myeloid differentiation primary response pro

10

Metagene 163

- 37509_at Cluster Incl. AF046059:Homo sapiens cytokine receptor related protein 4
 37185_at Cluster Incl. Y00630:Human mRNA for Arg-Serpin (plasminogen activator-i
15 1207_at X66365 /FEATURE=cds /DEFINITION=HSSTHPKF H.sapiens mRNA PLSTIRE for seri
 358_at AF000545 /FEATURE=cds /DEFINITION=HSAF000545 Homo sapiens putative purine

Metagene 164

- 20** 35013_at Cluster Incl. AF013512:untitled /cds=(106,1551) /gb=AF013512 /gi=265381
 37244_at Cluster Incl. AA746355:oa56f02.r1 Homo sapiens cDNA /clone=IMAGE-130898
 38977_at Cluster Incl. U89436:Human tyrosyl-tRNA synthetase mRNA, complete cds /
 39008_at Cluster Incl. M13699:Human ceruloplasmin (ferroxidase) mRNA, complete c
 39799_at Cluster Incl. M94856:Human fatty acid binding protein homologue (PA-FAB
25 33433_at Cluster Incl. AL049943:Homo sapiens mRNA; cDNA DKFZp564F0522 (from
 clon
 34333_at Cluster Incl. AL021707:Human DNA sequence from clone 508I15 on chromoso
 37320_at Cluster Incl. D14694:Human mRNA for KIAA0024 gene, complete cds /cds=(1
 1500_at X51630 /FEATURE=mRNA /DEFINITION=HSWT1 Human Wilms tumor WT1 mRNA
30 for zi

Metagene 165

- 31736_at Cluster Incl. AA975427:oq28g02.s1 Homo sapiens cDNA, 3 end /clone=IMAG
35 31944_at Cluster Incl. AI028290:ov84f11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 33004_g_at Cluster Incl. AI275502:ql74d06.x1 Homo sapiens cDNA, 3 end /clone=IM
 33690_at Cluster Incl. AL080190:Homo sapiens mRNA; cDNA DKFZp434A202 (from
 clone
 32872_at Cluster Incl. AL049279:Homo sapiens mRNA; cDNA DKFZp564I083 (from clone

	34936_at	Cluster Incl. AB012130:Homo sapiens SBC2 mRNA for sodium bicarbonate co
	35419_g_at	Cluster Incl. J04178:Human abnormal beta-hexosaminidase alpha chain (
	35439_at	Cluster Incl. D26121:Human mRNA for ZFM1 protein alternatively spliced
	36707_s_at	Cluster Incl. X89059:H.sapiens mRNA for unknown protein expressed in
5	37487_at	Cluster Incl. AB029016:Homo sapiens mRNA for KIAA1093 protein, partial
	39286_at	Cluster Incl. D64109:Homo sapiens mRNA for tob family, complete cds /cd
	39637_at	Cluster Incl. U14528:Human sulfate transporter (DTD) mRNA, complete cds
	39969_at	Cluster Incl. AA255502:zr85b06.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	41091_at	Cluster Incl. U05237:Human fetal Alz-50-reactive clone 1 (FAC1) mRNA, c
10	41438_at	Cluster Incl. AL049923:Homo sapiens mRNA; cDNA DKFZp547E2210 (from
	clon	
	41465_at	Cluster Incl. AJ236885:Homo sapiens mRNA for ZBP-89 protein /cds=(391,2
	41612_at	Cluster Incl. AB007872:Homo sapiens KIAA0412 mRNA, partial cds /cds=(36
	32127_at	Cluster Incl. U90030:Homo sapiens bicaudal-D (BICD) mRNA, alternatively
15	34211_at	Cluster Incl. AL079697:DKFZp434E1930_r1 Homo sapiens cDNA, 5 end /clon
	34234_f_at	Cluster Incl. AI688640:wd40b07.x1 Homo sapiens cDNA, 3 end /clone=IM
	34684_at	Cluster Incl. L36140:Homo sapiens (clone 1311) DNA helicase (RECQL) mRN
	35632_at	Cluster Incl. U26710:Human cbl-b mRNA, complete cds /cds=(322,3270) /gb
	35985_at	Cluster Incl. AB023137:Homo sapiens mRNA for KIAA0920 protein, complete
20	36905_at	Cluster Incl. AB009356:Homo sapiens mRNA for TGF-beta activated kinase
	37280_at	Cluster Incl. U59912:Human chromosome 4 Mad homolog Smad1 mRNA, complet
	38639_at	Cluster Incl. AF040963:Homo sapiens Mad4 homolog (Mad4) mRNA, complete
	39419_at	Cluster Incl. AB011088:Homo sapiens mRNA for KIAA0516 protein, partial
	40464_g_at	Cluster Incl. U70322:Human transportin (TRN) mRNA, complete cds /cds=
25	33829_at	Cluster Incl. Y12670:Homo sapiens mRNA for leptin receptor gene-related
	33862_at	Cluster Incl. AF017786:Homo sapiens phosphatidic acid phosphohydrolase
	34337_s_at	Cluster Incl. AJ010014:Homo sapiens mRNA for M96A protein /cds=(243,2
	35373_at	Cluster Incl. M61906:Human P13-kinase associated p85 mRNA sequence /cds
	37026_at	Cluster Incl. AF001461:Homo sapiens Kruppel-like zinc finger protein Zf
30	37661_at	Cluster Incl. J04027:Human plasma membrane Ca2+ pumping ATPase mRNA, co
	37710_at	Cluster Incl. L08895:Homo sapiens MADS/MEF2-family transcription factor
	39450_s_at	Cluster Incl. AF050145:Homo sapiens iduronate-2-sulfatase (IDS) mRNA,
	40191_s_at	Cluster Incl. AI761647:wg66h09.x1 Homo sapiens cDNA, 3 end /clone=IM
	40589_at	Cluster Incl. U40572:Human beta2-syntrophin (SNT B2) mRNA, complete cds
35	40604_at	Cluster Incl. Y13493:Homo sapiens mRNA for protein kinase Dyrk2 /cds=(3
	40928_at	Cluster Incl. W26496:30d2 Homo sapiens cDNA /gb=W26496 /gi=1307195 /ug=
	40949_at	Cluster Incl. AF035812:Homo sapiens dynein light intermediate chain 2 (
	32588_s_at	Cluster Incl. X78992:H.sapiens ERF-2 mRNA /cds=(66,1544) /gb=X78992 /
	33102_at	Cluster Incl. D67031:Homo sapiens ADDL mRNA for adducin-like protein, c

- 33207_at Cluster Incl. AI095508:qb29a06.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 1785_at S66431 /FEATURE= /DEFINITION=S66431 RBP2=retinoblastoma binding protein
 1591_s_at J03242 /FEATURE= /DEFINITION=HUMGFIL2 Human insulin-like growth factor
- 5** 1325_at U59423 /FEATURE= /DEFINITION=HSU59423 Human Smad1 mRNA, complete cds
 514_at U26710 /FEATURE= /DEFINITION=HSU26710 Human cbl-b mRNA, complete cds
 479_at U53446 /FEATURE= /DEFINITION=HSU53446 Human mitogen-responsive phosphopro
 447_g_at U89896 /FEATURE= /DEFINITION=HSU89896 Homo sapiens casein kinase I gamm
- 10** Metagene 166
- 32497_s_at Cluster Incl. S70609:glycine transporter type 1b [human, substantia n
 34041_at Cluster Incl. U83171:Human macrophage-derived chemokine precursor (MDC)
15 35382_at Cluster Incl. AF043244:Homo sapiens apoptosis repressor ARC (ARC) mRNA,
 37467_at Cluster Incl. K02882:Human germline IgD chain gene, C-region, C-delta-1
 36185_at Cluster Incl. D32050:Human mRNA for alanyl-tRNA synthetase, complete cd
 404_at X52425 /FEATURE=mRNA /DEFINITION=HSIL4R Human IL-4-R mRNA for the interle
- 20** Metagene 167
- 31536_at Cluster Incl. AB020693:Homo sapiens mRNA for KIAA0886 protein, complete
 38139_at Cluster Incl. AF017445:Homo sapiens GDP-L-fucose pyrophosphorylase (GFP
 38500_at Cluster Incl. AB002450:Homo sapiens mRNA from chromosome 5q21-22, clone
25 32624_at Cluster Incl. AL050050:Homo sapiens mRNA; cDNA DKFZp566D133 (from clone
 34678_at Cluster Incl. AL096713:Homo sapiens mRNA; cDNA DKFZp564E1616 (from clon
- 36814_at Cluster Incl. AB029032:Homo sapiens mRNA for KIAA1109 protein, partial
30 36921_at Cluster Incl. U02556:Human RP3 mRNA, complete cds /cds=(68,418) /gb=U02
 37537_at Cluster Incl. L04510:Human nucleotide binding protein mRNA, complete cd
 37638_at Cluster Incl. D50857:Human DOCK180 protein mRNA, complete cds /cds=(23,
 38984_at Cluster Incl. AB007896:Homo sapiens KIAA0436 mRNA, partial cds /cds=(0,
 39794_at Cluster Incl. D29956:Human mRNA for KIAA0055 gene, complete cds /cds=(3
35 40086_at Cluster Incl. D87450:Human mRNA for KIAA0261 gene, partial cds /cds=(0,
 40140_at Cluster Incl. D76444:Homo sapiens hkf-1 mRNA, complete cds /cds=(922,29
 40411_at Cluster Incl. D80003:Human mRNA for KIAA0181 gene, partial cds /cds=(0,
 40831_at Cluster Incl. AL050190:Homo sapiens mRNA; cDNA DKFZp586B0923 (from clon

- 32779_s_at Cluster Incl. U23850:Human inositol 1,4,5 trisphosphate receptor type
 33865_at Cluster Incl. AA127624:zk89b09.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 36626_at Cluster Incl. X87176:H.sapiens mRNA for 17-beta-hydroxysteroid dehydrog
 38033_at Cluster Incl. AL049934:Homo sapiens mRNA; cDNA DKFZp564M1416 (from
5 clon
 38441_s_at Cluster Incl. X59408:H.sapiens, gene for Membrane cofactor protein /c
 39509_at Cluster Incl. AI692348:wd85g12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40615_at Cluster Incl. AA780049:zj24f06.s1 Homo sapiens cDNA, 3 end /clone=4512
 1912_s_at M74088 /FEATURE= /DEFINITION=HUMFAPAPC Human APC gene mRNA,
10 complete c
 1913_at U47414 /FEATURE= /DEFINITION=HSU47414 Human cyclin G2 mRNA, complete cds
 1725_s_at Oncogene E6-Ap, Papillomavirus
 1728_at L13689 /FEATURE=mRNA /DEFINITION=HUMBMI1X Human prot-oncogene (BMI-1)
 mR
15 1079_g_at M31661 /FEATURE= /DEFINITION=HUMPRLR Human prolactin (PRL)
 receptor mR
 393_s_at X90976 /FEATURE= /DEFINITION=HSRNAML11 H.sapiens mRNA for an
 acute myel
 192_at U18062 /FEATURE= /DEFINITION=HSU18062 Human TFIID subunit TAFII55 (TAFII5
20
 Metagene 168

 31724_at Cluster Incl. L38518:Homo sapiens sonic hedgehog protein (SHH) mRNA, co
 37413_at Cluster Incl. J05257:Homo sapiens (clones MDP4, MDP7) microsomal dipept
25 37514_s_at Cluster Incl. AB008047:Homo sapiens sMAP mRNA for small MBL-associate
 38544_at Cluster Incl. M13981:Human inhibin A-subunit mRNA, complete cds /cds=(1
 40003_at Cluster Incl. U36221:Human pancreatic zymogen granule membrane protein
 36829_at Cluster Incl. AF022991:Homo sapiens Rigui (RIGUI) mRNA, complete cds /c
 39878_at Cluster Incl. AI524125:th09d11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
30 2030_at N95031 /FEATURE= /DEFINITION=N95031 zb32b01.s1 Soares_parathyroid_tumor_
 1246_at U35234 /FEATURE= /DEFINITION=HSU35234 Human protein tyrosine phosphatase

 Metagene 169

35 33572_at Cluster Incl. U78722:Homo sapiens zinc finger protein 165 (Zpf165) mRNA
 38554_at Cluster Incl. AA903720:ok60c02.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 39957_at Cluster Incl. AF150247:AF150247 Homo sapiens cDNA /clone=CBFBCC09
 /gb=A
 41417_at Cluster Incl. AC003108:Human Chromosome 16 BAC clone CIT987SK-327O24 /c

	41447_at	Cluster Incl. AB023207:Homo sapiens mRNA for KIAA0990 protein, complete
	34699_at	Cluster Incl. AL050105:Homo sapiens mRNA; cDNA DKFZp586H0519 (from clon
	36060_at	Cluster Incl. U51920:Human signal recognition particle (SRP54) mRNA, co
5	37604_at	Cluster Incl. U44111:Human histamine N-methyltransferase (HNMT) gene /c
	37902_at	Cluster Incl. L13278:Homo sapiens zeta-crystallin/quinone reductase mRN
	38318_at	Cluster Incl. AL050128:Homo sapiens mRNA; cDNA DKFZp586G051 (from clone
	38654_at	Cluster Incl. X65488:H.sapiens U21.1 mRNA /cds=(41,2461) /gb=X65488 /gi
10	39005_s_at	Cluster Incl. AB018257:Homo sapiens mRNA for KIAA0714 protein, partia
	39065_s_at	Cluster Incl. D83077:Homo sapiens mRNA for TPRD, complete cds /cds=(1
	40048_at	Cluster Incl. D43951:Human mRNA for KIAA0099 gene, complete cds /cds=(5
	40066_at	Cluster Incl. AF046024:Homo sapiens UBA3 (UBA3) mRNA, complete cds /cds
	40125_at	Cluster Incl. L10284:Homo sapiens integral membrane protein, calnexin,
15	40844_at	Cluster Incl. D63875:Human mRNA for KIAA0155 gene, complete cds /cds=(8
	41131_f_at	Cluster Incl. U01923:Human BTK region clone fip-3 mRNA /cds=UNKNOWN /
	41132_r_at	Cluster Incl. U01923:Human BTK region clone fip-3 mRNA /cds=UNKNOWN /
	41785_at	Cluster Incl. U73824:Human p97 mRNA, complete cds /cds=(306,3029) /gb=U
	32150_at	Cluster Incl. X82834:H.sapiens mRNA for golgin /cds=(207,6764) /gb=X828
20	32846_s_at	Cluster Incl. D13629:Human mRNA for KIAA0004 gene, complete cds /cds=
	33443_at	Cluster Incl. Z99129:Human DNA sequence from clone 425C14 on chromosome
	34394_at	Cluster Incl. AB018327:Homo sapiens mRNA for KIAA0784 protein, partial
	35848_at	Cluster Incl. AL049432:Homo sapiens mRNA; cDNA DKFZp586J231 (from clone
	36128_at	Cluster Incl. L40397:Homo sapiens (clone S31i125) mRNA, 3 end of cds /
25	37000_at	Cluster Incl. AL035304:H.sapiens gene from PAC 295C6, similar to rat PO
	37306_at	Cluster Incl. D38549:Human mRNA for KIAA0068 gene, partial cds /cds=(0,
	37389_at	Cluster Incl. AI346580:qp51f08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	37693_at	Cluster Incl. L40393:Homo sapiens (clone S171) mRNA, complete cds /cds=
	38802_at	Cluster Incl. Y12711:H.sapiens mRNA for putative progesterone binding p
30	40903_at	Cluster Incl. AL049929:Homo sapiens mRNA; cDNA DKFZp547O0510 (from clon
	41573_at	Cluster Incl. X68560:H.sapiens SPR-2 mRNA for GT box binding protein /c
	33113_at	Cluster Incl. U65093:Human msg1-related gene 1 (mrg1) mRNA, complete cd
	950_at	D87127 /FEATURE= /DEFINITION=D87127 Homo sapiens mRNA for translocation p
35		
	Metagene 170	
	31503_at	Cluster Incl. W28732:50h7 Homo sapiens cDNA /gb=W28732 /gi=1308680 /ug=
	31699_at	Cluster Incl. S67334:phosphatidylinositol 3-kinase p110 beta isoform=11

- 31996_at Cluster Incl. AI798834:we93c04.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 33634_at Cluster Incl. AF038007:Homo sapiens FIC1 mRNA, complete cds /cds=(0,375
- 33647_s_at Cluster Incl. AA224768:nc12d09.r1 Homo sapiens cDNA /clone=IMAGE-1007
- 35597_at Cluster Incl. AJ000480:Homo sapiens mRNA for C8FW phosphoprotein /cds=(
- 5** 35934_at Cluster Incl. L19161:Human translation initiation factor eIF-2 gamma su
- 36262_at Cluster Incl. Z12173:H.sapiens GNS mRNA encoding glucosamine-6-sulphata
- 36263_g_at Cluster Incl. Z12173:H.sapiens GNS mRNA encoding glucosamine-6-sulpha
- 36696_at Cluster Incl. AB000359:Homo sapiens PIGCP1 pseudogene /cds=(0,416) /gb=
- 38230_at Cluster Incl. U81984:Human endothelial PAS domain protein 1 (EPAS1) mRN
- 10** 41390_at Cluster Incl. X69086:H.sapiens mRNA for utrophin /cds=(0,10301) /gb=X69
- 32115_r_at Cluster Incl. X68486:H.sapiens mRNA for A2a adenosine receptor /cds=(
- 34725_at Cluster Incl. M73077:Human glucocorticoid receptor repression factor 1
- 40493_at Cluster Incl. L05424:Human hyaluronate receptor (CD44) gene /cds=(136,2
- 41144_g_at Cluster Incl. U12022:Human calmodulin (CALM1) gene /cds=(199,648) /gb
- 15** 41782_g_at Cluster Incl. U22815:Human LAR-interacting protein 1a mRNA, complete
- 33372_at Cluster Incl. AI189226:qd04h11.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 36630_at Cluster Incl. Z50781:H.sapiens mRNA for leucine zipper protein /cds=(13
- 39522_at Cluster Incl. D49817:Homo sapiens mRNA for 6-phosphofructo-2-kinase/fru
- 39523_at Cluster Incl. AF038897:Homo sapiens syntaxin 16 mRNA, complete cds /cds
- 20** 40608_at Cluster Incl. AA013087:ze27c09.r1 Homo sapiens cDNA, 5' end /clone=IMAG
- 40984_at Cluster Incl. W28255:44b8 Homo sapiens cDNA /gb=W28255 /gi=1308203 /ug=
- 2082_s_at L08599 /FEATURE= /DEFINITION=HUMUVOECAD Human uvomorulin (E-cadherin)
- 1793_at M80629 /FEATURE= /DEFINITION=HUMCHED Human cdc2-related protein kinase (
- 25** 1735_g_at M60556 /FEATURE=mRNA#1 /DEFINITION=HUMTGFB3B Human transforming growth
- 1617_at D21205 /FEATURE= /DEFINITION=HUMERFP Human mRNA for estrogen responsive
- 1439_s_at X75346 /FEATURE=cds /DEFINITION=HSMAPKAP H.sapiens mRNA for MAP kinase
- 30** 1244_at U18671 /FEATURE=mRNA /DEFINITION=HSU18671 Human Stat2 gene, complete cds
- 1034_at U14394 /FEATURE= /DEFINITION=HSU14394 Human tissue inhibitor of metallopro
- 867_s_at U12471 /FEATURE=cds#2 /DEFINITION=HSU12471 Human thrombospondin-1 gene,
- 696_at Homeotic Protein Hox5.4
- 35** 672_at J03764 /FEATURE=cds /DEFINITION=HUMPA1A Human, plasminogen activator inhi
- 591_s_at M33684 /FEATURE=cds /DEFINITION=HUMPPP1A5 Human (clone lambda-16-1) no
- 594_s_at M55265 /FEATURE=mRNA /DEFINITION=HUMACKII Human casein kinase II alpha

352_at D30036 /FEATURE= /DEFINITION=HUMPITPA Human mRNA for phosphatidylinositol

Metagene 171

- 5 39236_s_at Cluster Incl. AL050372:Homo sapiens mRNA; cDNA DKFZp434A091 (from clo
40733_f_at Cluster Incl. D89377:Homo sapiens mRNA for MSX-2, complete cds /cds=(
32133_at Cluster Incl. AB011161:Homo sapiens mRNA for KIAA0589 protein, partial
35147_at Cluster Incl. AB002360:Human mRNA for KIAA0362 gene, partial cds /cds=(
38663_at Cluster Incl. AI033692:ow26f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
10 40150_at Cluster Incl. AA205857:zq50e04.r1 Homo sapiens cDNA, 5 end /clone=IMAG
36096_at Cluster Incl. AL080222:Homo sapiens mRNA; cDNA DKFZp566D1146 (from
clon
36136_at Cluster Incl. AF010315:Homo sapiens Pig11 (PIG11) mRNA, complete cds /c
37331_g_at Cluster Incl. U24266:Human pyrroline-5-carboxylate dehydrogenase (P5C
15 37342_s_at Cluster Incl. AF070531:Homo sapiens clone 24764 mRNA sequence /cds=UN
32553_at Cluster Incl. M94046:Human zinc finger protein (MAZ) mRNA /cds=UNKNOWN
568_at M80335 /FEATURE= /DEFINITION=HUMPKACATO Homo sapiens protein kinase A cat

Metagene 172

- 20 36213_at Cluster Incl. AB016816:Homo sapiens MASL1 mRNA, complete cds /cds=(0,31
40329_at Cluster Incl. AL031228:dJ1033B10.10 (membrane protein with histidine ri
32706_at Cluster Incl. X89887:Homo sapiens mRNA for WD repeat protein (HIRA) /cd
33258_g_at Cluster Incl. D26535:Human gene for dihydrolipoamide succinyltransfer
25 36000_at Cluster Incl. X98054:H.sapiens mRNA for G13 protein /cds=(33,2144) /gb=
41207_at Cluster Incl. AF043897:Homo sapiens C90RF3 large isoform, mRNA sequence
32514_s_at Cluster Incl. AF032906:Homo sapiens cathepsin Z precursor (CTSZ) mRNA
2034_s_at U10906 /FEATURE= /DEFINITION=HSU10906 Human cyclin-dependent kinase
in

30

Metagene 173

- 38172_at Cluster Incl. AB003151:Homo sapiens DNA, chromosome 21q22.2, PAC clone
41451_s_at Cluster Incl. W28498:50e2 Homo sapiens cDNA /gb=W28498 /gi=1308653 /u
35 36491_at Cluster Incl. D82345:Homo sapiens mRNA for NB thymosin beta, complete c
36496_at Cluster Incl. AF014398:Homo sapiens myo-inositol monophosphatase 2 mRNA
38328_at Cluster Incl. H10201:ym02c07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
38331_at Cluster Incl. Y07566:H.sapiens mRNA for RIT protein /cds=(145,804) /gb=
39043_at Cluster Incl. AF006084:Homo sapiens Arp2/3 protein complex subunit p41-

	39059_at	Cluster Incl. AF034544:Homo sapiens delta7-sterol reductase mRNA, compl
	39338_at	Cluster Incl. AI201310:qf71b11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	40134_at	Cluster Incl. AF047436:Homo sapiens F1Fo-ATPase synthase f subunit mRNA
	32229_at	Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mR
5	33422_at	Cluster Incl. AF052155:Homo sapiens clone 24761 mRNA sequence /cds=UNKN
	33423_g_at	Cluster Incl. AF052155:Homo sapiens clone 24761 mRNA sequence /cds=UN
	36671_at	Cluster Incl. M27396:Human asparagine synthetase mRNA, complete cds /cd
	36687_at	Cluster Incl. N50520:yy89b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	37325_at	Cluster Incl. D14697:Human mRNA for KIAA0003 gene, complete cds /cds=(1
10	37679_at	Cluster Incl. Y10313:Homo sapiens mRNA IFRD1 (PC4) interferon-related d
	38744_at	Cluster Incl. N95406:zb80g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	38815_at	Cluster Incl. Y08999:H.sapiens mRNA for Sop2p-like protein /cds=(33,114
	41535_at	Cluster Incl. AF006484:Homo sapiens putative oral tumor suppressor prot
	2050_s_at	M29870 /FEATURE= /DEFINITION=HUMRACA Human ras-related C3
15	botulinum to	
	Metagene 174	
	31911_at	Cluster Incl. AF000989:Homo sapiens thymosin beta 4 Y isoform (TB4Y) mR
20	32474_at	Cluster Incl. X96744:H.sapiens PAX7 gene, exon 1 (and joined CDS) /cds=
	33580_r_at	Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosom
	33637_g_at	Cluster Incl. U87459:Human autoimmunogenic cancer/testis antigen NY-E
	34093_at	Cluster Incl. AI829701:wf09d11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	34573_at	Cluster Incl. U14187:Human receptor tyrosine kinase ligand LERK-3 (EPLG
25	35090_g_at	Cluster Incl. AB005060:Homo sapiens mRNA for NTAK, complete cds /cds=
	32274_r_at	Cluster Incl. AF052148:Homo sapiens clone 24507 mRNA sequence /cds=UN
	33469_r_at	Cluster Incl. X68679:H. sapiens mRNA for DOWN 16 /cds=(23,1018) /gb=X
	34529_at	Cluster Incl. W26760:12d6 Homo sapiens cDNA /gb=W26760 /gi=1305844 /ug=
	35911_r_at	Cluster Incl. AJ003147:Homo sapiens complete genomic sequence between
30	36729_g_at	Cluster Incl. M76446:Human alpha-A1-adrenergic receptor mRNA, complet
	38882_r_at	Cluster Incl. AF096870:Homo sapiens estrogen-responsive B box protein
	37587_at	Cluster Incl. S43855:recoverin=photoreceptor protein [human, retina, mR
	37898_r_at	Cluster Incl. AI985964:wr79d08.x1 Homo sapiens cDNA, 3 end /clone=IM
	41125_r_at	Cluster Incl. D45421:Human mRNA for phosphodiesterase I alpha, comple
35	35782_at	Cluster Incl. AB014557:Homo sapiens mRNA for KIAA0657 protein, partial
	37687_i_at	Cluster Incl. M31932:Human IgG low affinity Fc fragment receptor (FcR
	39448_r_at	Cluster Incl. W27095:20c10 Homo sapiens cDNA /gb=W27095 /gi=1306467 /
	39500_s_at	Cluster Incl. AL049299:Homo sapiens mRNA; cDNA DKFZp564P233 (from clo
	39919_at	Cluster Incl. AI423340:tf36c07.x1 Homo sapiens cDNA, 3 end /clone=IMAG

	41251_at	Cluster Incl. L40410:Homo sapiens thyroid receptor interactor (TRIP3) m
	32557_at	Cluster Incl. AI762438:wg57a07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	1542_at X04571	/FEATURE=cds /DEFINITION=HSEGFRE Human mRNA for kidney epidermal
	778_s_at	D16827 /FEATURE=cds /DEFINITION=HUMSSTR5 Human gene for fifth
5	somatosta	
	Metagene 175	
	36260_at	Cluster Incl. AB002448:Homo sapiens mRNA from chromosome 5q21-22, clone
10	39670_at	Cluster Incl. AL050034:Homo sapiens mRNA; cDNA DKFZp566G0224 (from
	clon	
	40038_at	Cluster Incl. W02490:za48b02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
	41111_at	Cluster Incl. U68418:Human branched chain aminotransferase precursor (B
	31790_at	Cluster Incl. AL049801:Novel human gene mapping to chromosome 13, simila
15	31852_at	Cluster Incl. AL050390:Homo sapiens mRNA; cDNA DKFZp564O043 (from
	clone	
	32685_at	Cluster Incl. AB002349:Human mRNA for KIAA0351 gene, complete cds /cds=
	34181_at	Cluster Incl. X55330:H.sapiens mRNA for aspartylglucosaminidase /cds=(1
	37199_at	Cluster Incl. AI760932:wi70d01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
20	37252_at	Cluster Incl. U44755:Human PSE-binding factor PTF delta subunit mRNA, c
	38344_at	Cluster Incl. R40666:yf79c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	40486_g_at	Cluster Incl. AA176780:zp32a10.s1 Homo sapiens cDNA, 3 end /clone=IM
	41167_at	Cluster Incl. M64929:Human protein phosphatase 2A alpha subunit mRNA, c
	32153_s_at	Cluster Incl. U49869:Human ubiquitin gene, complete cds /cds=(94,783)
25	33933_at	Cluster Incl. X63187:H.sapiens HE4 mRNA for extracellular proteinase in
	36989_at	Cluster Incl. L19711:Human dystroglycan (DAG1) mRNA, complete cds /cds=
	38821_at	Cluster Incl. AJ002030:Homo sapiens mRNA for putative progesterone bind
	32565_at	Cluster Incl. U66619:Human SWI/SNF complex 60 KDa subunit (BAF60c) mRNA
	745_at D50495	/FEATURE=mRNA /DEFINITION=HUMTEF Homo sapiens mRNA for
30	transcripti	
	456_at U66619	/FEATURE= /DEFINITION=HSU66619 Human SWI/SNF complex 60 KDa
	subuni	
	Metagene 176	
35	33754_at	Cluster Incl. U43203:Human thyroid transcription factor 1 (TTF-1) mRNA,
	40277_at	Cluster Incl. AI799984:wc46f12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	Metagene 177	

- 31950_at Cluster Incl. Y00345:Human mRNA for polyA binding protein /cds=(502,240
38690_at Cluster Incl. AL080097:Homo sapiens mRNA; cDNA DKFZp564P0462 (from
clon
- 5** 39003_at Cluster Incl. Z50022:H.sapiens mRNA for surface glycoprotein /cds=(93,6
33905_at Cluster Incl. AF072242:Homo sapiens methyl-CpG binding protein MBD2 (MB
33930_at Cluster Incl. AB020724:Homo sapiens mRNA for KIAA0917 protein, partial
34304_s_at Cluster Incl. AL050290:Homo sapiens mRNA; cDNA DKFZp586G1923 (from cl
34796_at Cluster Incl. X63679:H.sapiens mRNA for TRAMP protein /cds=(121,1245) /
- 10** 35367_at Cluster Incl. AB006780:Homo sapiens mRNA for galectin-3, complete cds /
38801_at Cluster Incl. AI742846:wg46h09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
40910_at Cluster Incl. U56637:Human capping protein alpha subunit isoform 1 mRNA
40953_at Cluster Incl. S80562:acidic calponin [human, kidney, mRNA, 1607 nt] /cd
- 15** Metagene 178
- 39696_at Cluster Incl. AB028974:Homo sapiens mRNA for KIAA1051 protein, partial
35312_at Cluster Incl. D21063:Human mRNA for KIAA0030 gene, partial cds /cds=(0,
35314_at Cluster Incl. D63880:Human mRNA for KIAA0159 gene, complete cds /cds=(7
20 967_g_at X97795 /FEATURE=cds /DEFINITION=HSRAD54 H.sapiens mRNA
homologous to S.
947_at D55716 /FEATURE=/DEFINITION=HUMP1CDC47 Human mRNA for P1cdc47,
complete
- 25** Metagene 179
- 33942_s_at Cluster Incl. AF004563:Homo sapiens hUNC18b alternatively-spliced mRN
35009_at Cluster Incl. U33837:Human glycoprotein receptor gp330 precursor, mRNA,
38211_at Cluster Incl. AL050276:Homo sapiens mRNA; cDNA DKFZp566F123 (from
30 clone
38855_s_at Cluster Incl. D82343:Homo sapiens mRNA for AMY, complete cds /cds=(28
39266_at Cluster Incl. AF070632:Homo sapiens clone 24405 mRNA sequence /cds=UNKN
39615_at Cluster Incl. AB028949:Homo sapiens mRNA for KIAA1026 protein, partial
40646_at Cluster Incl. U20350:Human G protein-coupled receptor V28 mRNA, complet
35 40746_at Cluster Incl. L20814:Human glutamate receptor 2 (HBGR2) mRNA, complete
41395_at Cluster Incl. AB003791:Homo sapiens mRNA for keratan sulfate Gal-6-sulf
33235_at Cluster Incl. AB023155:Homo sapiens mRNA for KIAA0938 protein, complete
34257_at Cluster Incl. AB014605:Homo sapiens mRNA for KIAA0705 protein, complete
36042_at Cluster Incl. X75958:H.sapiens trkB mRNA for protein-tyrosine kinase /c

	36059_at	Cluster Incl. AB011540:Homo sapiens mRNA for MEGF7, partial cds /cds=(0
	37242_at	Cluster Incl. U79260:Human clone 23745 mRNA, complete cds /cds=(609,102
	37259_at	Cluster Incl. Z81326:H.sapiens mRNA for protease inhibitor 12 (PI12; ne
	38704_at	Cluster Incl. AB007934:Homo sapiens mRNA for KIAA0465 protein, partial
5	39014_at	Cluster Incl. D84239:Homo sapiens mRNA for IgG Fc binding protein, comp
	39058_at	Cluster Incl. U01147:Human guanine nucleotide regulatory protein (ABR)
	39758_f_at	Cluster Incl. J04182:Homo sapiens lysosomal membrane glycoprotein-1 (
	33890_at	Cluster Incl. AB008109:Homo sapiens mRNA for RGS5, complete cds /cds=(8
	34808_at	Cluster Incl. AB023216:Homo sapiens mRNA for KIAA0999 protein, partial
10	35354_at	Cluster Incl. AL022326:dJ333H23.2.2 (Synaptogyrin 1A (SYNGR1A)) /cds=(4
	36134_at	Cluster Incl. U79299:Human neuronal olfactomedin-related ER localized p
	36948_at	Cluster Incl. AL109701:Homo sapiens mRNA full length insert cDNA clone
	40278_at	Cluster Incl. AB029003:Homo sapiens mRNA for KIAA1080 protein, partial
	40936_at	Cluster Incl. AI651806:wb55f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
15	41498_at	Cluster Incl. AB020718:Homo sapiens mRNA for KIAA0911 protein, complete
	41830_at	Cluster Incl. AB007963:Homo sapiens mRNA for KIAA0494 protein, complete
	33182_at	Cluster Incl. AI018523:ou47d07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	185_at	U04840 /FEATURE= /DEFINITION=HSU04840 Human onconeural ventral antigen-1
20	Metagene 180	
	31478_at	Cluster Incl. M16653:Human pancreatic elastase IIB mRNA, complete cds /
	34060_g_at	Cluster Incl. AA586695:nn42h06.s1 Homo sapiens cDNA, 3 end /clone=IM
	34067_at	Cluster Incl. AL022314:dJ1170K4.2 (novel Trypsin family protein with cl
25	34586_s_at	Cluster Incl. U51003:Human DLX-2 (Dlx2) mRNA, complete cds /cds=UNKNO
	34463_at	Cluster Incl. M55983:Human DNase I mRNA, complete cds /cds=(159,1007) /
	35378_at	Cluster Incl. AI051683:oy77h08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35899_at	Cluster Incl. AF109401:Homo sapiens neurotrophic factor artemin precurs
	36765_at	Cluster Incl. AL080154:Homo sapiens mRNA; cDNA DKFZp434I114 (from clone
30	37885_at	Cluster Incl. AF038169:Homo sapiens clone 23790 unknown protein mRNA, c
	38529_at	Cluster Incl. X68968:H.sapiens mRNA for acetyl-CoA carboxylase /cds=(0,
	38901_at	Cluster Incl. AB020698:Homo sapiens mRNA for KIAA0891 protein, partial
	41002_at	Cluster Incl. U59299:Homo sapiens putative monocarboxylate transporter
	41118_at	Cluster Incl. AI921843:wp07a11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35	32048_at	Cluster Incl. AL049675:Human gene from PAC 886K2, chromosome 1 /cds=UNK
	32717_at	Cluster Incl. AF029729:Homo sapiens neuralized mRNA, complete cds /cds=
	38624_at	Cluster Incl. AF054506:Homo sapiens erythroid K-CI cotransporter splici
	38629_at	Cluster Incl. AF047863:untitled /cds=(17,1075) /gb=AF047863 /gi=2909668
	38707_r_at	Cluster Incl. S75174:E2F-4=transcription factor [human, Nalm6 and HeL

- 39689_at Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32752_at Cluster Incl. W72440:zd65e10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 36168_at Cluster Incl. X66945:H.sapiens N-sam mRNA for fibroblast growth factor
 39915_at Cluster Incl. AB001535:Homo sapiens mRNA, complete cds /cds=(445,4956)
5 40919_at Cluster Incl. M81830:Human somatostatin receptor isoform 2 (SSTR2) gene
 41321_s_at Cluster Incl. AA528077:nh90a11.s1 Homo sapiens cDNA, 3 end /clone=IM
 41793_at Cluster Incl. AI288757:qm11h01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 1910_s_at M14745 /FEATURE=cds /DEFINITION=HUMBCL2C Human bcl-2 mRNA
 1419_g_at D29675 /FEATURE=exon /DEFINITION=HUMNOSB Human inducible nitric
10 oxide
 716_at D87002 /FEATURE=cds#5 /DEFINITION=D87002 Homo sapiens immunoglobulin lamb
 420_at X65633 /FEATURE=cds /DEFINITION=HSACTHR H.sapiens ACTH-R gene for adrenoc
 Metagene 181
15
 40358_at Cluster Incl. M57609:Human DNA-binding protein (GLI3) mRNA, complete cd
 37605_at Cluster Incl. L10347:Human pro-alpha1 type II collagen (COL2A1) gene ex
 40808_at Cluster Incl. U03749:Human chromogranin A (CHGA) gene, promoter and /cd
20 Metagene 182
 31672_g_at Cluster Incl. D82351:Human retropseudogene MSSP-1 DNA, complete cds /
 40036_at Cluster Incl. AF035940:Homo sapiens MAGOH mRNA, complete cds /cds=(65,5
 31792_at Cluster Incl. M20560:Human lipocortin-III mRNA, complete cds /cds=(46,1
25 34196_at Cluster Incl. AI337901:qt34f05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 37646_at Cluster Incl. D26018:Human mRNA for KIAA0039 gene, partial cds /cds=(0,
 38651_at Cluster Incl. U60061:Human FEZ2 mRNA, partial cds /cds=(0,461) /gb=U600
 39787_at Cluster Incl. AB029821:Homo sapiens mRNA for phosphatidylethanolamine N
 33924_at Cluster Incl. AB029014:Homo sapiens mRNA for KIAA1091 protein, partial
30 37312_at Cluster Incl. D50917:Human mRNA for KIAA0127 gene, complete cds /cds=(2
 40242_at Cluster Incl. L36529:Human (clone N5-4) protein p84 mRNA, complete cds
 32530_at Cluster Incl. X56468:Human mRNA for 14.3.3 protein, a protein kinase re
 1108_s_at M18391 /FEATURE= /DEFINITION=HUMTKR Human tyrosine kinase receptor
35 (ep
 Metagene 183
 36413_at Cluster Incl. Z82200:Human DNA sequence from clone 333E23 on chromosome

- 34046_at Cluster Incl. Z83844:Human DNA sequence from clone 37E16 on chromosome
- 38521_at Cluster Incl. X59350:H.sapiens mRNA for B cell membrane protein CD22 /c
- 41045_at Cluster Incl. U77643:Homo sapiens K12 protein precursor mRNA, complete
- 32116_at Cluster Incl. AB002405:Homo sapiens mRNA for LAK-4p, complete cds /cds=
- 5 32660_at Cluster Incl. AB002340:Human mRNA for KIAA0342 gene, complete cds /cds=
- 36465_at Cluster Incl. U51127:Human interferon regulatory factor 5 (Humirf5) mRNA
- 37618_at Cluster Incl. M16937:Human homeo box c1 protein, mRNA, complete cds /cd
- 38091_at Cluster Incl. Z49107:H.sapiens mRNA for galectin /cds=(87,1058) /gb=Z49
- 766_at AB006782 /FEATURE= /DEFINITION=AB006782 Homo sapiens mRNA for galectin-9
- 10 384_at X71874 /FEATURE=cds#1 /DEFINITION=HSPROSCHY H.sapiens genes for proteasom
- 344_s_at D13146 /FEATURE=mRNA#1 /DEFINITION=HUM3CNP3 Homo sapiens gene for 2,3
- Metagene 184
- 15 32913_i_at Cluster Incl. AC005175:Homo sapiens chromosome 19, cosmid R31449 /cds
- 37771_at Cluster Incl. AB020688:Homo sapiens mRNA for KIAA0881 protein, complete
- 34706_at Cluster Incl. AB011090:Homo sapiens mRNA for KIAA0518 protein, partial
- 35753_at Cluster Incl. AB007510:Homo sapiens mRNA for PRP8 protein, complete cds
- 20 41356_at Cluster Incl. W27619:35c7 Homo sapiens cDNA /gb=W27619 /gi=1307567 /ug=
- 2075_s_at L36719 /FEATURE=mRNA /DEFINITION=HUMMKK3A Homo sapiens MAP kinase kina,
- 1587_at M38258 /FEATURE= /DEFINITION=HUMRARGA Human retinoic acid receptor gamma
- 1089_i_at M64936 /FEATURE= /DEFINITION=HUMRIRT Homo sapiens retinoic acid-
- 25 induci
- 704_at Nuclear Factor 1, A Type
- 160022_at X03663 /FEATURE=cds /DEFINITION=HSCFMS Human mRNA for c-fms proto-onco
- 30 Metagene 185
- 35719_at Cluster Incl. AB011178:Homo sapiens mRNA for KIAA0606 protein, partial
- 37628_at Cluster Incl. M69177:Human monoamine oxidase B (MAOB) mRNA, complete cd
- 38681_at Cluster Incl. U62962:Human Int-6 mRNA, complete cds /cds=(22,1359) /gb=
- 35 39072_at Cluster Incl. L07648:Human MXI1 mRNA, complete cds /cds=(208,894) /gb=L
- 40213_at Cluster Incl. M88163:Human global transcription activator homologous se
- 1389_at J03779 /FEATURE=mRNA /DEFINITION=HUMCALLA Human common acute lymphoblast
- 654_at L07648 /FEATURE= /DEFINITION=HUMMXI1A Human MXI1 mRNA, complete cds

202_at M65217 /FEATURE= /DEFINITION=HUMHSF2 Human heat shock factor 2 (HSF2) mRNA

Metagene 186

- 5** 32991_f_at Cluster Incl. M86933:Human amelogenin (AMELY) mRNA, complete cds /cds
 34644_at Cluster Incl. AB021288:Homo sapiens mRNA for beta 2-microglobulin, comp
 37521_s_at Cluster Incl. H82458:yv80b07.r1 Homo sapiens cDNA, 5' end /clone=IMAG
 39972_at Cluster Incl. Z94155:H.sapiens mRNA for P2Y-like G-protein coupled rece
 41007_at Cluster Incl. AF052497:Homo sapiens clone B18 unknown mRNA
- 10** /cds=UNKNOWN
 41430_at Cluster Incl. AB011113:Homo sapiens mRNA for KIAA0541 protein, partial
 33391_r_at Cluster Incl. S57235:CD68=110kda transmembrane glycoprotein [human, p
 40975_s_at Cluster Incl. AL050258:Novel human mRNA similar to mouse tuftelin-int
 1988_at X76079 /FEATURE=exons#1-4 /DEFINITION=HSPDGF H.sapiens mRNA for platelet
- 15** 1018_at U81787 /FEATURE= /DEFINITION=HSU81787 Human Wnt10B mRNA, complete cds
 662_at L13848 /FEATURE= /DEFINITION=HUMRNAHELA Human RNA helicase A mRNA, comple
 160042_s_at X58431 /FEATURE=mRNA#1 /DEFINITION=HSHOX22 Human Hox2.2 gene for a h

20

Metagene 187

- 34912_at Cluster Incl. AF052941:Homo sapiens DAP-kinase related protein 1 mRNA,
 37530_s_at Cluster Incl. U79716:Human reelin (RELN) mRNA, complete cds /cds=(175
- 25** 33315_at Cluster Incl. M29204:Human DNA-binding factor mRNA, complete cds /cds=(
 39811_at Cluster Incl. AA402538:zu48g06.r1 Homo sapiens cDNA, 5' end /clone=IMAG
 566_at M79462 /FEATURE= /DEFINITION=HUMPML1 Human PML-1 mRNA, complete CDS

Metagene 188

30

- 37425_g_at Cluster Incl. AB029343:Homo sapiens HCR (a-helix coiled-coil rod homo
 39307_s_at Cluster Incl. X81637:H.sapiens clathrin light chain b gene /cds=UNKNO
 40686_at Cluster Incl. AI985272:ws06b05.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 31814_i_at Cluster Incl. AB009462:Homo sapiens hLRp105 mRNA for LDL receptor rel
- 35** 35627_at Cluster Incl. U40571:Human alpha1-syntrophin (SNT A1) mRNA, complete cd
 35979_at Cluster Incl. AF081287:Homo sapiens serine phosphatase FCP1a (FCP1) mRN
 36053_at Cluster Incl. AF041248:Homo sapiens cyclin-dependent kinase inhibitor (
 36461_at Cluster Incl. U41804:Human putative T1/ST2 receptor binding protein pre
 39772_at Cluster Incl. AF007157:Homo sapiens clone 23856 unknown mRNA, partial c

34410_at Cluster Incl. U49260:Human mevalonate pyrophosphate decarboxylase (MPD)
 37706_at Cluster Incl. U28811:Human cysteine-rich fibroblast growth factor recep
 1842_at Oncogene Tls/Chop, Fusion Activated
 1100_at L76191 /FEATURE=mRNA /DEFINITION=HUMI1R Homo sapiens interleukin-1 recep

5

Metagene 189

41467_at Cluster Incl. AF070071:Homo sapiens MutS homolog (MSH5) mRNA, complete
 32623_at Cluster Incl. AJ225028:Homo sapiens mRNA for GABA-B R1a receptor /cds=(
 10 35161_at Cluster Incl. AB020667:Homo sapiens mRNA for KIAA0860 protein, complete
 35650_at Cluster Incl. AB002354:Human mRNA for KIAA0356 gene, complete cds /cds=
 38004_at Cluster Incl. X96753:H.sapiens mRNA for melanoma-associated chondroitin
 39370_at Cluster Incl. W28807:52a3 Homo sapiens cDNA /gb=W28807 /gi=1308755 /ug=
 40070_at Cluster Incl. D50912:Human mRNA for KIAA0122 gene, partial cds /cds=(0,
 15 32260_at Cluster Incl. X86809:H.sapiens mRNA for major astrocytic phosphoprotein
 33350_s_at Cluster Incl. Z78315:HSZ78315 Homo sapiens cDNA /clone=2.120-(CEPH) /
 34396_at Cluster Incl. AB023195:Homo sapiens mRNA for KIAA0978 protein, partial
 37377_i_at Cluster Incl. M13452:Human lamin A mRNA, 3end /cds=(0,1547) /gb=M1345
 37378_r_at Cluster Incl. M13452:Human lamin A mRNA, 3end /cds=(0,1547) /gb=M1345
 20 38743_f_at Cluster Incl. X06409:Human mRNA fragment for activated c-raf-1 (exons
 39532_at Cluster Incl. L36463:Homo sapiens ras interactor (RIN1) mRNA, complete
 40175_at Cluster Incl. AI141670:ot08b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40221_at Cluster Incl. L39059:Homo sapiens transcription factor SL1 mRNA, comple
 41268_g_at Cluster Incl. AB028972:Homo sapiens mRNA for KIAA1049 protein, partia
 25 1778_g_at L36463 /FEATURE= /DEFINITION=HUMA Homo sapiens ras interactor (RIN1)
 m
 160024_at X78342 /FEATURE=cds /DEFINITION=HSPISSLRE H.sapiens PISSLRE mRNA
 /NOTE

30 Metagene 190

32480_at Cluster Incl. X07495:Human mRNA for cp19 homeobox from HOX-3 locus /cds
 32324_at Cluster Incl. X57346:H.sapiens mRNA for HS1 protein /cds=(372,1112) /gb
 32045_at Cluster Incl. AB002331:Human mRNA for KIAA0333 gene, partial cds /cds=(
 35 1573_at M12783 /FEATURE=mRNA /DEFINITION=HUMSISPDG Human c-sis/platelet-derived

Metagene 191

- 32625_at Cluster Incl. X15357:Human mRNA for natriuretic peptide receptor (ANP-A
 33706_at Cluster Incl. AB006198:Homo sapiens mRNA for SART-1, complete cds /cds=
 36846_s_at Cluster Incl. AA121509:zk88c10.s1 Homo sapiens cDNA, 3 end /clone=IM
 40782_at Cluster Incl. AF061741:Homo sapiens retinal short-chain dehydrogenase/r
 5 33871_s_at Cluster Incl. J02876:Human placental folate binding protein mRNA, com
 34325_at Cluster Incl. AJ005893:Homo sapiens mRNA for JM26 protein, complete CDS
 36115_at Cluster Incl. L29217:Homo sapiens clk3 mRNA, complete cds /cds=(56,1528
 38730_at Cluster Incl. AB020671:Homo sapiens mRNA for KIAA0864 protein, partial
 41850_s_at Cluster Incl. U63825:Human hepatitis delta antigen interacting protei
 10
 Metagene 192
 32410_at Cluster Incl. X17651:Human Myf-4 mRNA for myogenic determination factor
 35068_at Cluster Incl. U88063:Human Agouti related protein (Art) mRNA, complete
 15 37447_at Cluster Incl. AF015257:Homo sapiens flow-induced endothelial G protein-
 37596_at Cluster Incl. U09117:Human phospholipase c delta 1 mRNA, complete cds /
 38356_at Cluster Incl. M19481:Human follistatin gene /cds=(0,953) /gb=M19481 /gi
 40161_at Cluster Incl. L32137:Human germline oligomeric matrix protein (COMP) mR
 40162_s_at Cluster Incl. AC003107:Human DNA from chromosome 19-specific cosmid R
 20 33850_at Cluster Incl. W28892:53c11 Homo sapiens cDNA /gb=W28892 /gi=1308840 /ug
 Metagene 193
 31734_at Cluster Incl. AJ000041:Homo sapiens mRNA for HOXC11 /cds=(44,958) /gb=A
 25 33069_f_at Cluster Incl. U06641:Human UDP glucuronosyltransferase mRNA, partial
 34549_g_at Cluster Incl. X55764:Human mRNA for cytochrome P-450 (11 Beta) /cds=(
 33520_at Cluster Incl. M13232:Human factor VII serine protease precursor mRNA, c
 38524_at Cluster Incl. U49184:Human occludin mRNA, complete cds /cds=(167,1735)
 41030_at Cluster Incl. X99350:H.sapiens HFH4 gene, exon 1 and joined CDS /cds=(2
 30 34264_at Cluster Incl. AB026894:Homo sapiens mRNA for NESCA, complete cds /cds=(
 34655_at Cluster Incl. AI951832:wx38b09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 34298_at Cluster Incl. X69532:H.sapiens gene for inter-alpha-trypsin inhibitor h
 35755_at Cluster Incl. U51336:Human inositol 1,3,4-trisphosphate 5/6-kinase mRNA
 37400_at Cluster Incl. J03068:Human DNF1552 (lung) mRNA, complete cds /cds=(292,
 35 1524_at U46194 /FEATURE= /DEFINITION=HSU46194 Human renal cell carcinoma antigen
 694_at Mucin 5b, Tracheobronchial

Metagene 194

- 31432_g_at Cluster Incl. U12255:Human IgG Fc receptor hFcRn mRNA, complete cds /
- 34957_at Cluster Incl. Y18504:Homo sapiens X5L gene /cds=(112,1089) /gb=Y18504 /
- 39607_at Cluster Incl. AL080178:Homo sapiens mRNA; cDNA DKFZp434K171 (from clone
- 5** 37186_s_at Cluster Incl. U11863:Human clone HP-DAO2 diamine oxidase, copper/topa
- 37908_at Cluster Incl. U31384:Human G protein gamma-11 subunit mRNA, complete cd
- Metagene 195
- 10** 34607_at Cluster Incl. AB023135:Homo sapiens mRNA for activation-inducible lymph
- 32287_s_at Cluster Incl. AJ001685:Homo sapiens NKG2E gene /cds=(45,767) /gb=AJ00
- 33462_at Cluster Incl. D13626:Human mRNA for KIAA0001 gene, complete cds /cds=(2
- 41054_at Cluster Incl. AB006628:Homo sapiens mRNA for KIAA0290 gene, partial cds
- 37539_at Cluster Incl. AB023176:Homo sapiens mRNA for KIAA0959 protein, partial
- 15** 41177_at Cluster Incl. AW024285:wt69d06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 36203_at Cluster Incl. X16277:Human gene for ornithine decarboxylase ODC (EC 4.1
- 2002_s_at U27467 /FEATURE= /DEFINITION=HSU27467 Human Bcl-2 related (Bfl-1) mRNA
- 1630_s_at Tyrosine Kinase Syk
- 20** 998_s_at X59770 /FEATURE=mRNA /DEFINITION=HSIL1R2II H.sapiens IL-1R2 mRNA for ty
- 907_at M13792 /FEATURE=cds /DEFINITION=HUMADAG Human adenosine deaminase (ADA) g
- 478_g_at U51127 /FEATURE= /DEFINITION=HSU51127 Human interferon regulatory
- 25** facto
- 265_s_at M24736 /FEATURE= /DEFINITION=HUMELAM1A Human endothelial leukocyte adhe
- Metagene 196
- 30**
- 33648_at Cluster Incl. W28800:52g12 Homo sapiens cDNA /gb=W28800 /gi=1308811 /ug
- 40432_at Cluster Incl. AA522891:ni41b12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 37362_at Cluster Incl. X54871:H.sapiens mRNA for ras-related protein Rab5b /cds=
- 35** Metagene 197
- 35919_at Cluster Incl. J05068:human transcobalamin I mRNA, complete cds /cds=(75
- 34733_at Cluster Incl. X85237:H.sapiens mRNA for splicing factor SF3a120 /cds=(9
- 38657_s_at Cluster Incl. M20471:Human brain-type clathrin light-chain a mRNA, co

- 39018_at Cluster Incl. AF026977:Homo sapiens microsomal glutathione S-transferase
- 39685_at Cluster Incl. AL050282:Homo sapiens mRNA; cDNA DKFZp586H2219 (from
clon
- 32830_g_at Cluster Incl. X97544:H.sapiens mRNA for TIM17 preprotein translocase
- 5 33820_g_at Cluster Incl. X13794:H.sapiens lactate dehydrogenase B gene exon 1 an
- 34307_at Cluster Incl. U81006:Human p76 mRNA, complete cds /cds=(133,2124) /gb=U
- 37025_at Cluster Incl. AL120815:DKFZp762F172_r1 Homo sapiens cDNA, 5 end /clone
- 37367_at Cluster Incl. X76228:H.sapiens mRNA for vacuolar H⁺ ATPase E subunit /c
- 38054_at Cluster Incl. AF029890:Homo sapiens hepatitis B virus X interacting pro
- 10 40637_at Cluster Incl. Y00371:Human hsc70 gene for 71 kd heat shock cognate prot
- 41253_s_at Cluster Incl. AI983043:wz30b11.x1 Homo sapiens cDNA, 3 end /clone=IM
- 32547_at Cluster Incl. X56253:Human MPR46 gene for 46kd mannose 6-phosphate rece
- 32564_at Cluster Incl. AA083129:zn31a06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 2010_at U33760 /FEATURE= /DEFINITION=HSU33760 Human cyclin A/CDK2-associated p19
- 15 1624_at Stimulatory Gdp/Gtp Exchange Protein For C-Ki-Ras P21 And Smg P21
- 1179_at Heat Shock Protein, 70 Kda
- 1180_g_at Heat Shock Protein, 70 Kda
- 1009_at U51004 /FEATURE= /DEFINITION=HSU51004 Homo sapiens protein kinase C inhi
- 869_at U14193 /FEATURE= /DEFINITION=HSU14193 Human TFIIA gamma subunit mRNA,
- 20 com
- Metagene 198
- 37155_at Cluster Incl. AB020675:Homo sapiens mRNA for KIAA0868 protein, partial
- 25 32686_at Cluster Incl. D86096:Human DNA for prostaglandin E receptor EP3 subtype
- 38429_at Cluster Incl. U29344:Human breast carcinoma fatty acid synthase mRNA, c
- 103_at Z19585 /FEATURE=cds /DEFINITION=HSTHROMB4 H.sapiens mRNA for
thrombospond
- 30 Metagene 199
- 31680_at Cluster Incl. M55630:Human topoisomerase.I pseudogene 2 /cds=UNKNOWN /g
- 31788_at Cluster Incl. AB014537:Homo sapiens mRNA for KIAA0637 protein, complete
- 34199_at Cluster Incl. AJ131244:Homo sapiens mRNA for Sec24 protein (Sec24A isof
- 35 34215_at Cluster Incl. L03426:Human XE7 mRNA, complete alternate coding regions
- 35662_at Cluster Incl. U20536:Human cysteine protease Mch2 isoform alpha (Mch2)
- 36552_at Cluster Incl. AL080220:Homo sapiens mRNA; cDNA DKFZp586P0123 (from
clon

- 38296_at Cluster Incl. AL050196:Homo sapiens mRNA; cDNA DKFZp586D2223 (from
clon
- 39436_at Cluster Incl. AF079221:Homo sapiens BCL2/adenovirus E1B 19kDa-interacti
- 34817_s_at Cluster Incl. U70671:Human ataxin-2 related protein mRNA, partial cds
- 5 1295_at L19067 /FEATURE= /DEFINITION=HUMNFKB65A Human NF-kappa-B transcription f
- Metagene 200
- 36736_f_at Cluster Incl. Y10275:H.sapiens mRNA for L-3-phosphoserine phosphatase
- 10 32679_at Cluster Incl. D13634:Human mRNA for KIAA0009 gene, complete cds /cds=(1
36090_at Cluster Incl. AL080162:Homo sapiens mRNA; cDNA DKFZp434N024 (from
clone
- 36500_at Cluster Incl. AF027974:Homo sapiens clone LM1955 H105e3 gene, partial c
- 37263_at Cluster Incl. U55206:Homo sapiens human gamma-glutamyl hydrolase (hGH)
- 15 39042_at Cluster Incl. X05615:Human mRNA for thyroglobulin /cds=(41,8344) /gb=X0
36582_g_at Cluster Incl. U09510:Human glycyl-tRNA synthetase mRNA, complete cds
37678_at Cluster Incl. U23070:Human putative transmembrane protein (nma) mRNA, c
1536_at U77949 /FEATURE= /DEFINITION=HSU77949 Human Cdc6-related protein (HsCDC6
- 20 Metagene 201
- 33543_s_at Cluster Incl. U77718:Human desmosome associated protein pinin mRNA, c
- 34473_at Cluster Incl. AF051151:Homo sapiens Toll/interleukin-1 receptor-like pr
- 37445_at Cluster Incl. AB015633:Homo sapiens mRNA for type II membrane protein,
- 25 33791_at Cluster Incl. Y15227:Homo sapiens mRNA for leukemia associated gene 1 /
34654_at Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990
36031_at Cluster Incl. AB024401:Homo sapiens mRNA for p33, complete cds /cds=(45
36054_at Cluster Incl. AB020699:Homo sapiens mRNA for KIAA0892 protein, partial
38353_at Cluster Incl. AF042378:Homo sapiens spindle pole body protein spc98 hom
- 30 38626_at Cluster Incl. AB007859:Homo sapiens KIAA0399 mRNA, partial cds /cds=(0,
40404_s_at Cluster Incl. U18291:Human CDC16Hs mRNA, complete cds /cds=(24,1883)
40811_at Cluster Incl. AB011148:Homo sapiens mRNA for KIAA0576 protein, partial
32165_at Cluster Incl. L41887:Homo sapiens splicing factor, arginine/serine-rich
- 32841_at Cluster Incl. U19765:Human nucleic acid binding protein gene, complete
- 35 35738_at Cluster Incl. AI347088:qp60d09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
36953_at Cluster Incl. U44378:Human homozygous deletion target in pancreatic car
38400_at Cluster Incl. AI920820:wn82e10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
41790_at Cluster Incl. AL031230:dJ73M23.2 (NAD+-dependent succinic semialdehyde

	2064_g_at	L20046 /FEATURE= /DEFINITION=HUMERCC5A Human ERCC5 excision
	repair pro	
	1686_g_at	X82554 /FEATURE=mRNA /DEFINITION=HSSPHAR H.sapiens SPHAR gene
	for cycl	
5	Metagene 202	
	39597_at	Cluster Incl. AB020650:Homo sapiens mRNA for KIAA0843 protein, complete
	41389_s_at	Cluster Incl. U46193:Human renal cell carcinoma antigen RAGE-3 mRNA,
10	31822_at	Cluster Incl. L12579:Human alternatively spliced CUTL1 mRNA, complete c
	36083_at	Cluster Incl. U01160:Human transmembrane 4 superfamily protein (SAS) mR
	36553_at	Cluster Incl. AA669799:ag36c04.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	40772_at	Cluster Incl. AA284298:zc30c10.T7 Homo sapiens cDNA, 3 end /clone=IMAG
	32237_at	Cluster Incl. D87454:Human mRNA for KIAA0265 gene, partial cds /cds=(0,
15	38410_at	Cluster Incl. X72964:H.sapiens mRNA for caltractin /cds=(47,565) /gb=X7
	41590_at	Cluster Incl. AI652660:wb30c10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	1212_at	U86529 /FEATURE= /DEFINITION=HSU86529 Human glutathione transferase Zeta
	Metagene 203	
20	33605_at	Cluster Incl. AF019415:untitled /cds=(105,926) /gb=AF019415 /gi=3955194
	33606_g_at	Cluster Incl. AF019415:untitled /cds=(105,926) /gb=AF019415 /gi=39551
	40004_at	Cluster Incl. X91868:H.sapiens mRNA for SIX1 protein /cds=(275,1129) /g
	40327_at	Cluster Incl. U57052:Human Hoxb-13 mRNA, complete cds /cds=(54,908) /gb
25	40056_at	Cluster Incl. D87989:Human mRNA for UDP-galactose transporter related i
	34865_at	Cluster Incl. AI360249:qy84f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	38473_at	Cluster Incl. M63180:Human threonyl-tRNA synthetase mRNA, complete cds
	40167_s_at	Cluster Incl. AF038187:Homo sapiens clone 23714 mRNA sequence /cds=UN
30	Metagene 204	
	34460_at	Cluster Incl. AB014512:Homo sapiens mRNA for KIAA0612 protein, partial
	38889_at	Cluster Incl. AF104304:Homo sapiens Smad anchor for receptor activation
	38954_at	Cluster Incl. Y18423:Homo sapiens VIP2R gene, exons 1-2 (and joined CDS
35	40035_at	Cluster Incl. AB012917:Homo sapiens mRNA for serine protease (TLSP), co
	41077_at	Cluster Incl. AB011115:Homo sapiens mRNA for KIAA0543 protein, partial
	41421_at	Cluster Incl. AB020716:Homo sapiens mRNA for KIAA0909 protein, partial
	41473_at	Cluster Incl. L05779:Human cytosolic epoxide hydrolase mRNA, complete c
	41649_at	Cluster Incl. AF038177:Homo sapiens clone 23899 mRNA sequence /cds=UNKN

	33263_at	Cluster Incl. X67098:H.sapiens rTS alpha mRNA containing four open read
	33788_at	Cluster Incl. AB002390:Human mRNA for KIAA0392 gene, partial cds /cds=(
	34178_at	Cluster Incl. AI884738:wl84b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	34701_at	Cluster Incl. U83192:Homo sapiens post-synaptic density protein 95 (PSD
5	35652_g_at	Cluster Incl. AF002715:Homo sapiens MAP kinase kinase kinase (MTK1) m
	37192_at	Cluster Incl. U28389:Human dematin 52 kDa subunit mRNA, complete cds /c
	38711_at	Cluster Incl. AB014527:Homo sapiens mRNA for KIAA0627 protein, partial
	39408_at	Cluster Incl. Z80345:H.sapiens SCAD gene, 5 UTR exon 1 and 2 (and joine
	40428_i_at	Cluster Incl. AW043812:wy81b07.x1 Homo sapiens cDNA, 3 end /clone=IM
10	41749_at	Cluster Incl. U53003:Human GT335 mRNA, complete cds /cds=(84,890) /gb=U
	33408_at	Cluster Incl. AB023151:Homo sapiens mRNA for KIAA0934 protein, partial
	35265_at	Cluster Incl. U31501:Human fragile X mental retardation syndrome relate
	36118_at	Cluster Incl. AJ000882:Homo sapiens mRNA for steroid receptor coactivat
	38376_at	Cluster Incl. L46590:Homo sapiens very long chain acyl-CoA dehydrogenas
15	38794_at	Cluster Incl. X53390:Human mRNA for upstream binding factor (hUBF) /cds
	38817_at	Cluster Incl. AF047437:Homo sapiens sperm acrosomal protein mRNA, compl
	487_g_at	U60521 /FEATURE= /DEFINITION=HSU60521 Human protease proMch6
	(Mch6) mRN	
20	Metagene 205	
	33801_at	Cluster Incl. AF104222:Homo sapiens CD2 cytoplasmic domain binding prot
	36841_at	Cluster Incl. AA811338:ob81g05.s1 Homo sapiens cDNA /clone=IMAGE-133781
	39401_at	Cluster Incl. W28264:44c9 Homo sapiens cDNA /gb=W28264 /gi=1308212 /ug=
25	37016_at	Cluster Incl. D13900:Homo sapiens mRNA for mitochondrial short-chain en
	38480_s_at	Cluster Incl. U66867:Human ubiquitin conjugating enzyme 9 (hUBC9) mRN
	1939_at	M22898 /FEATURE=mRNA /DEFINITION=HUMP53A11 Human phosphoprotein p53
	gene	
	1754_at	AF006041 /FEATURE= /DEFINITION=AF006041 Homo sapiens Fas-binding protein
30	1374_g_at	M31523 /FEATURE= /DEFINITION=HUMTFAA Human transcription factor
	(E2A)	
	1199_at	D13748 /FEATURE= /DEFINITION=HUM4AI Human mRNA for eukaryotic initiation
	838_s_at	U45328 /FEATURE= /DEFINITION=HSU45328 Human ubiquitin-conjugating
	enzym	
35	Metagene 206	
	38234_at	Cluster Incl. M99438:Human transducin-like enhancer protein (TLE3) mRNA
	33763_at	Cluster Incl. AI829671:wf09b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG

- 35761_at Cluster Incl. AL050073:Homo sapiens mRNA; cDNA DKFZp566E2346 (from
clon
356_at AB017430 /FEATURE= /DEFINITION=AB017430 Homo sapiens mRNA for kinesin-lik
- 5** Metagene 207
- 32957_g_at Cluster Incl. AC002550:Human Chromosome 16 BAC clone CIT987SK-A-101F1
35204_at Cluster Incl. U52840:Homo sapiens semaphorin F homolog mRNA, complete c
36938_at Cluster Incl. U70063:Human acid ceramidase mRNA, complete cds /cds=(17,
10 1145_g_at Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 4, K-Sam IV
461_at U70063 /FEATURE= /DEFINITION=HSU70063 Human acid ceramidase mRNA, complet
- Metagene 208
- 15** 38143_at Cluster Incl. L33404:Human stratum corneum chymotryptic enzyme mRNA, co
31891_at Cluster Incl. U58515:Human chitinase (HUMTCHIT) mRNA, exon 1b form, par
39385_at Cluster Incl. M22324:Human aminopeptidase N/CD13 mRNA encoding aminopep
39723_at Cluster Incl. AF062536:Homo sapiens cullin 1 mRNA, complete cds /cds=(1
36939_at Cluster Incl. D49958:Homo sapiens mRNA for membrane glycoprotein M6, co
20 37676_at Cluster Incl. AF056490:Homo sapiens cAMP-specific phosphodiesterase 8A
33105_at Cluster Incl. W28790:54g3 Homo sapiens cDNA /gb=W28790 /gi=1308945 /ug=
- Metagene 209
- 25** 34119_at Cluster Incl. AA704268:zj22a08.s1 Homo sapiens cDNA, 3 end /clone=4509
39641_at Cluster Incl. X52486:Human mRNA for uracil-DNA glycosylase /cds=(79,105
32122_at Cluster Incl. L31573:Human sulfite oxidase mRNA, complete cds /cds=(903
35203_at Cluster Incl. AB002381:Human mRNA for KIAA0383 gene, partial cds /cds=(
35214_at Cluster Incl. AF061016:Homo sapiens UDP-glucose dehydrogenase (UGDH) mR
30 36451_at Cluster Incl. AI743299:wg91b04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
39369_at Cluster Incl. AB023152:Homo sapiens mRNA for KIAA0935 protein, partial
40521_at Cluster Incl. AL050259:Homo sapiens mRNA; cDNA DKFZp547D0710 (from
clon
32149_at Cluster Incl. AA532495:nj54a10.s1 Homo sapiens cDNA /clone=IMAGE-996282
35 32169_at Cluster Incl. AB020682:Homo sapiens mRNA for KIAA0875 protein, partial
34827_at Cluster Incl. AF045458:Homo sapiens serine/threonine kinase ULK1 (ULK1)
35356_at Cluster Incl. W21884:58c2 Homo sapiens cDNA /clone=(not-directional) /g
36093_at Cluster Incl. AB014514:Homo sapiens mRNA for KIAA0614 protein, partial
36625_at Cluster Incl. L40401:Homo sapiens (clone zap128) mRNA, 3 end of cds /c

	38103_at	Cluster Incl. AB014542: Homo sapiens mRNA for KIAA0642 protein, partial
	Metagene 210	
5	34585_at	Cluster Incl. L07919: Human homeodomain protein DLX-2 mRNA, 3 end /cds=
	37841_at	Cluster Incl. M16541: Human butyrylcholinesterase, mRNA, complete cds /c
	35285_at	Cluster Incl. AF007216: Homo sapiens sodium bicarbonate cotransporter (H
	41533_at	Cluster Incl. U79298: Human clone 23803 mRNA, partial cds /cds=(0,1123)
10	Metagene 211	
	31498_f_at	Cluster Incl. U19147: Human GAGE-6 protein mRNA, complete cds /cds=(81
	31953_f_at	Cluster Incl. U19144: Human GAGE-3 protein mRNA, complete cds /cds=(99
	31954_f_at	Cluster Incl. AA447559: zw81e11.s1 Homo sapiens cDNA, 3 end /clone=IM
15	31960_f_at	Cluster Incl. U19143: Human GAGE-2 protein mRNA, complete cds /cds=(83
	33671_f_at	Cluster Incl. U19145: Human GAGE-4 protein mRNA, complete cds /cds=(82
	33680_f_at	Cluster Incl. AF058988: Homo sapiens melanoma antigen related GAGE-7 m
	35601_at	Cluster Incl. L00022: Human Ig active epsilon1 5 UT, V-D-J region subgro
	37065_f_at	Cluster Incl. U19146: Human GAGE-5 protein mRNA, complete cds /cds=(74
20	Metagene 212	
	32310_f_at	Cluster Incl. AI341574: qq94h09.x1 Homo sapiens cDNA, 3 end /clone=IM
	32883_at	Cluster Incl. X77744: H.sapiens F11 mRNA /cds=UNKNOWN /gb=X77744
25	/gi=456	
	41455_at	Cluster Incl. AB018255: Homo sapiens mRNA for KIAA0712 protein, complete
	32139_at	Cluster Incl. Y09538: H.sapiens mRNA for ZNF185 gene /cds=(40,1398) /gb=
	36812_at	Cluster Incl. U92715: Homo sapiens breast cancer antiestrogen resistance
	37221_at	Cluster Incl. M31158: Human cAMP-dependent protein kinase subunit RII-be
30	34312_at	Cluster Incl. AI040324: oy33a12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	34335_at	Cluster Incl. AI765533: wi81c01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35289_at	Cluster Incl. AJ011679: Homo sapiens mRNA for Rab6 GTPase activating pro
	36660_at	Cluster Incl. AF000231: Homo sapiens rab11a GTPase mRNA, complete cds /c
	36998_s_at	Cluster Incl. Y08262: H.sapiens mRNA for SCA2 protein /cds=(0,2746) /g
35	38370_at	Cluster Incl. U90902: Human clone 23612 mRNA sequence /cds=UNKNOWN
	/gb=U	
	Metagene 213	

	34591_at	Cluster Incl. S79854:type 3 iodothyronine deiodinase=selenoenzyme [huma
	39220_at	Cluster Incl. T92248:ye18d03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	39632_at	Cluster Incl. X75308:H.sapiens mRNA for collagenase 3 /cds=(4,1419) /gb
5	Metagene 214	
	39317_at	Cluster Incl. D86324:Homo sapiens mRNA for CMP-N-acetylneuraminic acid
	33337_at	Cluster Incl. AF002668:Homo sapiens putative fatty acid desaturase MLD
	34251_at	Cluster Incl. M92299:Human homeobox 2.1 protein (HOX2A) mRNA, complete
10	39738_at	Cluster Incl. Z82215:Homo sapiens DNA sequence from PAC 68O2 on chromos
	33418_at	Cluster Incl. AL096752:Homo sapiens mRNA; cDNA DKFZp434A012 (from clone
	35301_at	Cluster Incl. AL049941:Homo sapiens mRNA; cDNA DKFZp564E2222 (from clon
15	Metagene 215	
	35426_at	Cluster Incl. AC004410:Homo sapiens chromosome 19, fosmid 39554 /cds=(0
	35442_at	Cluster Incl. AB007958:Homo sapiens mRNA, chromosome 1 specific transcr
20	37102_at	Cluster Incl. AA203717:zx52f12.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	37873_g_at	Cluster Incl. AF072468:Homo sapiens (JH8) mRNA, partial cds /cds=(0,1
	41657_at	Cluster Incl. AF035625:Homo sapiens serine threonine kinase 11 (STK11)
	35154_at	Cluster Incl. W68046:zd42a12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	36084_at	Cluster Incl. D38548:Human mRNA for KIAA0076 gene, complete cds /cds=(8
25	38284_at	Cluster Incl. AJ007041:Homo sapiens mRNA for trithorax homologue 2 /cds
	39050_at	Cluster Incl. AF026029:Homo sapiens poly(A) binding protein II (PABP2)
	39082_at	Cluster Incl. Y00097:Human mRNA for protein p68 /cds=(100,2121) /gb=Y00
	40867_at	Cluster Incl. J02902:Human protein phosphatase 2A regulatory subunit al
	32177_s_at	Cluster Incl. AC004084:Homo sapiens BAC clone RG158O17 from 7q22-q31.
30	33425_at	Cluster Incl. X97548:H.sapiens mRNA for TIF1beta zinc finger protein /c
	33913_at	Cluster Incl. M33509:Human HLA-B-associated transcript 2 (BAT2) mRNA, c
	35813_at	Cluster Incl. AA192359:zp91c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	36158_at	Cluster Incl. AF086947:untitled /cds=(334,4119) /gb=AF086947 /gi=413912
	36162_at	Cluster Incl. X64364:H.sapiens mRNA for M6 antigen /cds=(57,866) /gb=X6
35	36598_s_at	Cluster Incl. L36818:Human (clone 51C-3) 51C protein mRNA, complete c
	38021_at	Cluster Incl. U53204:Human plectin (PLEC1) mRNA, complete cds /cds=(51,
	38795_s_at	Cluster Incl. X56687:H.sapiens mRNA for autoantigen NOR-90 /cds=(179,
	38799_at	Cluster Incl. AF068706:Homo sapiens gamma2-adaptin (G2AD) mRNA, complet
	40980_at	Cluster Incl. W26477:30b5 Homo sapiens cDNA /gb=W26477 /gi=1307176 /ug=

- 41337_at Cluster Incl. AF072902:Homo sapiens gp130 associated protein GAM mRNA,
 41526_at Cluster Incl. AF072836:Homo sapiens Sox-like transcriptional factor mRN
 1707_g_at U01337 /FEATURE=expanded_cds /DEFINITION=HSU01337 Human Ser/Thr
 protei
- 5** 1131_at L11285 /FEATURE= /DEFINITION=HUMMEK2NF Homosapiens ERK activator kinase
 993_at X54637 /FEATURE=cds /DEFINITION=HSTYK2 Human tyk2 mRNA for non-receptor p
 922_at J02902 /FEATURE=mRNA /DEFINITION=HUMP2A Human protein phosphatase 2A regu
 564_at M69013 /FEATURE= /DEFINITION=HUMGTPBRPA Human guanine nucleotide-binding
 519_g_at U07132 /FEATURE= /DEFINITION=HSU07132 Human steroid hormone receptor
- 10** Ne
 294_s_at Protein Kinase Pitslre, Alpha, Alt. Splice 1-Feb
 175_s_at U33053 /FEATURE= /DEFINITION=HSU33053 Human lipid-activated protein
 kin
 110_at X96753 /FEATURE=cds /DEFINITION=HSMCSP H.sapiens mRNA for melanoma-associ
- 15** Metagene 216
- 35045_r_at Cluster Incl. X60655:H.sapiens EVX1 mRNA /cds=(228,1451) /gb=X60655 /
 37098_at Cluster Incl. D38537:Human mRNA for protoporphyrinogen oxidase, complet
20 40044_at Cluster Incl. U16282:Human ELL mRNA, complete cds /cds=(12,1877) /gb=U1
 40266_at Cluster Incl. AB028959:Homo sapiens mRNA for KIAA1036 protein, complete
 40898_at Cluster Incl. U46751:Human phosphotyrosine independent ligand p62 for t
 1983_at X68452 /FEATURE=cds /DEFINITION=HSCYCD2 H.sapiens mRNA for cyclin D2
- 25** Metagene 217
- 39244_at Cluster Incl. M28211:Homo sapiens GTP-binding protein (RAB4) mRNA, comp
 40654_at Cluster Incl. U88871:Human HsPex7p (HsPEX7) mRNA, complete cds /cds=(81
 41662_at Cluster Incl. AL050272:Homo sapiens mRNA; cDNA DKFZp566B183 (from
30 clone
 35651_at Cluster Incl. AF002715:Homo sapiens MAP kinase kinase kinase (MTK1) mRN
 37910_at Cluster Incl. U52112:host cell factor 1 /cds=(344,6451) /gb=U52112 /gi=
 39386_at Cluster Incl. D14811:Human mRNA for KIAA0110 gene, complete cds /cds=(3.
 39713_at Cluster Incl. AJ132440:Homo sapiens mRNA for PLU-1 protein /cds=(89,472
35 40456_at Cluster Incl. AL049963:Homo sapiens mRNA; cDNA DKFZp564A132 (from
 clone
 33403_at Cluster Incl. AL050260:Homo sapiens mRNA; cDNA DKFZp547E1010 (from
 clon
 34356_at Cluster Incl. U52960:Human RNA polymerase II complex component SRB7 mRN

- 34413_at Cluster Incl. AF038203:Homo sapiens clone 23596 mRNA sequence /cds=UNKN
 34786_at Cluster Incl. AB018285:Homo sapiens mRNA for KIAA0742 protein, partial
 37045_at Cluster Incl. D87443:Human mRNA for KIAA0254 gene, complete cds /cds=(5
 37715_at Cluster Incl. AF045184:Homo sapiens nuclear receptor coactivator NCoA-6
 5 38481_at Cluster Incl. M63488:Human replication protein A 70kDa subunit mRNA com
 38820_at Cluster Incl. AF051894:Homo sapiens 15 kDa selenoprotein mRNA, complete
 1969_s_at X77743 /FEATURE=cds /DEFINITION=HSCDKAK H.sapiens CDK activating
 kinas
 1011_s_at U54778 /FEATURE= /DEFINITION=HSU54778 Human 14-3-3 epsilon mRNA,
 10 compl
 831_at U28042 /FEATURE= /DEFINITION=HSU28042 Human DEAD box RNA helicase-like pr
 781_at X98001 /FEATURE=cds /DEFINITION=HSGGII H.sapiens mRNA for geranylgeranyl
 744_at D50487 /FEATURE= /DEFINITION=HUMHRH1 Human mRNA for RNA helicase
 (HRH1),
 15 621_at M28211 /FEATURE= /DEFINITION=HUMRAB4A Homo sapiens GTP-binding protein (R
 Metagene 218
 32397_r_at Cluster Incl. AA079018:zm94e12.s1 Homo sapiens cDNA, 3' end /clone=IM
 20 32879_at Cluster Incl. AL080233:Homo sapiens mRNA; cDNA DKFZp586L111 (from
 clone
 35412_at Cluster Incl. D13705:Human mRNA for fatty acids omega-hydroxylase (cyto
 37061_at Cluster Incl. U29615:Human chitotriosidase precursor mRNA, complete cds
 33714_at Cluster Incl. Y10043:Homo sapiens mRNA for high mobility group protein
 25 34221_at Cluster Incl. D83778:Human mRNA for KIAA0194 gene, partial cds /cds=(0,
 Metagene 219
 38903_at Cluster Incl. AF099731:Homo sapiens connexin 31.1 (GJB5) gene, complete
 30 40294_at Cluster Incl. U66676:HSU66676 Homo sapiens cDNA /gb=U66676 /gi=1906561
 40712_at Cluster Incl. D26579:Homo sapiens mRNA for transmembrane protein, compl
 37013_at Cluster Incl. X16295:Human mRNA for angiotensin I converting enzyme (AC
 32523_at Cluster Incl. M20470:Human lymphocyte clathrin light-chain B mRNA, comp
 35 Metagene 220
 35007_at Cluster Incl. AC004940:Homo sapiens PAC clone DJ0978E18 from 7p21 /cds=
 39268_at Cluster Incl. AF033382:Homo sapiens potassium channel mRNA, complete cd
 34180_at Cluster Incl. AB002292:Human mRNA for KIAA0294 gene, complete cds /cds=

	36025_at	Cluster Incl. AB002335:Human mRNA for KIAA0337 gene, complete cds /cds=
	35780_at	Cluster Incl. AF035292:Homo sapiens clone 23584 mRNA sequence /cds=UNKN
	35781_g_at	Cluster Incl. AF035292:Homo sapiens clone 23584 mRNA sequence /cds=UN
	37657_at	Cluster Incl. Y16270:Homo sapiens PALM gene, exon 1 and joined CDS /cds
5	Metagene 221	
	33485_at	Cluster Incl. D23660:Human mRNA for ribosomal protein, complete cds /cd
	41688_at	Cluster Incl. AI688299:wc87h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
10	39798_at	Cluster Incl. R87876:yo45h01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
	40435_at	Cluster Incl. J03592:Human ADP/ATP translocase mRNA, 3 end, clone pHAT
	40436_g_at	Cluster Incl. J03592:Human ADP/ATP translocase mRNA, 3 end, clone pH
	33889_s_at	Cluster Incl. D79985:Human mRNA for KIAA0163 gene, complete cds /cds=
	34784_at	Cluster Incl. Z83844:Human DNA sequence from clone 37E16 on chromosome
15	37404_at	Cluster Incl. AF030152:Homo sapiens regulator of G protein signaling 12
	1273_r_at	L22005 /FEATURE= /DEFINITION=HUMCDC34H Human ubiquitin conjugating
	enz	
	Metagene 222	
20	33614_at	Cluster Incl. X80822:H.sapiens mRNA for ORF /cds=(133,555) /gb=X80822 /
	32340_s_at	Cluster Incl. M85234:Human nuclease sensitive element binding protein
	32963_s_at	Cluster Incl. W27549:32d11 Homo sapiens cDNA /gb=W27549 /gi=1307353 /
	37922_at	Cluster Incl. L02648:Homo sapiens (clone V6) transcobalamin II (TCN2) m
25	38635_at	Cluster Incl. Z69043:H.sapiens mRNA translocon-associated protein delta
	33819_at	Cluster Incl. X13794:H.sapiens lactate dehydrogenase B gene exon 1 and
	34367_at	Cluster Incl. AF006043:Homo sapiens 3-phosphoglycerate dehydrogenase mR
	Metagene 223	
30	31410_at	Cluster Incl. AF023614:Homo sapiens transmembrane activator and CAML in
	31559_at	Cluster Incl. U26209:Human renal sodium/dicarboxylate cotransporter (NA
	31594_at	Cluster Incl. Y16788:Homo sapiens hHa3-I gene, complete CDS /cds=(0,121
	31947_r_at	Cluster Incl. X74143:H.sapiens HBF-2 mRNA for transcription factor /c
35	32000_g_at	Cluster Incl. AI344681:qp09h03.x1 Homo sapiens cDNA, 3 end /clone=IM
	32498_at	Cluster Incl. L35318:Human rearranged metabotropic glutamate receptor t
	33016_at	Cluster Incl. AI052224:oz21a02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	33080_s_at	Cluster Incl. AB007943:Homo sapiens mRNA for KIAA0474 protein, comple
	34066_at	Cluster Incl. AJ012590:Homo sapiens mRNA for glucose 1-dehydrogenase /c

	34558_at	Cluster Incl. U30185:Human orphan opioid receptor mRNA, complete cds /c
	34568_at	Cluster Incl. X82634:Homo sapiens mRNA for hair keratin acidic 3-II /cd
	35505_at	Cluster Incl. AI290660:qm12b10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35590_s_at	Cluster Incl. X81832:H.sapiens mRNA for glucose-dependant insulinotro
5	32269_at	Cluster Incl. W26805:13a12 Homo sapiens cDNA /gb=W26805 /gi=1305889 /ug
	32897_at	Cluster Incl. AJ237672:Homo sapiens mRNA for methylenetetrahydrofolate
	32923_r_at	Cluster Incl. M58378:Human synapsin I (SYN1) gene /cds=(0,2117) /gb=M
	33967_at	Cluster Incl. M31525:Human MHC class II lymphocyte antigen (HLA-DNA) ge
	36237_at	Cluster Incl. AB009698:Homo sapiens mRNA for hOAT1-2, complete cds /cds
10	38530_at	Cluster Incl. W26021:18c10 Homo sapiens cDNA /gb=W26021 /gi=1306306 /ug
	39290_f_at	Cluster Incl. W28257:44c1 Homo sapiens cDNA /gb=W28257 /gi=1308205 /u
	39645_r_at	Cluster Incl. AF033105:Homo sapiens X-arrestin mRNA, complete cds /cd
	39657_at	Cluster Incl. X07695:Human mRNA for cytokeratin 4 C-terminal region /cd
	40300_g_at	Cluster Incl. AF091890:Homo sapiens G-protein coupled receptor RE2 mR
15	41382_at	Cluster Incl. AJ000342:Homo sapiens mRNA for DMBT1 6 kb transcript vari
	31861_at	Cluster Incl. L14754:Human DNA-binding protein (SMBP2) mRNA, complete c
	32699_s_at	Cluster Incl. X64116:H.sapiens PVR gene for poliovirus receptor (exon
	33293_at	Cluster Incl. AB023167:Homo sapiens mRNA for KIAA0950 protein, partial
	33719_at	Cluster Incl. AF010242:AF010242 Homo sapiens cDNA /gb=AF010242 /gi=2612
20	32162_r_at	Cluster Incl. AI817548:wk24e08.x1 Homo sapiens cDNA, 3 end /clone=IM
	32228_at	Cluster Incl. AB020706:Homo sapiens mRNA for KIAA0899 protein, partial
	33416_at	Cluster Incl. AI332820:qp96e06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	33449_at	Cluster Incl. AF054185:Homo sapiens proteasome subunit HSPC mRNA, compl
	36615_at	Cluster Incl. M83751:Human arginine-rich protein (ARP) gene, complete c
25	37746_r_at	Cluster Incl. U15131:Human p126 (ST5) mRNA, complete cds /cds=(114,35
	39473_r_at	Cluster Incl. W29065:56g2 Homo sapiens cDNA /gb=W29065 /gi=1309094 /u
	39474_s_at	Cluster Incl. AF045800:Homo sapiens gremlin mRNA, complete cds /cds=(
	39868_at	Cluster Incl. AL046394:DKFZp434M217_r1 Homo sapiens cDNA, 5 end /clone
	40565_at	Cluster Incl. AI358867:qy24a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
30	40622_r_at	Cluster Incl. AL096740:Homo sapiens mRNA; cDNA DKFZp586K2123 (from cl
	41500_at	Cluster Incl. AI761818:wi62g02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41525_at	Cluster Incl. N25429:yx76b02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	33110_at	Cluster Incl. AI356682:qy22a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	33211_at	Cluster Incl. AW051889:wz04f05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35	2032_s_at	U07375 /FEATURE=cds /DEFINITION=HSU07375 Human integrin alpha v gene,
	2005_s_at	U31317 /FEATURE= /DEFINITION=HSU31317 Human JAK family tyrosine
	protei	
	2013_at	U35117 /FEATURE= /DEFINITION=HSU35117 Human transcription factor Dp-2 mR
	1925_at	Z36714 /FEATURE=mRNA /DEFINITION=HSCYCLF H.sapiens mRNA for cyclin F

- 1894_f_at Neurofibromatosis 2 Tumor Suppressor
- 1627_at Tyrosine Kinase
- 1483_at L34059 /FEATURE= /DEFINITION=HUMCA4A Homo sapiens cadherin-4 mRNA, compl
- 1469_at U12779 /FEATURE= /DEFINITION=HSU12779 Human MAP kinase activated protein
- 5 1415_at D26561 /FEATURE=cds#3 /DEFINITION=D26561 Homo sapiens cellular DNA conta
- 1008_f_at U50648 /FEATURE=mRNA /DEFINITION=HSIIPKR17 Human interferon-inducible
- 882_at M37435 /FEATURE= /DEFINITION=HUMCSDF1 Human macrophage-specific colony-st
- 534_s_at U20391 /FEATURE=mRNA#1 /DEFINITION=HSU20391 Human folate receptor
- 10 (FOLR
- 385_at X71874 /FEATURE=cds#2 /DEFINITION=HSPROSCHY H.sapiens genes for proteasom
- 240_at M64231 /FEATURE=mRNA /DEFINITION=HUMSPERSYN Human spermidine synthase gen
- 15 Metagene 224
- 41362_at Cluster Incl. X91249:H.sapiens mRNA for white gene protein /cds=(30,205
- 41453_at Cluster Incl. U49089:Human neuroendocrine-dlg (NE-dlg) mRNA, complete c
- 38285_at Cluster Incl. AF039397:untitled /cds=(30,974) /gb=AF039397 /gi=2746761
- 20 39078_at Cluster Incl. U43286:Human selenophosphate synthetase 2 (SPS2) mRNA, co
- 40765_at Cluster Incl. D87438:Human mRNA for KIAA0251 gene, partial cds /cds=(0,
- 32212_at Cluster Incl. AL049703:Human gene from PAC 179D3, chromosome X, isoform
- 34352_at Cluster Incl. AA631698:np79a08.s1 Homo sapiens cDNA /clone=IMAGE-113250
- 35276_at Cluster Incl. AB000712:Homo sapiens hCPE-R mRNA for CPE-receptor, compl
- 25 35297_at Cluster Incl. AC002400:Human Chromosome 16 BAC clone CIT987SK-A-735G6 /
- 37659_at Cluster Incl. L42572:Homo sapiens p87/89 gene, complete cds /cds=(92,23
- Metagene 225
- 30
- 40732_at Cluster Incl. D83243:Human NPAT mRNA, complete cds /cds=(66,4349) /gb=D
- 41027_at Cluster Incl. AF078096:Homo sapiens forkhead/winged helix-like transcri
- 34765_at Cluster Incl. D13645:Human mRNA for KIAA0020 gene, complete cds /cds=(4
- 37251_s_at Cluster Incl. AF016004:Homo sapiens m6b1 mRNA, complete cds /cds=(254
- 35 39382_at Cluster Incl. AB011089:Homo sapiens mRNA for KIAA0517 protein, partial
- 40488_at Cluster Incl. M18533:Homo sapiens dystrophin (DMD) mRNA, complete cds /
- 41229_at Cluster Incl. AI222594:qg58g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 32242_at Cluster Incl. AL038340:DKFZp566K192_s1 Homo sapiens cDNA, 3 end /clone
- 32243_g_at Cluster Incl. AL038340:DKFZp566K192_s1 Homo sapiens cDNA, 3 end /clo

- 36159_s_at Cluster Incl. U29185:Homo sapiens prion protein (PrP) gene, complete
 37327_at Cluster Incl. X00588:Human mRNA for precursor of epidermal growth facto
 38803_at Cluster Incl. AF052142:Homo sapiens clone 24665 mRNA sequence /cds=UNKN
 40240_at Cluster Incl. AC004131:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-
 5 40642_at Cluster Incl. AI312646:qp77f01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41531_at Cluster Incl. AI445461:tj34g07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41815_at Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from
 clone
 32521_at Cluster Incl. AF056087:Homo sapiens secreted frizzled related protein m
 10 1519_at J04102 /FEATURE= /DEFINITION=HUMETS2A Human erythroblastosis virus oncog
 892_at M90657 /FEATURE= /DEFINITION=HUML6A Human tumor antigen (L6) mRNA,
 comple
 339_at AF035752 /FEATURE= /DEFINITION=AF035752 Homo sapiens caveolin-2 mRNA, com
 15 Metagene 226
 31426_at Cluster Incl. U34806:Human G protein-coupled receptor (GPR15) gene, com
 31626_i_at Cluster Incl. AF047485:Homo sapiens amine oxidase pseudogene mRNA, sp
 31700_at Cluster Incl. AF027957:Homo sapiens G protein-coupled receptor (GPR35)
 20 31745_at Cluster Incl. AF007194:Homo sapiens mucin (MUC3) mRNA, partial cds /cds
 31930_f_at Cluster Incl. X63096:H.sapiens mRNA for rhesus polypeptide (RhVIII) /
 31975_at Cluster Incl. X55503:H.sapiens pseudogene for metallothionein and AG/CT
 31993_f_at Cluster Incl. U80764:Human EST clone 122887 mariner transposon Hsmar1
 32010_at Cluster Incl. Z82180:Human DNA sequence from clone E81G9 on chromosome
 25 33670_at Cluster Incl. X74439:H.sapiens mRNA for estrogen receptor gene 5flankin
 33685_at Cluster Incl. AC004755:Homo sapiens chromosome 19, fosmid 37502 /cds=(0
 34139_at Cluster Incl. AL049651:Human DNA sequence from clone 753D10 on chromoso
 34166_at Cluster Incl. S80071:hPROT=brain-specific L-proline transporter [human,
 34167_s_at Cluster Incl. AA984230:am82g03.s1 Homo sapiens cDNA, 3 end /clone=IM
 30 36332_at Cluster Incl. U40391:Human serotonin N-acetyltransferase gene, complete
 36375_at Cluster Incl. X74614:H.sapiens ODF2 (allele 2) gene for outer dense fib
 36407_at Cluster Incl. AL050220:Homo sapiens mRNA; cDNA DKFZp586J1923 (from clon
 33521_at Cluster Incl. M63962:Human gastric H,K-ATPase catalytic subunit gene, c
 34005_at Cluster Incl. X73079:Homo sapiens encoding Polymeric immunoglobulin rec
 35 34469_at Cluster Incl. X84746:H.sapiens Histo-blood group AB0 gene, exon 1 /cds=
 34963_at Cluster Incl. AA557228:nl75c09.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 35492_at Cluster Incl. AC004523:Homo sapiens chromosome 19, cosmid F22329 /cds=(
 35864_at Cluster Incl. Y00970:Human mRNA for acrosin (EC 3.4.21.10) /cds=(16,128
 35910_f_at Cluster Incl. AJ003147:Homo sapiens complete genomic sequence between

	36276_at	Cluster Incl. X67734:H.sapiens mRNA for transient axonal glycoprotein (
	37070_at	Cluster Incl. D14720:Homo sapiens gene for peripheral myelin protein ze
	37429_g_at	Cluster Incl. AI140857:qa83c11.s1 Homo sapiens cDNA, 3 end /clone=IM
	37853_at	Cluster Incl. AI857458:wl57e02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
5	38558_at	Cluster Incl. M29273:Human myelin-associated glycoprotein (MAG) mRNA, c
	38607_at	Cluster Incl. AF027204:Homo sapiens putative tetraspan transmembrane pr
	38851_at	Cluster Incl. M63394:Human 3 nucleotide sequence mRNA /cds=UNKNOWN
	/gb=	
	38897_at	Cluster Incl. AJ000730:Homo sapiens mRNA for cationic amino acid transp
10	40299_at	Cluster Incl. AF091890:Homo sapiens G-protein coupled receptor RE2 mRNA
	40317_at	Cluster Incl. U57352:Human sodium channel 1 (hBNaC1) mRNA, complete cds
	31819_at	Cluster Incl. AI796281:wh49a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	32029_at	Cluster Incl. AF017995:Homo sapiens 3-phosphoinositide dependent protei
	36011_at	Cluster Incl. AF035531:Homo sapiens syntaxin 10 mRNA, complete cds /cds
15	36037_g_at	Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /c
	36883_at	Cluster Incl. X14640:Human mRNA for keratin 13 /cds=(42,1418) /gb=X1464
	36907_at	Cluster Incl. M88468:Homo sapiens mevalonate kinase mRNA, complete cds
	37191_at	Cluster Incl. D87463:Human mRNA for KIAA0273 gene, complete cds /cds=(4
	37285_at	Cluster Incl. X60364:Human ALAS mRNA for 5-aminolevulinate synthase pre
20	38309_r_at	Cluster Incl. AA805659:nz41b04.s1 Homo sapiens cDNA /clone=IMAGE-1290
	39335_at	Cluster Incl. AI074025:oy66g12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	34405_at	Cluster Incl. U47927:Human isopeptidase T (ISOT) mRNA, complete cds /cd
	38027_at	Cluster Incl. X53742:H.sapiens mRNA for fibulin-1 B /cds=(10,1815) /gb=
	38048_at	Cluster Incl. D84110:Homo sapiens mRNA for RBP-MS/type 4, complete cds
25	38058_at	Cluster Incl. Z22865:H.sapiens dermatopontin mRNA, complete CDS /cds=(1
	38752_r_at	Cluster Incl. AA426364:zv61b06.s1 Homo sapiens cDNA, 3 end /clone=IM
	39451_i_at	Cluster Incl. AF050145:Homo sapiens iduronate-2-sulfatase (IDS) mRNA,
	39472_s_at	Cluster Incl. W25985:17c6 Homo sapiens cDNA /gb=W25985 /gi=1306252 /u
	39490_f_at	Cluster Incl. W26381:29b11 Homo sapiens cDNA /gb=W26381 /gi=1307098 /
30	40595_at	Cluster Incl. AI345337:tb81g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41279_f_at	Cluster Incl. AF007134:Homo sapiens clone 23565 unknown mRNA, partial
	41799_at	Cluster Incl. W28595:48h8 Homo sapiens cDNA /gb=W28595 /gi=1308543 /ug=
	41825_at	Cluster Incl. W26652:34c6 Homo sapiens cDNA /gb=W26652 /gi=1307495 /ug=
	32525_r_at	Cluster Incl. W29012:55a6 Homo sapiens cDNA /gb=W29012 /gi=1308969 /u
35	33178_at	Cluster Incl. AF003837:Homo sapiens Jagged1 (JAG1) mRNA, complete cds /
	1804_at	X07730 /FEATURE= /DEFINITION=HSPSA Human mRNA for prostate specific anti
	1663_at	Retinoic Acid Receptor, Gamma 2
	1432_s_at	D16105 /FEATURE= /DEFINITION=HUMLTkLp2 Human mRNA for leukocyte
	tyrosi	

- 1353_g_at U11870 /FEATURE=mRNA /DEFINITION=HSU11870 Human interleukin-8 receptor
- 1177_at Dna-Binding Protein Ap-2, Alt. Splice 3
- 1122_f_at K03183 /FEATURE=cds /DEFINITION=HUMCGBBA3 Human chorionic gonadotropin
- 5 888_s_at M62302 /FEATURE=cds#1 /DEFINITION=HUMGDF1 Human growth/differentiation
- 729_i_at Mucin 3, Intestinal
- 730_r_at Mucin 3, Intestinal
- 10 731_f_at Mucin 3, Intestinal
- 678_at J04948 /FEATURE=mRNA /DEFINITION=HUMALP1GC Human alkaline phosphatase (AL
- 336_at D38081 /FEATURE= /DEFINITION=HUMHTAR Human mRNA for thromboxane A2 recept
- 15 121_at X69699 /FEATURE= /DEFINITION=HSPAX8A H.sapiens Pax8 mRNA
- Metagene 227
- 31723_at Cluster Incl. X70377:H.sapiens mRNA for cystatin D /cds=(4,432) /gb=X70
- 20 31732_at Cluster Incl. X00948:Human mRNA for prepro-relaxin H2 /cds=(0,557) /gb=
- 32001_s_at Cluster Incl. M80482:Human subtilisin-like protein (PACE4) mRNA, comp
- 35055_at Cluster Incl. X53281:H.sapiens BTF3b mRNA /cds=(239,727) /gb=X53281 /gi
- 35531_at Cluster Incl. AB007933:Homo sapiens mRNA for KIAA0464 protein, complete
- 36364_at Cluster Incl. L32961:Human 4-aminobutyrate aminotransferase (GABAT) mRN
- 25 36374_at Cluster Incl. U79293:Human clone 23948 mRNA sequence /cds=UNKNOWN /gb=U
- 36434_r_at Cluster Incl. AF017724:Homo sapiens glycine receptor alpha 3 subunit
- 34042_at Cluster Incl. U96769:Homo sapiens chondroadherin gene, 5flanking region
- 35428_g_at Cluster Incl. W28256:44b9 Homo sapiens cDNA /gb=W28256 /gi=1308204 /u
- 30 35437_at Cluster Incl. M88461:Human neuropeptide Y peptide YY receptor mRNA, com
- 35925_at Cluster Incl. AF040639:Homo sapiens aflatoxin B1-aldehyde reductase mRN
- 37142_at Cluster Incl. AF038421:Homo sapiens GPI-linked anchor protein (GFRA1) m
- 37485_at Cluster Incl. D88308:Homo sapiens mRNA for very-long-chain acyl-CoA syn
- 37486_f_at Cluster Incl. U68385:Human Meis1-related protein 2 (MRG2), mRNA, part
- 35 37833_at Cluster Incl. J02943:Human corticosteroid binding globulin mRNA, comple
- 38187_at Cluster Incl. D90041:Human liver arylamine N-acetyltransferase (EC 2.3.
- 38875_r_at Cluster Incl. AB011147:Homo sapiens mRNA for KIAA0575 protein, comple
- 39227_at Cluster Incl. AB006621:Homo sapiens mRNA for KIAA0283 gene, partial cds
- 39276_g_at Cluster Incl. M76558:Human neuronal DHP-sensitive, voltage-dependent,

	39616_at	Cluster Incl. AL050227:Homo sapiens mRNA; cDNA DKFZp586M0723 (from
	clon	
	39642_at	Cluster Incl. AL080199:Homo sapiens mRNA; cDNA DKFZp434E082 (from
	clone	
5	40015_at	Cluster Incl. AB002301:Human mRNA for KIAA0303 gene, partial cds /cds=(
	40016_g_at	Cluster Incl. AB002301:Human mRNA for KIAA0303 gene, partial cds /cds
	40377_at	Cluster Incl. AB014582:Homo sapiens mRNA for KIAA0682 protein, complete
	40673_at	Cluster Incl. U12778:Human acyl-CoA dehydrogenase mRNA, complete cds /c
	41048_at	Cluster Incl. D90070:Human ATL-derived PMA-responsive (APR) peptide mRN
10	41440_at	Cluster Incl. D82061:Homo sapiens mRNA for a member of the short-chain
	41660_at	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane rece
	31798_at	Cluster Incl. AA314825:EST186646 Homo sapiens cDNA, 5' end /clone=ATCC-
	32027_at	Cluster Incl. AF012281:Homo sapiens PDZ domain containing-protein (PDZK
	32043_at	Cluster Incl. AF098462:Homo sapiens stanniocalcin-related protein mRNA,
15	33799_at	Cluster Incl. U76248:Human hSIAH2 mRNA, complete cds /cds=(526,1500) /g
	34656_at	Cluster Incl. X82895:H.sapiens mRNA for DLG2 /cds=(87,1817) /gb=X82895
	35238_at	Cluster Incl. AB000509:Homo sapiens mRNA for TRAF5, complete cds /cds=(
	35976_at	Cluster Incl. U65092:Human melanocyte-specific gene 1 (msg1) mRNA, comp
	36499_at	Cluster Incl. D87469:Human mRNA for KIAA0279 gene, partial cds /cds=(0,
20	36859_at	Cluster Incl. AF067724:Homo sapiens nm23-H5 mRNA, complete cds /cds=(48
	37273_at	Cluster Incl. AF007153:Homo sapiens clone 23736 mRNA sequence /cds=UNKN
	37567_at	Cluster Incl. X98834:H.sapiens mRNA for zinc finger protein, Hsa12 /cds
	37639_at	Cluster Incl. X07732:Human hepatoma mRNA for serine protease hepsin /cd
	38254_at	Cluster Incl. AB020689:Homo sapiens mRNA for KIAA0882 protein, partial
25	38267_at	Cluster Incl. AI928365:wo96d08.x1 Homo sapiens cDNA, 3' end /clone=IMAG
	38342_at	Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0,
	39358_at	Cluster Incl. U37146:Human silencing mediator of retinoid and thyroid h
	39366_at	Cluster Incl. N36638:yx88f05.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-
	39378_at	Cluster Incl. U17999:HSU17999 Homo sapiens cDNA /clone=B49B32B27 /gb=U1
30	39781_at	Cluster Incl. U20982:Human insulin-like growth factor binding protein-4
	40511_at	Cluster Incl. X58072:Human hGATA3 mRNA for trans-acting T-cell specific
	40766_at	Cluster Incl. U24578:Human RP1 and complement C4B precursor (C4B) genes
	40791_at	Cluster Incl. X63564:H.sapiens mRNA for RNA polymerase II largest subun
	33353_at	Cluster Incl. W26466:32f11 Homo sapiens cDNA /gb=W26466 /gi=1307372 /ug
35	33446_at	Cluster Incl. W26407:29b8 Homo sapiens cDNA /gb=W26407 /gi=1307106 /ug=
	33821_at	Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromoso
	33825_at	Cluster Incl. X68733:H.sapiens gene for alpha1-antichymotrypsin, exon 1
	34785_at	Cluster Incl. AB028948:Homo sapiens mRNA for KIAA1025 protein, partial

- 34792_at Cluster Incl. AL049954:Homo sapiens mRNA; cDNA DKFZp564A1523 (from
clon
- 35352_at Cluster Incl. AB002305:Human mRNA for KIAA0307 gene, complete cds /cds=
35778_at Cluster Incl. AB011103:Homo sapiens mRNA for KIAA0531 protein, complete
5 35789_at Cluster Incl. AB028965:Homo sapiens mRNA for KIAA1042 protein, complete
35794_at Cluster Incl. AB023159:Homo sapiens mRNA for KIAA0942 protein, partial
35842_at Cluster Incl. AL049265:Homo sapiens mRNA; cDNA DKFZp564F053 (from
clone
- 36583_at Cluster Incl. U53225:Human sorting nexin 1 (SNX1) mRNA, complete cds /c
10 36634_at Cluster Incl. U72649:Human BTG2 (BTG2) mRNA, complete cds /cds=(71,547)
38078_at Cluster Incl. AF042166:Homo sapiens beta-filamin mRNA, complete cds /cd
38418_at Cluster Incl. X59798:Human PRAD1 mRNA for cyclin /cds=(147,1034) /gb=X5
39823_at Cluster Incl. U06631:Human (H326) mRNA, complete cds /cds=(176,1969) /g
40575_at Cluster Incl. AB011155:Homo sapiens mRNA for KIAA0583 protein, partial
15 41792_at Cluster Incl. L78207:Homo sapiens sulfonylurea receptor (SUR1) mRNA, co
2042_s_at M15024 /FEATURE= /DEFINITION=HUMCMYBLA Human c-myb mRNA,
complete cds
2020_at M73554 /FEATURE= /DEFINITION=HUMBCL1 Human bcl-1 mRNA, complete CDS
1909_at M14745 /FEATURE= /DEFINITION=HUMBCL2C Human bcl-2 mRNA
20 1798_at U41060 /FEATURE= /DEFINITION=HSU41060 Human breast cancer, estrogen regu
1737_s_at M62403 /FEATURE= /DEFINITION=HUMIGFBP5 Human insulin-like growth
facto
1237_at S81914 /FEATURE= /DEFINITION=S81914 IEX-1=radiation-inducible immediate-
1241_at U14603 /FEATURE= /DEFINITION=HSU14603 Human protein-tyrosine phosphatase
25 903_at L42373 /FEATURE=mRNA /DEFINITION=HUMPP2A Homo sapiens phosphatase 2A
B56-
310_s_at J03778 /FEATURE= /DEFINITION=HUMTAUA Human microtubule-associated
prote
260_at M16447 /FEATURE= /DEFINITION=HUMDHPRPRA Human dihydropteridine reductase (h
30
Metagene 228
- 35060_at Cluster Incl. U51224:Human U2AFBPL gene, complete cds /cds=(111,1550) /
32921_at Cluster Incl. X83300:H.sapiens SMA4 mRNA /cds=(66,488) /gb=X83300 /gi=6
35 35944_at Cluster Incl. AL031228:dJ1033B10.3 (GalT3 (beta3-Galactosyltransferase)
34801_at Cluster Incl. AB014610:Homo sapiens mRNA for KIAA0710 protein, complete
38090_at Cluster Incl. AL050371:Homo sapiens mRNA; cDNA DKFZp566G2246 (from
clon
40552_s_at Cluster Incl. AL049987:Homo sapiens mRNA; cDNA DKFZp564F112 (from clo

41814_at	Cluster Incl. M29877:Human alpha-L-fucosidase, complete cds /cds=UNKNOWN
33158_at	Cluster Incl. M97252:Homo sapiens Kallmann syndrome (KAL) mRNA, complet
Metagene 229	
5	
32058_at	Cluster Incl. AF070594:Homo sapiens clone 24570 HNK-1 sulfotransferase
33287_at	Cluster Incl. AA533071:nj19e03.s1 Homo sapiens cDNA, 3 end /clone=IMAG
35243_at	Cluster Incl. AA535884:nf90d04.s1 Homo sapiens cDNA, 3 end /clone=IMAG
36044_at	Cluster Incl. AF022912:Homo sapiens cGMP phosphodiesterase delta subuni
10	
36530_g_at	Cluster Incl. AI885381:w193b01.x1 Homo sapiens cDNA, 3 end /clone=IM
38311_at	Cluster Incl. AF055012:Homo sapiens clone 24615 mRNA sequence /cds=UNKN
38971_r_at	Cluster Incl. AJ011896:Homo sapiens mRNA for HIV-1, Nef-associated fa
39045_at	Cluster Incl. W26655:34c9 Homo sapiens cDNA /gb=W26655 /gi=1307498 /ug=
40151_s_at	Cluster Incl. Z48054:H.sapiens mRNA for peroxisomal targeting signal
15	
40462_at	Cluster Incl. AF055022:Homo sapiens clone 24684 mRNA sequence /cds=UNKN
34776_at	Cluster Incl. W27541:32c12 Homo sapiens cDNA /gb=W27541 /gi=1307345 /ug
32528_at	Cluster Incl. Z50853:H.sapiens mRNA for CLPP /cds=(19,852) /gb=Z50853 /
Metagene 230	
20	
32452_at	Cluster Incl. X66357:H.sapiens mRNA cdk3 for serine/threonine protein k
33630_s_at	Cluster Incl. AF026488:Homo sapiens beta III spectrin (SPTBN2) mRNA,
35569_at	Cluster Incl. AB015330:Homo sapiens HRIHFB2007 mRNA, partial cds /cds=(
36336_s_at	Cluster Incl. AC005390:Homo sapiens chromosome 19, cosmid R31180 /cds
25	
39262_at	Cluster Incl. U79266:Human clone 23627 mRNA, complete cds /cds=(184,104
31858_at	Cluster Incl. X07315:Human gene for PP15 (placental protein 15) /cds=(9
32622_at	Cluster Incl. L36983:Homo sapiens dynamin (DNM) mRNA, complete cds /cds
37993_at	Cluster Incl. X63422:H.sapiens mRNA for delta-subunit of mitochondrial
38310_at	Cluster Incl. AB014591:Homo sapiens mRNA for KIAA0691 protein, complete
30	
40164_at	Cluster Incl. X69550:H.sapiens mRNA for rho GDP-dissociation Inhibitor
40850_at	Cluster Incl. L37033:Human FK-506 binding protein homologue (FKBP38) mR
32157_at	Cluster Incl. S57501:protein phosphatase type 1 catalytic subunit [huma
32209_at	Cluster Incl. AF052151:Homo sapiens clone 24574 mRNA sequence /cds=UNKN
33863_at	Cluster Incl. U65785:Human 150 kDa oxygen-regulated protein ORP150 mRNA
35	
33887_at	Cluster Incl. D84064:Homo sapiens mRNA for Hrs, complete cds /cds=(60,2
34310_at	Cluster Incl. Y00486:Human APRT gene for adenine phosphoribosyltransfer
36678_at	Cluster Incl. D21261:Human mRNA for KIAA0120 gene, complete cds /cds=(7
37741_at	Cluster Incl. M77836:Human pyrroline 5-carboxylate reductase mRNA, comp
38434_at	Cluster Incl. M95627:Homo sapiens angio-associated migratory cell prote

- 39812_at Cluster Incl. X79865:H.sapiens Mrp17 mRNA /cds=(137,733) /gb=X79865 /gi
- 41267_at Cluster Incl. AB028972:Homo sapiens mRNA for KIAA1049 protein, partial
- 32543_at Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds
- 32608_at Cluster Incl. AF000560:Homo sapiens TTF-I interacting peptide 20 mRNA,
- 5** 1775_at L24559 /FEATURE= /DEFINITION=HUMDNSPOLA Homo sapiens DNA polymerase
alph
- 1397_at L32976 /FEATURE= /DEFINITION=HUMMLK3A Human protein kinase (MLK-3)
mRNA,
- 1274_s_at L22005 /FEATURE= /DEFINITION=HUMCDC34H Human ubiquitin conjugating
10 enz
- 1224_at X66363 /FEATURE=cds /DEFINITION=HSSTHPKD H.sapiens mRNA PCTAIRE-1 for se
- 954_s_at Protein Phosphatase 1, Alpha Catalytic Subunit
- 858_at S90469 /FEATURE= /DEFINITION=S90469 cytochrome P450 reductase [human, pla
- 691_g_at J02783 /FEATURE=mRNA /DEFINITION=HUMTHBP Human thyroid hormone
15 binding
- 499_at U33822 /FEATURE= /DEFINITION=HSU33822 Human tax1-binding protein TXBP181
- 335_r_at Spliceosomal Protein Sap 62
- 187_at U07349 /FEATURE= /DEFINITION=HSU07349 Human B lymphocyte serine/threonine
- 20** Metagene 231
- 31386_at Cluster Incl. M20812:Human kappa-immunoglobulin germline pseudogene (co
- 31393_r_at Cluster Incl. AB011076:Homo sapiens mRNA for UTF1, complete cds /cds=
- 31554_at Cluster Incl. X55019:H.sapiens mRNA for acetylcholine receptor delta su
- 25** 31621_s_at Cluster Incl. M36860:Human elastin mRNA, complete cds /cds=(49,2241)
- 31669_s_at Cluster Incl. AF039307:Homo sapiens homeobox A11 (HOXA11) gene, compl
- 32988_at Cluster Incl. Z30643:H.sapiens mRNA for chloride channel (putative) 213
- 35096_at Cluster Incl. U18244:Human excitatory amino acid transporter 4 mRNA, co
- 32282_at Cluster Incl. U66047:Human clone Z3-1 placenta expressed mRNA from chro
- 30** 34508_r_at Cluster Incl. AI971726:wr07a08.x1 Homo sapiens cDNA, 3 end /clone=IM
- 34894_r_at Cluster Incl. AC003965:Homo sapiens chromosome 16, cosmid clone 325D7
- 34907_at Cluster Incl. AB014541:Homo sapiens mRNA for KIAA0641 protein, complete
- 34970_r_at Cluster Incl. AI655458:tt13a03.x1 Homo sapiens cDNA, 3 end /clone=IM
- 37418_at Cluster Incl. M36653:Human Oct-2 factor mRNA, complete cds /cds=UNKNOWN
- 35** 37490_at Cluster Incl. L27213:Homo sapiens anion exchange protein mRNA, complete
- 37517_at Cluster Incl. AB028962:Homo sapiens mRNA for KIAA1039 protein, partial
- 38166_r_at Cluster Incl. AF010403:Homo sapiens ALR mRNA, complete cds /cds=(0,15
- 38880_at Cluster Incl. AB011168:Homo sapiens mRNA for KIAA0596 protein, partial
- 40359_at Cluster Incl. M91083:Human DNA-binding protein (HRC1) mRNA, complete cd

	40376_at	Cluster Incl. X83573:Homo sapiens ARSE gene, complete CDS /cds=(67,1836
	41034_s_at	Cluster Incl. U92315:Homo sapiens hydroxysteroid sulfotransferase SUL
	32701_at	Cluster Incl. U51269:Human armadillo repeat protein mRNA, complete cds
	35201_at	Cluster Incl. X16135:Human mRNA for novel heterogeneous nuclear RNP pro
5	35986_at	Cluster Incl. AL050395:Homo sapiens mRNA; cDNA DKFZp586D1020 (from clon
	38265_at	Cluster Incl. AI538172:ti75f08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39803_s_at	Cluster Incl. U84570:Human A2 mRNA, complete cds /cds=(239,883) /gb=U
	33361_at	Cluster Incl. AF052149:Homo sapiens clone 24733 mRNA sequence /cds=UNKN
10	36208_at	Cluster Incl. D42040:Human mRNA for KIAA9001 gene, complete cds /cds=(1
	37042_at	Cluster Incl. U09577:Homo sapiens lysosomal hyaluronidase (LUCA2/HYAL2)
	38019_at	Cluster Incl. L37043:Homo sapiens casein kinase I epsilon mRNA, complet
	39920_r_at	Cluster Incl. AF095154:Homo sapiens C1q-related factor mRNA, complete
	40598_at	Cluster Incl. W20138:zb40d12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
15	40904_at	Cluster Incl. AI857673:wk96c02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41305_at	Cluster Incl. M95549:Homo sapiens sodium/glucose cotransporter-like pro
	1944_f_at	AF001359 /FEATURE= /DEFINITION=AF001359 Homo sapiens DNA mismatch repa
	1742_at	S61953 /FEATURE= /DEFINITION=S61953 c-erbB3=receptor tyrosine kinase {al
20	1395_at	L25081 /FEATURE= /DEFINITION=HUMRHOC A Homo sapiens GTPase (rhoC) mRNA, c
	884_at	M59911 /FEATURE= /DEFINITION=HUMINTA3A Human integrin alpha-3 chain mRNA,
	806_at	U56998 /FEATURE= /DEFINITION=HSU56998 Human putative serine/threonine pro
25	477_at	U51127 /FEATURE= /DEFINITION=HSU51127 Human interferon regulatory factor
Metagene 232		
	36091_at	Cluster Incl. AF051323:Homo sapiens Src-associated adaptor protein (SAP
30	37565_at	Cluster Incl. X85750:H.sapiens mRNA for transcript associated with mono
	39428_at	Cluster Incl. AF055581:Homo sapiens adaptor protein Lnk mRNA, complete
	39733_at	Cluster Incl. AF055001:Homo sapiens clone 24560 unknown mRNA, complete
	36207_at	Cluster Incl. D67029:Human SEC14L mRNA, complete cds /cds=(303,2450) /g
	36672_at	Cluster Incl. L13977:Human prolylcarboxypeptidase mRNA, complete cds /c
35	38745_at	Cluster Incl. X76488:H.sapiens mRNA for lysosomal acid lipase /cds=(145
	40568_at	Cluster Incl. L35249:Homo sapiens vacuolar H ⁺ -ATPase Mr 56,000 subunit
	32578_at	Cluster Incl. AW005997:wz91c01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	677_s_at	J04430 /FEATURE=mRNA /DEFINITION=HUMACP5 Human tartrate-resistant acid

317_at D55696 /FEATURE= /DEFINITION=D55696 Homo sapiens mRNA for cysteine protea

Metagene 233

- 5** 36925_at Cluster Incl. L26336:Human heat shock protein HSPA2 gene, complete cds
 37943_at Cluster Incl. AB002319:Human mRNA for KIAA0321 gene, partial cds /cds=(
 32261_at Cluster Incl. AF072810:Homo sapiens transcription factor WSTF mRNA, com
 2053_at M34064 /FEATURE= /DEFINITION=HUMNCADH Human N-cadherin mRNA, complete
 cd
10 645_at L26336 /FEATURE=cds /DEFINITION=HUMHSPA2A Human heat shock protein HSPA2

Metagene 234

- 31997_at Cluster Incl. X15674:Human pTR5 mRNA for repetitive sequence /cds=UNKNO
15 33581_at Cluster Incl. AF023259:Homo sapiens RNA-binding protein (RBMS3) mRNA, c
 36378_at Cluster Incl. AF085807:Homo sapiens uroplakin Ia mRNA, partial cds /cds
 32335_r_at Cluster Incl. AB009010:Homo sapiens mRNA for polyubiquitin UbC, compl
 33546_at Cluster Incl. AI923984:wn49d12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 34530_at Cluster Incl. W73822:zd52f10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
20 35956_s_at Cluster Incl. U18467:Human pregnancy-specific beta 1-glycoprotein 7 (
 36747_at Cluster Incl. AF052172:Homo sapiens clone 24617 mRNA sequence /cds=UNKN
 37088_at Cluster Incl. AF059681:Homo sapiens serine/threonine kinase 13 (STK13)
 39684_at Cluster Incl. U37707:Human dl3 mRNA, complete cds /cds=(336,2093) /gb=
 35990_at Cluster Incl. AB007947:Homo sapiens mRNA for KIAA0478 protein, complete
25 37195_at Cluster Incl. M14565:Human cholesterol side-chain cleavage enzyme P450s
 37210_at Cluster Incl. S78296:neurofilament-66 [human, fetal brain, mRNA, 3197 n
 39383_at Cluster Incl. AB007882:Homo sapiens KIAA0422 mRNA, partial cds /cds=(0,
 38024_at Cluster Incl. AB020678:Homo sapiens mRNA for KIAA0871 protein, complete
 40236_at Cluster Incl. D29990:Human mRNA for cationic amino acid transporter 2,
30 41276_at Cluster Incl. W27641:37d11 Homo sapiens cDNA /gb=W27641 /gi=1307715 /ug
 1855_at X14445 /FEATURE=expanded_cds /DEFINITION=HSINT2 Human int-2 proto-oncoge
 1661_i_at Antigen, Prostate Specific, Alt. Splice Form 2
 1567_at S77812 /FEATURE= /DEFINITION=S77812 flt=vascular endothelial growth fact

35 Metagene 235

- 37463_r_at Cluster Incl. L21990:Human spliceosomal protein (SAP 62) gene, comple
 41073_at Cluster Incl. AI743745:wg53d06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 38775_at Cluster Incl. X13916:Human mRNA for LDL-receptor related protein /cds=(

- 657_at L11373 /FEATURE= /DEFINITION=HUMPC43ABB Human protocadherin 43 mRNA,
comp
- 635_s_at L42374 /FEATURE=mRNA /DEFINITION=HUMPP2ABA Homo sapiens protein
phospha
- 5** 272_at K02054 /FEATURE=mRNA /DEFINITION=HUMGRP5E Human gastrin-releasing peptide
- Metagene 236
- 10** 33610_at Cluster Incl. AL049977:Homo sapiens mRNA; cDNA DKFZp564C122 (from
clone
- 33611_g_at Cluster Incl. AL049977:Homo sapiens mRNA; cDNA DKFZp564C122 (from clo
- 39581_at Cluster Incl. AA570193:nf38c11.s1 Homo sapiens cDNA /clone=IMAGE-916052
- 32044_at Cluster Incl. D13635:Human mRNA for KIAA0010 gene, complete cds /cds=(3
- 34749_at Cluster Incl. U83461:Human putative copper uptake protein (hCTR2) mRNA,
- 15** 37542_at Cluster Incl. D86961:Human mRNA for KIAA0206 gene, partial cds /cds=(0,
- 39023_at Cluster Incl. AF020038:Homo sapiens NADP-dependent isocitrate dehydroge
- 39032_at Cluster Incl. AJ222700:Homo sapiens mRNA for.TSC-22 protein /cds=(191,6
- 32210_at Cluster Incl. M83088:Human phosphoglucomutase 1 (PGM1) mRNA, complete c
- 33849_at Cluster Incl. U02020:Human pre-B cell enhancing factor (PBEF) mRNA, com
- 20** 37692_at Cluster Incl. AI557240:PT2.1_15_C11.r Homo sapiens cDNA, 3 end /clone_
- 2014_s_at U39064 /FEATURE= /DEFINITION=HSU39064 Human MAP kinase kinase 6
mRNA,
- Metagene 237
- 25**
- 31705_at Cluster Incl. X99977:H.sapiens ARS gene, component B /cds=(26,337) /gb=
- 37163_at Cluster Incl. AL050374:Homo sapiens mRNA; cDNA DKFZp586C1619 (from
clon
- 821_s_at U78793 /FEATURE= /DEFINITION=HSU78793 Human folate receptor alpha
- 30** (hFR)
- 542_at S74445 /FEATURE= /DEFINITION=S74445 cellular retinoic acid-binding protei
- 543_g_at S74445 /FEATURE= /DEFINITION=S74445 cellular retinoic acid-binding prot
- Metagene 238
- 35**
- 38228_g_at Cluster Incl. AB006909:Homo sapiens mRNA for A-type microphthalmia as
- 34688_at Cluster Incl. AB029001:Homo sapiens mRNA for KIAA1078 protein, partial
- 34697_at Cluster Incl. AF074264:Homo sapiens LDL receptor-related protein 6 (LRP
- 40780_at Cluster Incl. AF016507:Homo sapiens C-terminal binding protein 2 mRNA,

	40260_g_at	Cluster Incl. AL009266:H. sapiens cDNA similar to C. elegans RNA bind
	1955_s_at	AF035528 /FEATURE= /DEFINITION=AF035528 Homo sapiens Smad6 mRNA,
	compl	
5	Metagene 239	
	41699_f_at	Cluster Incl. AL080149:Homo sapiens mRNA; cDNA DKFZp434B094 (from clo
	37181_at	Cluster Incl. X76538:H.sapiens Mpv17 mRNA /cds=(29,559) /gb=X76538 /gi=
	39429_at	Cluster Incl. X99050:H.sapiens mRNA; UV Radiation Resistance Associated
10	40095_at	Cluster Incl. J03037:Human carbonic anhydrase II mRNA, complete cds /cd
	40444_s_at	Cluster Incl. AB002382:Human mRNA for KIAA0384 gene, complete cds /cd
	36623_at	Cluster Incl. AB011406:Homo sapiens mRNA for alkalin phosphatase, compl
	Metagene 240	
15		
	37510_at	Cluster Incl. AF036715:Homo sapiens syntaxin 8 mRNA, complete cds /cds=
	40331_at	Cluster Incl. AF035819:Homo sapiens macrophage receptor MARCO mRNA, com
	40068_at	Cluster Incl. U26648:Homo sapiens syntaxin 5 mRNA, complete cds /cds=(2
	34359_at	Cluster Incl. AA524058:ng33b12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
20	34789_at	Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular se
	35270_at	Cluster Incl. W16505:zb05e12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
	37329_at	Cluster Incl. AF053070:Homo sapiens NADH-ubiquinone dehydrogenase 51 kD
	40255_at	Cluster Incl. AC004531:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-
25	Metagene 241	
	33678_i_at	Cluster Incl. X02344:Homo sapiens beta 2 gene /cds=(0,1337) /gb=X0234
	32336_at	Cluster Incl. X05236:Human fibroblast mRNA for aldolase A /cds=(146,124
	31887_at	Cluster Incl. J04469:Human mitochondrial creatine kinase (CKMT) gene, c
30	32028_at	Cluster Incl. U85773:Human phosphomannomutase (PMM2) mRNA, complete cds
	34746_at	Cluster Incl. W28085:41g9 Homo sapiens cDNA /gb=W28085 /gi=1308033 /ug=
	36507_at	Cluster Incl. D30612:Homo sapiens mRNA for repressor protein, partial c
	37188_at	Cluster Incl. X92720:H.sapiens mRNA for phosphoenolpyruvate carboxykina
	38640_at	Cluster Incl. AI582831:tn36c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35	39004_at	Cluster Incl. AI432190:tg77f11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39074_at	Cluster Incl. U79241:Human clone 23759 mRNA, partial cds /cds=(0,1315)
	40778_at	Cluster Incl. AF035555:Homo sapiens short chain L-3-hydroxyacyl-CoA deh
	40807_at	Cluster Incl. X86018:H.sapiens mRNA for MUF1 protein /cds=(0,1853) /gb=
	34828_at	Cluster Incl. AL037557:DKFZp564H2472_r1 Homo sapiens cDNA, 5 end /clon

- 34868_at Cluster Incl. AB029012:Homo sapiens mRNA for KIAA1089 protein, partial
 37311_at Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878
 37719_at Cluster Incl. AF070539:Homo sapiens clone 24433 myelodysplasia/myeloid
 39183_at Cluster Incl. X66363:H.sapiens mRNA PCTAIRE-1 for serine/threonine prot
- 5**
- Metagene 242
- 31773_at Cluster Incl. U06715:Human cytochrome B561, HCYTO B561, mRNA, partial c
 41057_at Cluster Incl. AI760162:wg58e09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
10 41058_g_at Cluster Incl. AI760162:wg58e09.x1 Homo sapiens cDNA, 3 end /clone=IM
 32723_at Cluster Incl. L02547:Homo sapiens (clone pZ50-19) cleavage stimulation
 40459_at Cluster Incl. S69189:peroxisomal acyl-coenzyme A oxidase [human, liver,
 41757_at Cluster Incl. W25933:15b2 Homo sapiens cDNA /gb=W25933 /gi=1306056 /ug=
 36651_at Cluster Incl. X15525:H.sapiens lysosomal acid phosphatase gene (EC 3.1.
15 37293_at Cluster Incl. D43948:Human mRNA for KIAA0097 gene, complete cds /cds=(4
 38124_at Cluster Incl. X55110:Human mRNA for neurite outgrowth-promoting protein
 38804_at Cluster Incl. AF053641:Homo sapiens brain cellular apoptosis susceptibi
 40571_at Cluster Incl. U90942:Human myosin heavy chain 12 (MYO5A) mRNA, complete
 40613_at Cluster Incl. AL031775:dJ30M3.2 (novel protein) /cds=(0,260) /gb=AL0317
20 32572_at Cluster Incl. X98296:H.sapiens mRNA for ubiquitin hydrolase /cds=(59,77
 1450_g_at D00763 /FEATURE= /DEFINITION=HUMPSC9 Human mRNA for proteasome
 subunit
 577_at M94250 /FEATURE=expanded_cds /DEFINITION=HUMMKXX Human retinoic acid
 indu
- 25**
- Metagene 243
- 39625_at Cluster Incl. AL050204:Homo sapiens mRNA; cDNA DKFZp586F1223 (from
 clon
30 35648_at Cluster Incl. AB007902:Homo sapiens KIAA0442 mRNA, partial cds /cds=(0,
 36082_at Cluster Incl. S71326:BGPC=biliary glycoprotein adhesion molecule {alter
 37225_at Cluster Incl. D79994:Human mRNA for KIAA0172 gene, partial cds /cds=(0,
 33436_at Cluster Incl. Z46629:Homo sapiens SOX9 mRNA /cds=(359,1888) /gb=Z46629
 36133_at Cluster Incl. AL031058:Human DNA sequence from clone 512B11 on chromoso
35 36636_at Cluster Incl. M12267:Human ornithine aminotransferase mRNA, complete cd
 988_at X16354 /FEATURE= /DEFINITION=HSTM1CEA Human mRNA for transmembrane
 carcin
- Metagene 244

	34016_s_at	Cluster Incl. X78338:Synthetic adenovirus transformed human retina ce
	37322_s_at	Cluster Incl. X82460:H.sapiens mRNA for 15-hydroxy prostaglandin dehy
	32570_at	Cluster Incl. L76465:Homo sapiens NAD+-dependent 15 hydroxyprostaglandi
5		
	Metagene 245	
	36537_at	Cluster Incl. AB011093:Homo sapiens mRNA for KIAA0521 protein, partial
	36095_at	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /
10	38740_at	Cluster Incl. X79067:H.sapiens ERF-1 mRNA 3 end /cds=UNKNOWN
	/gb=X7906	
	287_at	L19871 /FEATURE= /DEFINITION=HUMATF3X Human activating transcription fact
	Metagene 246	
15		
	36295_at	Cluster Incl. U09412:Human zinc finger protein ZNF134 mRNA, complete cd
	41402_at	Cluster Incl. AL080121:Homo sapiens mRNA; cDNA DKFZp564O0823 (from
	clon	
	37932_at	Cluster Incl. Y12490:Homo sapiens mRNA for Golgi-associated microtubule
20	36170_at	Cluster Incl. D83198:Homo sapiens mRNA expressed in thyroid gland /cds=
	Metagene 247	
	37844_at	Cluster Incl. AI263885:qi08d08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
25	38870_at	Cluster Incl. U97145:Homo sapiens RET ligand 2 (RETL2) mRNA, complete c
	39345_at	Cluster Incl. AI525834:PT1.3_06_D01.r Homo sapiens cDNA, 5 end /clone_
	41236_at	Cluster Incl. U79252:Human clone 23679 mRNA, complete cds /cds=(973,144
	32774_at	Cluster Incl. AI541050:pec1.2-1.E08.r Homo sapiens cDNA, 5 end /clone_
	38832_r_at	Cluster Incl. AF053356:Homo sapiens chromosome 7q22 sequence /cds=(25
30		
	Metagene 248	
	35107_at	Cluster Incl. AF053712:Homo sapiens osteoprotegerin ligand mRNA, comple
	40659_at	Cluster Incl. U12767:Human mitogen induced nuclear orphan receptor (MIN
35	41385_at	Cluster Incl. AB023204:Homo sapiens mRNA for KIAA0987 protein, partial
	38381_at	Cluster Incl. U32315:Human syntaxin 3 mRNA, complete cds /cds=(38,907)
	1911_s_at	M60974 /FEATURE= /DEFINITION=HUMGADD45 Human growth arrest and
	DNA-dam	

Metagene 249

- 34898_at Cluster Incl. M30704:Human amphiregulin (AR) mRNA, complete cds, clones
 37883_i_at Cluster Incl. AI375033:ta66e10.x1 Homo sapiens cDNA, 3 end /clone=IM
 5 37884_f_at Cluster Incl. AI375033:ta66e10.x1 Homo sapiens cDNA, 3 end /clone=IM
 37989_at Cluster Incl. J03802:Human renal carcinoma parathgrad hormone-like pept
 36633_at Cluster Incl. AA114830:zk88e06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 615_s_at M24351 /FEATURE=expanded_cds /DEFINITION=HUMPTH14 Human
 parathyroid hor
 10 469_at U66406 /FEATURE= /DEFINITION=HSU66406 Human putative EPH-related PTK rece

Metagene 250

- 34274_at Cluster Incl. AB029039:Homo sapiens mRNA for KIAA1116 protein, complete
 15 38030_at Cluster Incl. AB002330:Human mRNA for KIAA0332 gene, partial cds /cds=(
 762_f_atAB000905 /FEATURE=cds /DEFINITION=AB000905 Homo sapiens DNA for H4 hist

Metagene 251

- 20 41852_at Cluster Incl. U22377:Human Zn-15 related zinc finger protein (rlf) mRNA
 34737_at Cluster Incl. AF058718:Homo sapiens putative 13 S Golgi transport compl
 36032_at Cluster Incl. AL031427:dJ167A19.3 (novel protein) /cds=(123,557) /gb=AL
 37961_at Cluster Incl. U90907:Human clone 23907 mRNA sequence /cds=UNKNOWN
 /gb=U
 25 41213_at Cluster Incl. X67951:H.sapiens mRNA for proliferation-associated gene (
 33912_at Cluster Incl. Y13834:Homo sapiens mRNA for farnesylated-proteins conver
 35299_at Cluster Incl. AB000409:Homo sapiens mRNA for MNK1, complete cds /cds=(1
 501_g_at U37143 /FEATURE= /DEFINITION=HSU37143 Human cytochrome P450
 monooxygena

30

Metagene 252

- 36215_at Cluster Incl. M34181:Human testis-specific cAMP-dependent protein kinas
 39666_at Cluster Incl. U31382:Human G protein gamma-4 subunit mRNA, complete cds
 35 32103_at Cluster Incl. M20786:Human alpha-2-plasmin inhibitor gene /cds=(4,1479)
 33803_at Cluster Incl. J02973:Human thrombomodulin gene, complete cds /cds=(541,
 35230_at Cluster Incl. AF070530:Homo sapiens clone 24751 unknown mRNA /cds=(0,12
 32788_at Cluster Incl. D42063:Human mRNA for RanBP2 (Ran-binding protein 2), com
 36573_at Cluster Incl. U78524:Human Gu binding protein mRNA, partial cds /cds=(0

	38438_at	Cluster Incl. M58603:Human nuclear factor kappa-B DNA binding subunit (
	Metagene 253	
5	31419_r_at	Cluster Incl. AF023203:Homo sapiens homeobox protein Ogl2 (OGL12) mRNA
	34104_i_at	Cluster Incl. AI147237:qb36f02.x1 Homo sapiens cDNA, 3' end /clone=IM
	36338_at	Cluster Incl. W28504:48e7 Homo sapiens cDNA /gb=W28504 /gi=1308515 /ug=
	32877_i_at	Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-9542
	34454_r_at	Cluster Incl. U32576:Human apolipoprotein apoC-IV (APOC4) gene, compl
10	35446_at	Cluster Incl. AA767013:oa42a08.s1 Homo sapiens cDNA /clone=IMAGE-130760
	37831_at	Cluster Incl. AB011117:Homo sapiens mRNA for KIAA0545 protein, partial
	38538_at	Cluster Incl. AB014602:Homo sapiens mRNA for KIAA0702 protein, complete
	38597_f_at	Cluster Incl. D50402:Human mRNA for NRAMP1, complete cds /cds=(175,18
	39965_at	Cluster Incl. AI570572:tm78c02.x1 Homo sapiens cDNA, 3' end /clone=IMAG
15	41117_s_at	Cluster Incl. AB016243:Homo sapiens gene for regulatory factor 2 of s
	31815_r_at	Cluster Incl. AB009462:Homo sapiens hLRp105 mRNA for LDL receptor rel
	33268_at	Cluster Incl. L25270:Human XE169 mRNA, complete cds /cds=(531,5213) /gb
	33275_at	Cluster Incl. AB016194:Homo sapiens elk1 oncogene, complete cds /cds=(3
	33768_at	Cluster Incl. L19267:Homo sapiens 59 protein mRNA, 3' end /cds=(0,1661)
20	34722_at	Cluster Incl. U44385:Human tissue inhibitor of metalloproteinases-2 (TI
	38699_at	Cluster Incl. X00734:Human beta-tubulin gene (5-beta) with ten Alu fami
	39002_at	Cluster Incl. AJ010063:Homo sapiens telethonin gene /cds=(10,513) /gb=A
	33882_at	Cluster Incl. AB020664:Homo sapiens mRNA for KIAA0857 protein, partial
	36114_r_at	Cluster Incl. M19309:Human slow skeletal muscle troponin T mRNA, clon
25	37387_r_at	Cluster Incl. X55885:Human mRNA for a presumptive KDEL receptor /cds=
	37760_at	Cluster Incl. AB015019:Homo sapiens mRNA for BAP2-alpha protein, comple
	40580_r_at	Cluster Incl. M24398:Human parathymosin mRNA, complete cds /cds=(300,
	40888_f_at	Cluster Incl. W28170:43a12 Homo sapiens cDNA /gb=W28170 /gi=1308118 /
	2091_at	H23429 /FEATURE= /DEFINITION=H23429 ym52d12.s1 Soares infant brain 1N1B
30	2076_s_at	L37361 /FEATURE= /DEFINITION=HUMEFL3 Homo sapiens (clone hELK-L)
	ELK r	
	2078_s_at	M13228 /FEATURE=cds /DEFINITION=HUMNMCY1A Human N-myc
	oncogene protein	
	991_g_at	X51602 /FEATURE=cds /DEFINITION=HSFLT Human flt mRNA for receptor-
35	relat	
	632_at	L40027 /FEATURE=mRNA /DEFINITION=HUMGLYSYN Homo sapiens glycogen
	synthase	
	540_at	S67070 /FEATURE= /DEFINITION=S67070 heat shock protein HSP72 homolog [hum
	258_at	M16441 /FEATURE=cds#1 /DEFINITION=HUMTNFAB Human tumor necrosis factor an

Metagene 254

- 5** 31899_at Cluster Incl. D14659:Human mRNA for KIAA0103 gene, complete cds /cds=(6
 38336_at Cluster Incl. AB023230:Homo sapiens mRNA for KIAA1013 protein, partial
 39701_at Cluster Incl. AB006625:Homo sapiens mRNA for KIAA0287 gene, partial cds
 35803_at Cluster Incl. S82240:RhoE=26 kda GTPase homolog [human, HeLa cell line,
 37403_at Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X0590

10 Metagene 255

- 33982_f_at Cluster Incl. X59244:Human ZNF43 mRNA /cds=(337,2748) /gb=X59244 /gi=
 36303_f_at Cluster Incl. U35376:Human repressor transcriptional factor (ZNF85) m
 36783_f_at Cluster Incl. M55422:Human Krueppel-related zinc finger protein (H-pl
15 34721_at Cluster Incl. U42031:Human 54 kDa progesterone receptor-associated immu
 36489_at Cluster Incl. D00860:Homo sapiens mRNA for phosphoribosyl pyrophosphate
 38753_at Cluster Incl. AF039022:Homo sapiens exportin t mRNA, complete cds /cds=
 40931_at Cluster Incl. AL080084:Homo sapiens mRNA; cDNA DKFZp564G2362 (from
 clon

20

Metagene 256

- 33998_at Cluster Incl. U91618:Human proneurotensin/proneuromedin N mRNA, complet
 34526_s_at Cluster Incl. AF052108:Homo sapiens clone 23687 mRNA sequence /cds=UN
25 39572_at Cluster Incl. AI401567:tg28f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39151_at Cluster Incl. AL031290:Human DNA sequence from clone 774I24 on chromoso

Metagene 257

- 30** 31966_at Cluster Incl. S48220:type I 5 iodothyronine deiodinase [human, mRNA, 22
 35965_at Cluster Incl. X51757:Human heat-shock protein HSP70B gene /cds=(0,1931)
 38937_at Cluster Incl. AF022152:Homo sapiens AP-3 complex beta3B subunit mRNA, c
 39352_at Cluster Incl. S70585:thyroid-stimulating hormone alpha subunit [human,
 752_s_at D85429 /FEATURE=expanded_cds /DEFINITION=D85429 Homo sapiens gene
35 for h
 117_at X51757 /FEATURE=cds /DEFINITION=HSP70B Human heat-shock protein HSP70B g

Metagene 258

- 35882_at Cluster Incl. AI075181:oy96b04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 38512_r_at Cluster Incl. D26158:Homo sapiens mRNA for PLE21 protein, complete cd
- 35150_at Cluster Incl. X60592:Human CDw40 mRNA for nerve growth factor receptor-
- 40257_at Cluster Incl. AI400011:tg85a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
5. 41539_at Cluster Incl. U77782:Human N-methyl-D-aspartate receptor 2C subunit pre
- 1019_g_at U81787 /FEATURE= /DEFINITION=HSU81787 Human Wnt10B mRNA, complete cds
- Metagene 259
- 10
- 38484_at Cluster Incl. D21267:Homo sapiens mRNA, complete cds /cds=(205,825) /gb
- 1924_at U11791 /FEATURE= /DEFINITION=HSU11791 Human cyclin H mRNA, complete cds
- 539_at S59184 /FEATURE= /DEFINITION=S59184 RYK=related to receptor tyrosine kina
- 147_at U82130 /FEATURE= /DEFINITION=HSU82130 Human tumor susceptibility protein (
- 15
- Metagene 260
- 34433_at Cluster Incl. AF035299:Homo sapiens clone 23863 mRNA, partial cds /cds=
- 37472_at Cluster Incl. U60337:Homo sapiens beta-mannosidase mRNA, complete cds /
- 20 39588_at Cluster Incl. AF055872:Homo sapiens Apo3/DR3 ligand (APO3L) mRNA, compl
- 39340_at Cluster Incl. M16424:Human beta-hexosaminidase alpha chain (HEXA) gene
- 39752_at Cluster Incl. AF040704:Homo sapiens putative tumor suppressor protein (
- 40077_at Cluster Incl. Z11559:H.sapiens mRNA for iron regulatory factor /cds=(10
- 40498_g_at Cluster Incl. AF040707:Homo sapiens candidate tumor suppressor gene 2
- 25 35815_at Cluster Incl. AL049470:Homo sapiens mRNA; cDNA DKFZp586L012 (from clone
- 36629_at Cluster Incl. AI635895:tz82a07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 38424_at Cluster Incl. AB018290:Homo sapiens mRNA for KIAA0747 protein, partial
- 39187_at Cluster Incl. AF001450:untitled /cds=(0,1568) /gb=AF001450 /gi=2245523
- 30 1103_at M11567 /FEATURE=mRNA /DEFINITION=HUMAGG Human angiogenin gene, complete
- Metagene 261
- 35 32441_at Cluster Incl. X52142:Human mRNA for CTP synthetase (EC 6.3.4.2) /cds=(7
- 36720_at Cluster Incl. AA873266:oh68e03.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 38606_at Cluster Incl. U32989:Human tryptophan oxygenase (TDO) mRNA, complete cd
- 33282_at Cluster Incl. U42408:Human ladinin (LAD) mRNA, complete cds /cds=(219,1
- 34668_at Cluster Incl. D88152:Homo sapiens mRNA for acetyl-coenzyme A transporte

	34669_at	Cluster Incl. X96717:H.sapiens mRNA for transcription factor TFE3 /cds=
	37228_at	Cluster Incl. U01038:Human pLK mRNA, complete cds /cds=(63,1874) /gb=U0
	37907_at	Cluster Incl. M34677:Human nested gene protein gene, complete cds /cds=
	39704_s_at	Cluster Incl. L17131:Human high mobility group protein (HMG-I(Y)) gen
5	40237_at	Cluster Incl. AF035444:Homo sapiens p17-Beckwith-Wiedemann region 1 C (
	Metagene 262	
	36423_at	Cluster Incl. W47047:zc38g10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
10	39947_at	Cluster Incl. AJ006352:Homo sapiens mRNA for ephrin-A4 protein, membran
	31844_at	Cluster Incl. AF000573:Homo sapiens homogentisate 1,2-dioxygenase gene,
	33292_at	Cluster Incl. AL008583:dJ327J16.1 (human ortholog of mouse outer arm Dy
	37589_at	Cluster Incl. AL109698:Homo sapiens mRNA full length insert cDNA clone
	37590_g_at	Cluster Incl. AL109698:Homo sapiens mRNA full length insert cDNA clon
15	33883_at	Cluster Incl. AB001466:Homo sapiens mRNA for Efs1, complete cds /cds=(6
	38440_s_at	Cluster Incl. AA015605:ze20c12.s1 Homo sapiens cDNA, 3 end /clone=IM
	38754_at	Cluster Incl. AI557295:PT2.1_16_D02.r Homo sapiens cDNA, 3 end /clone_
	Metagene 263	
20	37105_at	Cluster Incl. M16117:Human cathepsin G mRNA, complete cds /cds=(8,775)
	41088_at	Cluster Incl. X12433:Human pHS1-2 mRNA with ORF homologous to membrane
	40265_s_at	Cluster Incl. AI401287:tg92b04.x1 Homo sapiens cDNA, 3 end /clone=IM
25	Metagene 264	
	36354_at	Cluster Incl. AL049689:Novel human mRNA from chromosome 1, similar to T
	32918_at	Cluster Incl. AL080182:Homo sapiens mRNA; cDNA DKFZp434O151 (from clone
30	35454_at	Cluster Incl. AB007919:Homo sapiens mRNA for KIAA0450 protein, complete
	38131_at	Cluster Incl. AF010316:Homo sapiens Pig12 (PIG12) mRNA, complete cds /c
	40304_at	Cluster Incl. M69225:Human bullous pemphigoid antigen (BPAG1) mRNA, com
	41618_at	Cluster Incl. M91669:Human Bullous pemphigoid autoantigen BP180 gene, 3
	31791_at	Cluster Incl. Y16961:Homo sapiens mRNA for KET protein /cds=(27,2069) /
35	36822_at	Cluster Incl. U51334:Human putative RNA binding protein (RBP56) mRNA, c
	38669_at	Cluster Incl. D86959:Human mRNA for KIAA0204 gene, complete cds /cds=(5
	40783_s_at	Cluster Incl. L36151:Homo sapiens phosphatidylinositol 4-kinase mRNA,
	34820_at	Cluster Incl. M57399:Human nerve growth factor (HBNF-1) mRNA, complete

	36961_at	Cluster Incl. AL050286:Homo sapiens mRNA; cDNA DKFZp586A011 (from clone
	40885_s_at	Cluster Incl. N30151:yx81f01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	33192_g_at	Cluster Incl. AW051579:wy87g03.x1 Homo sapiens cDNA, 3 end /clone=IM
5	1147_at	V-Erba Related Ear-3 Protein
	Metagene 265	
	32392_s_at	Cluster Incl. M57951:Human bilirubin UDP-glucuronosyltransferase isoz
10	36266_at	Cluster Incl. U79275:Human clone 23947 mRNA, partial cds /cds=(0,401) /
	39206_s_at	Cluster Incl. X17406:Human mRNA for cartilage specific proteoglycan /
	39567_at	Cluster Incl. AB006190:Homo sapiens mRNA for aquaporin adipose, complet
	40039_g_at	Cluster Incl. W02490:za48b02.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	34293_at	Cluster Incl. AF004426:Homo sapiens microtubule-based motor (HsKIFC3) m
15	36455_at	Cluster Incl. L41162:Homo sapiens collagen alpha 3 type IX (COL9A3) mRN
	35323_at	Cluster Incl. U78525:Homo sapiens eukaryotic translation initiation fac
	39094_at	Cluster Incl. AI991631:wr12h09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41501_at	Cluster Incl. AF004849:Homo sapiens PKY protein kinase mRNA, complete c
20	Metagene 266	
	37819_at	Cluster Incl. AF007130:Homo sapiens clone 23750 unknown mRNA, partial c
	39610_at	Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148
25	39940_at	Cluster Incl. AL080094:Homo sapiens mRNA; cDNA DKFZp564O1262 (from clon
	35213_at	Cluster Incl. AF071185:Homo sapiens formin binding protein 21 mRNA, com
	39397_at	Cluster Incl. M64497:Human apolipoprotein AI regulatory protein (ARP-1)
	39714_at	Cluster Incl. AF042081:Homo sapiens SH3 domain binding glutamic acid-ri
30	40839_at	Cluster Incl. AL080177:Homo sapiens mRNA; cDNA DKFZp434K151 (from clone
	33936_at	Cluster Incl. D86181:Homo sapiens DNA for galactocerebrosidase /cds=(14
	35829_at	Cluster Incl. AL080181:Homo sapiens mRNA; cDNA DKFZp434O111 (from clone
	37393_at	Cluster Incl. L19314:Human HRY gene, complete cds /cds=(0,842) /gb=L193
35	38411_at	Cluster Incl. U90916:Human clone 23815 mRNA sequence /cds=UNKNOWN /gb=U
	38764_at	Cluster Incl. AF007142:Homo sapiens clone 23938 mRNA sequence /cds=UNKN
	39091_at	Cluster Incl. AF070523:Homo sapiens JWA protein mRNA, complete cds /cds
	41562_at	Cluster Incl. L13689:Human prot-oncogene (BMI-1) mRNA, complete cds /cd

1857_at AF010193 /FEATURE= /DEFINITION=AF010193 Homo sapiens MAD-related gene SM

Metagene 267

- 5** 31584_at Cluster Incl. X16064:Human mRNA for translationally controlled tumor pr
 32433_at Cluster Incl. Z97353:Human DNA sequence from clone 90L6 on chromosome 2
 33660_at Cluster Incl. U14966:Human ribosomal protein L5 mRNA, complete cds /cds
 35125_at Cluster Incl. X67309:H.sapiens gene for ribosomal protein S6 /cds=(42,7
 31869_at Cluster Incl. AB014540:Homo sapiens mRNA for KIAA0640 protein, partial
10 34685_at Cluster Incl. AI685944:tu38g02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39037_at Cluster Incl. L13773:Human AF-4 mRNA, complete cds /cds=(420,4052) /gb=
 39782_at Cluster Incl. X95592:H.sapiens mRNA for C1D protein /cds=(117,542) /gb=
 41152_f_at Cluster Incl. T89651:yd99a05.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 34381_at Cluster Incl. AI708889:as86g01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
15 35327_at Cluster Incl. U54559:Homo sapiens translation initiation factor eIF3 p4
 35814_at Cluster Incl. AF064603:Homo sapiens GA17 protein mRNA, complete cds /cd
 37385_at Cluster Incl. U40763:Human Clk-associated RS cyclophilin CARS-Cyp mRNA,
 37668_at Cluster Incl. M69039:Human pre-mRNA splicing factor SF2p32, complete se
 38106_at Cluster Incl. AJ012409:Homo sapiens mRNA for hypothetical protein, clon
20 39510_r_at Cluster Incl. AL049932:Homo sapiens mRNA; cDNA DKFZp564H2416 (from cl
 40211_at Cluster Incl. X12671:Human gene for heterogeneous nuclear ribonucleopro
 41292_at Cluster Incl. L22009:Human hnRNP H mRNA, complete cds /cds=(72,1421) /g
 723_s_at Small Nuclear Ribonucleoprotein, Polypeptide C, Alt. Splice 2
 571_at M86667 /FEATURE= /DEFINITION=HUMNAP H.sapiens NAP (nucleosome assembly pr

25

Metagene 268

- 32140_at Cluster Incl. Y08110:H.sapiens mRNA for mosaic protein LR11 /cds=(80,67
 38375_at Cluster Incl. AF112219:Homo sapiens esterase D mRNA, complete cds /cds=

30

Metagene 269

- 35906_at Cluster Incl. L29339:Homo sapiens Na⁺/glucose co-transporter (SGLT1) ge
 36766_at Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /
35 39301_at Cluster Incl. X85030:H.sapiens mRNA for skeletal muscle-specific calpai
 37629_at Cluster Incl. M55268:Human casein kinase II alpha subunit mRNA, complet
 34361_at Cluster Incl. U33849:Human lymphoma proprotein convertase (LPC) mRNA, c
 36937_s_at Cluster Incl. U90878:Homo sapiens carboxyl terminal LIM domain protei
 1114_at M22490 /FEATURE= /DEFINITION=HUMBMP2B Human bone morphogenetic protein-2

Metagene 270

- 2066_at L22474 /FEATURE= /DEFINITION=HUMBAXB Human Bax beta mRNA, complete cds
5 1481_at L23808 /FEATURE= /DEFINITION=HUMHME Human metalloproteinase (HME) mRNA,
 1482_g_at L23808 /FEATURE= /DEFINITION=HUMHME Human metalloproteinase
 (HME) mRNA

Metagene 271

- 10**
 33650_at Cluster Incl. W25911:14h11 Homo sapiens cDNA /gb=W25911 /gi=1306034 /ug
 35966_at Cluster Incl. X71125:H.sapiens mRNA for glutamine cyclotransferase /cds
 39243_s_at Cluster Incl. U94319:Human autoantigen DFS70 mRNA, partial cds /cds=(
 37597_s_at Cluster Incl. AF055006:Homo sapiens clone 24666 sec6 homolog mRNA, pa
15 40118_at Cluster Incl. X07290:Human HF.12 gene mRNA /cds=(0,589) /gb=X07290 /gi=

Metagene 272

- 37166_at Cluster Incl. Z29481:H.sapiens mRNA for 3-hydroxyanthranilic acid dioxy
20 40033_at Cluster Incl. AL022328:Human DNA sequence from clone 402G11 on chromoso
 31892_at Cluster Incl. X58288:H.sapiens hR-PTPu gene for protein tyrosine phosph
 34235_at Cluster Incl. AB018301:Homo sapiens mRNA for KIAA0758 protein, partial
 35716_at Cluster Incl. AB008164:Homo sapiens mRNA for ST1C2, complete cds /cds=(
 36906_at Cluster Incl. U73304:Human CB1 cannabinoid receptor (CNR1) gene, comple
25 39777_at Cluster Incl. AF075587:Homo sapiens protein associated with Myc mRNA, c
 37384_at Cluster Incl. D13640:Human mRNA for KIAA0015 gene, complete cds /cds=(1
 40994_at Cluster Incl. L15388:Human G protein-coupled receptor kinase (GRK5) mRN
 41000_at Cluster Incl. U68723:Human checkpoint suppressor 1 mRNA, complete cds /
 1368_at M27492 /FEATURE= /DEFINITION=HUMIL1RA Human interleukin 1 receptor mRNA,
30 1135_at L15388 /FEATURE= /DEFINITION=HUMGRK5A Human G protein-coupled receptor k
 692_s_at J02947 /FEATURE=mRNA /DEFINITION=HUMSODEC Human extracellular-
 superoxid

Metagene 273

- 35**
 34544_at Cluster Incl. X78925:H.sapiens HZF2 mRNA for zinc finger protein /cds=(
 32870_g_at Cluster Incl. AF073362:Homo sapiens endo/exonuclease Mre11 (MRE11A) m
 32901_s_at Cluster Incl. AC005192:Homo sapiens BAC clone RG163K11 from 7q31 /cds
 35916_s_at Cluster Incl. AA877215:ob15e02.s1 Homo sapiens cDNA, 3' end /clone=IM

	38220_at	Cluster Incl. U20938:Human lymphocyte dihydropyrimidine dehydrogenase m
	41474_at	Cluster Incl. Y08319:H.sapiens mRNA for kinesin-2 /cds=(18,2057) /gb=Y0
	41635_at	Cluster Incl. D14661:Human mRNA for KIAA0105 gene, complete cds /cds=(1
	31853_at	Cluster Incl. AF080227:Homo sapiens embryonic ectoderm development prot
5	31895_at	Cluster Incl. AB002803:Homo sapiens BACH1 mRNA, complete cds /cds=(118,
	32060_at	Cluster Incl. U15173:Homo sapiens BCL2/adenovirus E1B 19kD-interacting
	32067_at	Cluster Incl. S68271:CREM=cyclic AMP-responsive element modulator [huma
	32621_at	Cluster Incl. M97388:Human TATA binding protein-associated phosphoprote
	33705_at	Cluster Incl. L20971:Human phosphodiesterase mRNA, complete cds /cds=(7
10	38354_at	Cluster Incl. X52560:Human gene for nuclear factor NF-IL6 /cds=(0,1037)
	39039_s_at	Cluster Incl. AI557497:Pt2.1_16_A04.r Homo sapiens cDNA, 3 end/clon
	39040_at	Cluster Incl. W28360:46f9 Homo sapiens cDNA /gb=W28360 /gi=1308371 /ug=
	39379_at	Cluster Incl. AL049397:Homo sapiens mRNA; cDNA DKFZp586C1019 (from clon
15	39759_at	Cluster Incl. AL031781:dJ51J12.1 (human ortholog of zebrafish Quaking p
	41142_at	Cluster Incl. U62961:Human succinyl CoA-3-oxoacid CoA transferase precu
	41175_at	Cluster Incl. L20298:Homo sapiens transcription factor (CBFB) mRNA, 3
	41762_at	Cluster Incl. D64015:Homo sapiens mRNA for T-cluster binding protein, c
	32775_r_at	Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=
20	34336_at	Cluster Incl. D32053:Homo sapiens mRNA for Lysyl tRNA Synthetase, compl
	34857_at	Cluster Incl. Z24724:H.sapiens polyA site DNA /cds=UNKNOWN /gb=Z24724 /
	35307_at	Cluster Incl. Y13286:Homo sapiens mRNA for GDP dissociation inhibitor b
	37734_at	Cluster Incl. D80006:Human mRNA for KIAA0184 gene, partial cds /cds=(0,
	38402_at	Cluster Incl. U36336:Human lysosome-associated membrane protein-2b (LAM
25	38728_at	Cluster Incl. D86978:Human mRNA for KIAA0225 gene, partial cds /cds=(0,
	38774_at	Cluster Incl. U77942:Human syntaxin 7 mRNA, complete cds /cds=(79,864)
	41295_at	Cluster Incl. AL041780:DKFZp434A0418_s1 Homo sapiens cDNA, 3 end/clon
	41595_at	Cluster Incl. AB023164:Homo sapiens mRNA for KIAA0947 protein, partial
	41795_at	Cluster Incl. X17576:Human melanoma mRNA for nck protein, showing homol
30	1868_g_at	AF005775 /FEATURE= /DEFINITION=AF005775 Homo sapiens caspase-like apop
	1739_at	M99487 /FEATURE= /DEFINITION=HUMPSM Human prostate-specific membrane ant
	1448_at	D00762 /FEATURE= /DEFINITION=HUMPSC8 Human mRNA for proteasome subunit H
	1038_s_at	U19247 /FEATURE=mRNA /DEFINITION=HSINFGRA7 Homo sapiens
35	interferon-gam	
	890_at	M74524 /FEATURE= /DEFINITION=HUMHHR6A Human HHR6A (yeast RAD 6 homologue)
	583_s_at	M30257 /FEATURE= /DEFINITION=HUMCAM1V Human vascular cell adhesion mole

- 574_s_at M87507 /FEATURE= /DEFINITION=HUMIL1BCE Homo sapien interleukin-1
beta c
- 430_at X00737 /FEATURE=cds /DEFINITION=HSPNP Human mRNA for purine nucleoside ph
- 160_at U43899 /FEATURE= /DEFINITION=HSU43899 Human signal transducing adaptor mo
- 5**
- Metagene 274
- 31610_at Cluster Incl. U21049:Human DD96 mRNA, complete cds /cds=(0,344) /gb=U21
- 32275_at Cluster Incl. X04470:Human mRNA for antileukoprotease (ALP) from cervix
- 10** 36806_at Cluster Incl. X83877:H.sapiens mRNA for ABP/ZF /cds=(364,684) /gb=X8387
- 37482_at Cluster Incl. U37100:Homo sapiens aldose reductase-like peptide mRNA, c
- 38178_at Cluster Incl. L40802:Homo sapiens 17-beta-hydroxysteroid dehydrogenase
- 38495_s_at Cluster Incl. U27328:Human alpha (1,3/1,4) fucosyltransferase (FUT3)
- 38952_s_at Cluster Incl. M33653:Human (clones HT-[125,133]) alpha-2 type IV coll
- 15** 40356_at Cluster Incl. AB026833:Homo sapiens mRNA for chloride channel protein,
- 41368_at Cluster Incl. AA922934:oh10g06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 31864_at Cluster Incl. X98263:H.sapiens mRNA for M-phase phosphoprotein, mpp6 /c
- 35185_at Cluster Incl. AJ002962:Homo sapiens mRNA for hB-FABP /cds=(76,474) /gb=
- 35980_at Cluster Incl. AB011153:Homo sapiens mRNA for KIAA0581 protein, partial
- 20** 36832_at Cluster Incl. AB015630:Homo sapiens mRNA for type II membrane protein,
- 37637_at Cluster Incl. U27655:Human RGP3 mRNA, complete cds /cds=(287,1846) /gb=
- 39080_at Cluster Incl. M88458:Human ELP-1 mRNA sequence /cds=UNKNOWN
- /gb=M88458
- 32805_at Cluster Incl. U05861:Human hepatic dihydrodiol dehydrogenase gene /cds=
- 25** 32821_at Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 34810_at Cluster Incl. AC004382:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-
- 35369_at Cluster Incl. AB023154:Homo sapiens mRNA for KIAA0937 protein, partial
- 36963_at Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene,
- 37044_at Cluster Incl. D49490:Homo sapiens mRNA for protein disulfide isomerase-
- 30** 37343_at Cluster Incl. U01062:Human type 3 inositol 1,4,5-trisphosphate receptor
- 38469_at Cluster Incl. M35252:Human CO-029 /cds=(137,850) /gb=M35252 /gi=180925
- 40541_at Cluster Incl. X01630:Human mRNA for argininosuccinate synthetase /cds=(
- 40976_at Cluster Incl. AF052432:Homo sapiens katanin p80 subunit mRNA, complete
- 41294_at Cluster Incl. AJ238246:Homo sapiens mRNA for sarcolectin /cds=(61,1470)
- 35** 41489_at Cluster Incl. M99435:Human transducin-like enhancer protein (TLE1) mRNA
- 1063_s_at U02566 /FEATURE= /DEFINITION=HSU02566 Human receptor tyrosine kinase t
- 182_at U01062 /FEATURE=mRNA /DEFINITION=HUMIP3R3 Human type 3 inositol 1,4,5-tri

Metagene 275

- 34510_at Cluster Incl. AF070552:Homo sapiens clone 24767 mRNA sequence /cds=UNKN
- 38158_at Cluster Incl. D79987:Human mRNA for KIAA0165 gene, complete cds /cds=(1
- 33266_at Cluster Incl. AF015254:Homo sapiens serine/threonine kinase (STK-1) mRNA
- 5 37238_s_at Cluster Incl. AF014118:Homo sapiens membrane-associated kinase (Myt1)
- 37945_at Cluster Incl. U91316:Human acyl-CoA thioester hydrolase mRNA, complete
- 39375_g_at Cluster Incl. AL022325:Homo sapiens DNA sequence from Fosmid 27C3 on
- 34851_at Cluster Incl. AF011468:Homo sapiens serine/threonine kinase (BTAK) mRNA
- 36987_at Cluster Incl. M94362:Human lamin B2 (LAMB2) mRNA, partial cds /cds=(0,1
- 10 39872_at Cluster Incl. AL031588:dJ1163J1.3 (novel protein similar to mouse B99)
- 2028_s_at M96577 /FEATURE= /DEFINITION=HUME2F Homo sapiens (E2F-1) pRB-binding p
- 1943_at X51688 /FEATURE=mRNA /DEFINITION=HSCYCLINA Human mRNA for cyclin A
- 1854_at X13293 /FEATURE=cds /DEFINITION=HSBMYB Human mRNA for B-myb gene
- 15 1505_at D00596 /FEATURE=cds /DEFINITION=HUMTS1 Homo sapiens gene for thymidylate
- 982_at X74795 /FEATURE=cds /DEFINITION=HSP1CDC46 H.sapiens P1-Cdc46 mRNA
- 480_at U56816 /FEATURE= /DEFINITION=HSU56816 Human kinase Myt1 (Myt1) mRNA, comp
- 348_at D14678 /FEATURE= /DEFINITION=HUMMHCB Human mRNA for kinesin-related prote
- 20 Metagene 276
- 32393_s_at Cluster Incl. W27466:31c9 Homo sapiens cDNA /gb=W27466 /gi=1307270 /u
- 41436_at Cluster Incl. AJ224901:Homo sapiens mRNA for ZNF198 protein /cds=(184,4
- 25 33219_at Cluster Incl. AB029020:Homo sapiens mRNA for KIAA1097 protein, partial
- 33297_at Cluster Incl. AL031778:dJ34B21.3 (PUTATIVE novel protein) /cds=(297,557
- 34269_at Cluster Incl. AL050102:Homo sapiens mRNA; cDNA DKFZp586F1019 (from clon
- 35163_at Cluster Incl. AB028964:Homo sapiens mRNA for KIAA1041 protein, complete
- 30 35187_at Cluster Incl. AL080216:Homo sapiens mRNA; cDNA DKFZp586K1123 (from clon
- 36502_at Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete
- 36511_at Cluster Incl. AB020658:Homo sapiens mRNA for KIAA0851 protein, complete
- 36860_at Cluster Incl. AB028987:Homo sapiens mRNA for KIAA1064 protein, partial
- 35 36909_at Cluster Incl. X62048:H.sapiens Wee1 hu gene /cds=(170,2110) /gb=X62048
- 37962_r_at Cluster Incl. D63506:Homo sapiens mRNA for unc-18homologue, complete
- 39344_at Cluster Incl. U53209:Human transformer-2 alpha (htra-2 alpha) mRNA, com
- 39434_at Cluster Incl. AB011164:Homo sapiens mRNA for KIAA0592 protein, partial
- 39797_at Cluster Incl. AB002347:Human mRNA for KIAA0349 gene, partial cds /cds=(

	40108_at	Cluster Incl. D13630:Human mRNA for KIAA0005 gene, complete cds /cds=(8
	40485_at	Cluster Incl. AA176780:zp32a10.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	40517_at	Cluster Incl. AB002370:Human mRNA for KIAA0372 gene, complete cds /cds=
	40822_at	Cluster Incl. L41067:Homo sapiens NF-AT4c mRNA, complete cds /cds=(210,
5	41174_at	Cluster Incl. AF012086:Homo sapiens Ran binding protein 2 (RanBP2alpha)
	41747_s_at	Cluster Incl. U49020:Human myocyte-specific enhancer factor 2A (MEF2A
	32187_at	Cluster Incl. AB028973:Homo sapiens mRNA for KIAA1050 protein, partial
	32219_at	Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1
	33817_at	Cluster Incl. S63912:D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt]
10	34353_at	Cluster Incl. AB014548:Homo sapiens mRNA for KIAA0648 protein, partial
	34825_at	Cluster Incl. AL031775:dJ30M3.3 (novel protein similar to C. elegans Y6
	35268_at	Cluster Incl. AL050171:Homo sapiens mRNA; cDNA DKFZp586F1122 (from
	clon	
	35317_at	Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial
15	36580_at	Cluster Incl. AL050139:Homo sapiens mRNA; cDNA DKFZp586M141 (from
	clone	
	36942_at	Cluster Incl. D79996:Human mRNA for KIAA0174 gene, complete cds /cds=(6
	36970_at	Cluster Incl. D80004:Human mRNA for KIAA0182 gene, partial cds /cds=(0,
	37334_at	Cluster Incl. U23803:Human heterogeneous ribonucleoprotein A0 mRNA, com
20	37409_at	Cluster Incl. U88666:Homo sapiens serine kinase SRPK2 mRNA, complete cd
	37694_at	Cluster Incl. D87685:Human mRNA for KIAA0244 gene, partial cds /cds=(0,
	37703_at	Cluster Incl. Y08201:Homo sapiens mRNA for rab geranylgeranyl transfera
	38818_at	Cluster Incl. Y08685:H.sapiens mRNA for serine palmitoyltransferase, su
	39117_at	Cluster Incl. AB014562:Homo sapiens mRNA for KIAA0662 protein, partial
25	39131_at	Cluster Incl. N36842:yy35g03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	39132_at	Cluster Incl. AB010882:Homo sapiens mRNA for hSNF2H, complete cds /cds=
	39897_at	Cluster Incl. N36997:yy39g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	41283_at	Cluster Incl. AF052131:Homo sapiens clone 23930 mRNA sequence /cds=UNKN
	33125_at	Cluster Incl. AL043470:DKFZp434A0327_s1 Homo sapiens cDNA, 3 end /clon
30	33150_at	Cluster Incl. AI126004:qc50e12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	250_at	L41067 /FEATURE= /DEFINITION=HUMHFAT4A Homo sapiens NF-AT4c mRNA,
	complet	
	Metagene 277	
35		
	31682_s_at	Cluster Incl. D32039:Human pgH3 mRNA for proteoglycan PG-M(V3), compl
	41098_at	Cluster Incl. AB002379:Human mRNA for KIAA0381 gene, partial cds /cds=(
	41700_at	Cluster Incl. M62424:Human thrombin receptor mRNA, complete cds /cds=(2
	41872_at	Cluster Incl. AF073308:Homo sapiens nonsyndromic hearing impairment pro

- 40051_at Cluster Incl. D31762:Human mRNA for KIAA0057 gene, complete cds /cds=(7
 40126_at Cluster Incl. Z97200:Homo sapiens DNA sequence from PAC 79C4 on chromos
 41191_at Cluster Incl. AB023209:Homo sapiens mRNA for KIAA0992 protein, partial
 41738_at Cluster Incl. M64110:Human caldesmon mRNA, complete cds /cds=(111,1727)
 5 32764_at Cluster Incl. AI796048:wh41g06.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 33440_at Cluster Incl. U19969:Human two-handed zinc finger protein ZEB mRNA, par
 36638_at Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor
 36976_at Cluster Incl. D21255:Human mRNA for OB-cadherin-2, complete cds /cds=(4
 38038_at Cluster Incl. U21128:Human lumican mRNA, complete cds /cds=(84,1100) /g
 10 38125_at Cluster Incl. M14083:Human beta-migrating plasminogen activator inhibit
 38433_at Cluster Incl. M76125:Human tyrosine kinase receptor (axl) mRNA, complet
 41505_r_at Cluster Incl. AF055376:Homo sapiens short form transcription factor C
 41839_at Cluster Incl. L13698:Human gas1 gene, complete cds /cds=(410,1447) /gb=
 32585_at Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /c
 15 2087_s_at D21254 /FEATURE= /DEFINITION=HUMOSF4A Human mRNA for OB-
 cadherin-1, co
 2062_at L19182 /FEATURE= /DEFINITION=HUMMAC25X Human MAC25 mRNA, complete
 cds
 1815_g_at D50683 /FEATURE= /DEFINITION=D50683 Homo sapiens mRNA for TGF-
 20 betaIR
 1731_at M21574 /FEATURE=mRNA /DEFINITION=HUMPDGFRAA Human platelet-derived
 growt
 1278_at Tyrosine Kinase, Receptor Axl, Alt. Splice 2
 735_s_at Protein Kinase Ht31, Camp-Dependent
 25 661_at L13698 /FEATURE= /DEFINITION=HUMGAS1A Human gas1 gene, complete cds
 581_at M61916 /FEATURE= /DEFINITION=HUMLAM101 Human laminin B1 chain mRNA,
 compl
 340_at AJ001047 /FEATURE=cds /DEFINITION=HSMATRIL3 Homo sapiens mRNA for matril
 232_at M55210 /FEATURE=mRNA#1 /DEFINITION=HUMLB2A26 Human laminin B2 chain
 30 gene,
 128_at X82153 /FEATURE=cds /DEFINITION=HSOC2RNA H.sapiens mRNA for cathepsin O
 129_g_at X82153 /FEATURE=cds /DEFINITION=HSOC2RNA H.sapiens mRNA for
 cathepsin O
 35 Metagene 278
 33085_at Cluster Incl. U64863:Human hPD-1 (hPD-1) mRNA, complete cds /cds=(68,93
 32382_at Cluster Incl. AB015234:Homo sapiens mRNA for uroplakin 1b, complete cds
 41652_at Cluster Incl. AL031228:dJ1033B10.12 (collagen, type XI, alpha 2 (COL11A

- 34702_f_at Cluster Incl. M27826:Human endogenous retroviral protease mRNA, compl
 34703_f_at Cluster Incl. AA151971:zo30b03.r1 Homo sapiens cDNA, 5 end /clone=IM
 36051_s_at Cluster Incl. X58199:Human mRNA for beta adducin /cds=(322,2502) /gb=
 37968_at Cluster Incl. AF031137:Homo sapiens 1C7 precursor, mRNA, alternatively
5 736_f_atD87002 /FEATURE=cds#2 /DEFINITION=D87002 Homo sapiens immunoglobulin la

Metagene 279

- 34008_at Cluster Incl. AF084465:Homo sapiens Ras-like GTP-binding protein REM mR
10 34480_at Cluster Incl. AF016272:Homo sapiens Ksp-cadherin (CDH16) mRNA, complete
 38350_f_at Cluster Incl. AF005392:Homo sapiens alpha tubulin (TUBA2) gene, parti
 37382_at Cluster Incl. N25117:yx19c09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 39199_at Cluster Incl. W28661:49h1 Homo sapiens cDNA /gb=W28661 /gi=1308609 /ug=
 709_at J00314 /FEATURE=mRNA#1 /DEFINITION=HUMTBBM40 Human beta-tubulin gene,
15 clo
 685_f_atK03460 /FEATURE=cds /DEFINITION=HUMTUBA2H Human alpha-tubulin isotype H

Metagene 280

- 20** 32941_at Cluster Incl. M91196:Homo sapiens DNA-binding protein mRNA, complete cd
 33229_at Cluster Incl. U08316:Human insulin-stimulated protein kinase 1 (ISPK-1)
 34809_at Cluster Incl. H53921:yq87g03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-

Metagene 281

- 25**
 36734_at Cluster Incl. M21302:Human small proline rich protein (sprII) mRNA, clo
 40695_at Cluster Incl. J05272:Human IMP dehydrogenase type 1 mRNA complete cds /
 40745_at Cluster Incl. L13939:Homo sapiens beta adaptin (BAM22) mRNA, complete c
 31874_at Cluster Incl. Y07846:H.sapiens mRNA for GAR22 protein /cds=(132,1145) /
30 33736_at Cluster Incl. Y16522:Homo sapiens mRNA for hSLP-1 protein /cds=(44,1228
 39333_at Cluster Incl. M26576:Human alpha-1 collagen type IV gene /cds=(0,5009)
 39801_at Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3)
 34777_at Cluster Incl. D14874:Homo sapiens mRNA for adrenomedullin precursor, co
 36950_at Cluster Incl. X90872:H.sapiens mRNA for gp25L2 protein /cds=(91,735) /g
35 1424_s_at D78577 /FEATURE=expanded_cds /DEFINITION=D78576S2 Human DNA for
 14-3-3
 1346_at S72043 /FEATURE=mRNA /DEFINITION=S72043 GIF=growth inhibitory factor [hu

Metagene 282

- 32329_at Cluster Incl. X99142:H.sapiens mRNA for hair keratin, hHb6 /cds=(0,1451
 36731_g_at Cluster Incl. U66684:HSU66684 Homo sapiens cDNA /gb=U66684 /gi=190656
 37246_at Cluster Incl. AF070535:Homo sapiens clone 24432 mRNA sequence /cds=UNKN
5 38718_at Cluster Incl. AL050101:Homo sapiens mRNA; cDNA DKFZp586E1519 (from
 clon
 40116_at Cluster Incl. X15573:Human liver-type 1-phosphofructokinase (PFKL) mRNA
 36670_at Cluster Incl. L26339:Human autoantigen mRNA, complete cds /cds=(136,378
 37691_at Cluster Incl. X63380:Homo sapiens mRNA for serum response factor-relate
10 39108_at Cluster Incl. U22526:Human 2,3-oxidosqualene-lanosterol cyclase mRNA, c
 793_at X54936 /FEATURE=cds /DEFINITION=HSPLGF H.sapiens mRNA for placenta growth
 541_g_at S67070 /FEATURE= /DEFINITION=S67070 heat shock protein HSP72 homolog
 [h
 244_at M64673 /FEATURE= /DEFINITION=HUMHSF1 Human heat shock factor 1 (TCF5) mRN
15
 Metagene 283
 39210_at Cluster Incl. M58597:Human ELAM-1 ligand fucosyltransferase (ELFT) mRNA
 37974_at Cluster Incl. AL050178:Homo sapiens mRNA; cDNA DKFZp586J1822 (from clon
20 37978_at Cluster Incl. D78177:Homo sapiens mRNA for quinolinate phosphoribosyl t
 39337_at Cluster Incl. M37583:Human histone (H2A.Z) mRNA, complete cds /cds=(106
 39791_at Cluster Incl. M23114:Homo sapiens calcium-ATPase (HK1) mRNA, complete c
 40509_at Cluster Incl. J04058:Human electron transfer flavoprotein alpha-subunit
 32849_at Cluster Incl. D80000:Human mRNA for KIAA0178 gene, partial cds /cds=(0,
25 37677_at Cluster Incl. V00572:Human mRNA encoding phosphoglycerate kinase /cds=(
 1369_s_at M28130 /FEATURE=mRNA /DEFINITION=HUMIL8A Human interleukin 8
 (IL8) gen
 880_at M34539 /FEATURE= /DEFINITION=HUMFKBP Human FK506-binding protein (FKBP)
 m
30
 Metagene 284
 38915_at Cluster Incl. AB011135:Homo sapiens mRNA for KIAA0563 protein, complete
 40951_at Cluster Incl. AL049250:Homo sapiens mRNA; cDNA DKFZp564D113 (from
35 clone
 2000_at U26455 /FEATURE= /DEFINITION=HSU26455 Human phosphatidylinositol 3-kinas
 Metagene 285

	35008_at	Cluster Incl. AB002345:Human mRNA for KIAA0347 gene, complete cds /cds=
	37874_at	Cluster Incl. Z47553:H.sapiens mRNA for flavin-containing monooxygenase
	38850_at	Cluster Incl. M11119:Human endogenous retrovirus envelope region mRNA (
	39665_at	Cluster Incl. U33267:Human glycine receptor beta subunit (GLRB) mRNA, c
5	41679_at	Cluster Incl. AF035282:Homo sapiens clone 23703 mRNA sequence /cds=UNKN
	32664_at	Cluster Incl. D37931:Human mRNA for RNase 4, complete cds /cds=(27,470)
	32668_at	Cluster Incl. AL080076:Homo sapiens mRNA; cDNA DKFZp564C0362 (from clon
	33811_at	Cluster Incl. AI761567:wg66a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
10	34767_at	Cluster Incl. AI670788:tz10c02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35253_at	Cluster Incl. AB011143:Homo sapiens mRNA for KIAA0571 protein, complete
	36013_at	Cluster Incl. AF006621:Homo sapiens embryonic lung protein (HUEL) mRNA,
	36057_at	Cluster Incl. AB011084:Homo sapiens mRNA for KIAA0512 protein, complete
	36092_at	Cluster Incl. AL080213:Homo sapiens mRNA; cDNA DKFZp586I1823 (from clon
15	36506_at	Cluster Incl. AJ131693:Homo sapiens mRNA for AKAP450 protein /cds=(222,
	37934_at	Cluster Incl. AL080078:Homo sapiens mRNA; cDNA DKFZp564D1462 (from clon
	38990_at	Cluster Incl. AL031178:Human DNA sequence from clone 341E18 on chromoso
	39717_g_at	Cluster Incl. AI597616:tn15f08.x1 Homo sapiens cDNA, 3 end /clone=IM
20	40087_at	Cluster Incl. AF020202:Homo sapiens Munc13 mRNA, complete cds /cds=(224
	40471_at	Cluster Incl. Y09048:H.sapiens PxF gene /cds=(10,909) /gb=Y09048 /gi=25
	41225_at	Cluster Incl. AL049417:Homo sapiens mRNA; cDNA DKFZp586O1919 (from clon
	32148_at	Cluster Incl. AI701049:wc78b08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
25	34800_at	Cluster Incl. AL039458:DKFZp434N0910_s1 Homo sapiens cDNA, 3 end /clon
	36689_at	Cluster Incl. AL040446:DKFZp434D1414_r1 Homo sapiens cDNA, 5 end /clon
	38013_at	Cluster Incl. AL096842:Homo sapiens mRNA; cDNA DKFZp586D1519 (from clon
	40196_at	Cluster Incl. D88153:Homo sapiens mRNA for HYA22, complete cds /cds=(14
30	40916_at	Cluster Incl. AL035494:Human DNA sequence from clone 635G19 on chromoso
	41837_at	Cluster Incl. AA149431:z126a08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	32510_at	Cluster Incl. AF026947:Homo sapiens aflatoxin aldehyde reductase AFAR m
	33126_at	Cluster Incl. L13435:Human chromosome 3p21.1 gene sequence /cds=UNKNOWN
35	776_at	D13435 /FEATURE= /DEFINITION=HUMPIGF Human mRNA for PIG-F (phosphatidyl-i
	631_g_at	L39874 /FEATURE=expanded_cds /DEFINITION=HUMDODDA Homo sapiens deoxycyt

- 35071_s_at Cluster Incl. AF042377:Homo sapiens GDP-mannose 4,6 dehydratase mRNA,
 35562_at Cluster Incl. AI076718:oz16h09.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 36233_at Cluster Incl. AF091242:Homo sapiens ATP sulfurylase/APS kinase 2 mRNA,
5 36918_at Cluster Incl. Y15723:Homo sapiens mRNA for soluble guanylyl cyclase /cd
 1537_at X00588 /FEATURE=cds /DEFINITION=HSEGFPRE Human mRNA for precursor of epi
 1319_at X74764 /FEATURE=cds /DEFINITION=HSRPTK H.sapiens mRNA for receptor prote

Metagene 287

10

- 37113_at Cluster Incl. AF022795:Homo sapiens TGF beta receptor associated protei
 36957_at Cluster Incl. W22296:65A11 Homo sapiens cDNA /clone=(not-directional) /
 1606_at L36645 /FEATURE=mRNA /DEFINITION=HUMRPTKC Homo sapiens receptor protein-
 842_at U48251 /FEATURE= /DEFINITION=HSU48251 Homo sapiens protein kinase C-bindi

15

Metagene 288

- 34458_at Cluster Incl. AA586894:nn68c06.s1 Homo sapiens cDNA, 3' end /clone=IMAG
 40671_g_at Cluster Incl. AI148772:qc69h01.x1 Homo sapiens cDNA, 3' end /clone=IM
20 40672_at Cluster Incl. U57721:Human L-kynurenine hydrolase mRNA, complete cds /c
 41096_at Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 41471_at Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-
 31888_s_at Cluster Incl. AF001294:Homo sapiens IPL (IPL) mRNA, complete cds /cds
 39372_at Cluster Incl. W26480:30b8 Homo sapiens cDNA /gb=W26480 /gi=1307179 /ug=
25 40082_at Cluster Incl. D10040:Homo sapiens mRNA for long-chain acyl-CoA syntheta
 32190_at Cluster Incl. AL050118:Homo sapiens mRNA; cDNA DKFZp586C201 (from
 clone
 36109_at Cluster Incl. J04605:Human prolidase (imidodipeptidase) mRNA, complete
 36679_at Cluster Incl. X06272:Human mRNA for docking protein (signal recognition
30 38012_at Cluster Incl. U03272:Human fibrillin-2 mRNA, complete cds /cds=(0,8735)
 41534_at Cluster Incl. AB006755:Homo sapiens mRNA for PCDH7 (BH-Pcdh)a, complete
 33128_s_at Cluster Incl. W68521:zd36f07.r1 Homo sapiens cDNA, 5' end /clone=IMAG
 33168_at Cluster Incl. H24861:yl42e11.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-
 966_at X97795 /FEATURE=cds /DEFINITION=HSRAD54 H.sapiens mRNA homologous to S. c
35 837_s_at U43944 /FEATURE= /DEFINITION=HSU43944 Human breast cancer cytosolic
 NAD
 589_at M32313 /FEATURE=mRNA /DEFINITION=HUM5AR Human steroid 5-alpha-reductase
 m

Metagene 289

- 31800_at Cluster Incl. AL050136:Homo sapiens mRNA; cDNA DKFZp586L141 (from clone
- 5 31801_at Cluster Incl. AI808712:wf57c05.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 35177_at Cluster Incl. AB018268:Homo sapiens mRNA for KIAA0725 protein, partial
- 39017_at Cluster Incl. AJ238094:Homo sapiens mRNA for Lsm1 protein /cds=(188,589
- 35804_at Cluster Incl. AB022785:Homo sapiens ASH2L gene, complete cds, similar t
- 36956_at Cluster Incl. L20852:Human leukemia virus receptor 2 (GLVR2) mRNA, comp
- 10 1772_s_at L00634 /FEATURE= /DEFINITION=HUMFPTA Human farnesyl-protein transferas
- 1499_at L10413 /FEATURE= /DEFINITION=HUMFTA Human farnesyltransferase alpha-subu

Metagene 290

- 15 38282_at Cluster Incl. U41767:Human metargidin precursor mRNA, complete cds /cds
- 39394_at Cluster Incl. AF007149:Homo sapiens clone 23568, 23621, 23795, 23873 an
- 40494_at Cluster Incl. AF043733:Homo sapiens death effector domain-containing te
- 36936_at Cluster Incl. U58766:Human FX protein mRNA, complete cds /cds=(74,1039)
- 20 38066_at Cluster Incl. M81600:Human NAD(P)H-quinone oxireductase gene /cds=(111,
- 898_s_at L37360 /FEATURE= /DEFINITION=HUMEFL2 Homo sapiens (clone hEHK1-L)
- EHK1

Metagene 291

- 25 38592_s_at Cluster Incl. AI828210:wk81e09.x1 Homo sapiens cDNA, 3' end /clone=IM
- 35197_at Cluster Incl. AF038188:Homo sapiens clone 23940 mRNA sequence /cds=UNKN
- 38633_at Cluster Incl. U35113:Human metastasis-associated mta1 mRNA, complete cd
- 34406_at Cluster Incl. AB011174:Homo sapiens mRNA for KIAA0602 protein, partial
- 30 35828_at Cluster Incl. D42123:Homo sapiens mRNA for ESP1/CRP2, complete cds /cds
- 36644_at Cluster Incl. D29963:Homo sapiens mRNA for CD151, complete cds /cds=(84
- 41281_s_at Cluster Incl. AF060502:Homo sapiens peroxisome assembly protein PEX10
- 1642_at U35113 /FEATURE= /DEFINITION=HSU35113 Human metastasis-associated mta1 m
- 1643_g_at U35113 /FEATURE= /DEFINITION=HSU35113 Human metastasis-associated
- 35 mta1
- 1564_at M63167 /FEATURE= /DEFINITION=HUMRACPC Human rac protein kinase alpha mRN

Metagene 292

	36275_at	Cluster Incl. AB002438:Homo sapiens mRNA from chromosome 5q21-22, clone
	38152_at	Cluster Incl. AI632589:wb10h03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39939_at	Cluster Incl. D21337:Human mRNA for collagen /cds=(234,5270) /gb=D21337
	41094_at	Cluster Incl. Y10179:H.sapiens mRNA for prolactin-inducible protein /cd
5	32667_at	Cluster Incl. M58526:Human alpha-5 collagen type IV (COL4A5) mRNA, 3 e
	32792_at	Cluster Incl. AL031432:Human DNA sequence from clone 465N24 on chromoso
	37723_at	Cluster Incl. U47414:Human cyclin G2 mRNA, complete cds /cds=(135,1169)
	325_s_at	Prolactin-Induced Protein
10	Metagene 293	
	34503_at	Cluster Incl. AF007146:Homo sapiens clone 23686 and 23885 mRNA sequence
	37794_at	Cluster Incl. AF035281:Homo sapiens clone 23903 mRNA sequence /cds=UNKN
	38188_s_at	Cluster Incl. L28821:Homo sapiens alpha mannosidase II isozyme mRNA,
15	34712_at	Cluster Incl. AB023227:Homo sapiens mRNA for KIAA1010 protein, partial
	36033_at	Cluster Incl. AL049309:Homo sapiens mRNA; cDNA DKFZp564B176 (from clone
	36833_at	Cluster Incl. U78027:Homo sapiens Brutons tyrosine kinase (BTK), alpha-
	37915_at	Cluster Incl. AL080173:Homo sapiens mRNA; cDNA DKFZp434H071 (from
20	clone	
	40136_at	Cluster Incl. AB014576:Homo sapiens mRNA for KIAA0676 protein, partial
	41766_at	Cluster Incl. D55649:Human mRNA for alpha mannosidase II isozyme, compl
	32223_at	Cluster Incl. AB002363:Human mRNA for KIAA0365 gene, partial cds /cds=(
	35787_at	Cluster Incl. AI986201:wr81a01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
25	39923_at	Cluster Incl. AI935420:wo84c08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	40986_s_at	Cluster Incl. AA058852:zf65a1.1.s1 Homo sapiens cDNA, 3 end /clone=IM
	41243_at	Cluster Incl. AB007916:Homo sapiens mRNA for KIAA0447 protein, complete
	2026_at	M83215 /FEATURE= /DEFINITION=HUMAML1BP Human acute myeloid leukemia (AML
30	Metagene 294	
	32478_f_at	Cluster Incl. AL031133:dJ281H8.4 (Ubiquitin-Like protein SMT3 LIKE) /
	32272_at	Cluster Incl. K00558:human alpha-tubulin mRNA, complete cds /cds=(67,14
35	33458_r_at	Cluster Incl. AI688098:wc92f08.x1 Homo sapiens cDNA, 3 end /clone=IM
	37448_s_at	Cluster Incl. X56009:Human GSA mRNA for alpha subunit of GsGTP bindin
	35729_at	Cluster Incl. AB018270:Homo sapiens mRNA for KIAA0727 protein, partial
	36517_at	Cluster Incl. M96982:Homo sapiens U2 snRNP auxiliary factor small subun
	36913_at	Cluster Incl. U75679:Human histone stem-loop binding protein (SLBP) mRN

	37609_at	Cluster Incl. U01833:Human nucleotide-binding protein mRNA, complete cd
	39056_at	Cluster Incl. X53793:H.sapiens ADE2H1 mRNA showing homologies to SAICAR
	39368_at	Cluster Incl. AL031668:Human DNA sequence from clone 64K7 on chromosome
	40418_at	Cluster Incl. X74262:H.sapiens RbAp48 mRNA encoding retinoblastoma bind
5	41224_at	Cluster Incl. AB018331:Homo sapiens mRNA for KIAA0788 protein, partial
	32853_at	Cluster Incl. AB018262:Homo sapiens mRNA for KIAA0719 protein, complete
	33859_at	Cluster Incl. U96915:Homo sapiens sin3 associated polypeptide p18 (SAP1
	34891_at	Cluster Incl. AI540958:PEC1.2_15_H01.r Homo sapiens cDNA, 5 end /clone
	35810_at	Cluster Incl. AI525393:PT1.1_07_A11.r Homo sapiens cDNA, 5 end /clone_
10	36098_at	Cluster Incl. M72709:Human alternative splicing factor mRNA, complete c
	36188_at	Cluster Incl. D32257:Human GTF3A mRNA for Xenopus transcription factor
	36572_r_at	Cluster Incl. D31885:Human mRNA for KIAA0069 gene, partial cds /cds=(
	36608_at	Cluster Incl. D55654:Human mRNA for cytosolic malate dehydrogenase, com
	36620_at	Cluster Incl. X02317:Human mRNA for Cu/Zn superoxide dismutase (SOD) /c
15	37050_r_at	Cluster Incl. AI130910:qb81g08.x1 Homo sapiens cDNA, 3 end /clone=IM
	37333_at	Cluster Incl. X63692:H.sapiens mRNA for DNA (cytosin-5)-methyltransfera
	38068_at	Cluster Incl. M63175:Human autocrine motility factor receptor mRNA /cds
	38395_at	Cluster Incl. X61100:Human mRNA for mitochondrial 75 kDa iron sulphur p
	40957_at	Cluster Incl. D63881:Human mRNA for KIAA0160 gene, partial cds /cds=(0,
20	1030_s_at	U07806 /FEATURE= /DEFINITION=HSU07806 Human camptothecin resistant
	clo	
	155_s_at	U61397 /FEATURE= /DEFINITION=HSU61397 Human ubiquitin-homology
	domain p	
25	Metagene 295	
	32520_at	Cluster Incl. M24900:Human triiodothyronine recptor (THRA1, ear1), and
	1950_s_at	AB004922 /FEATURE=cds /DEFINITION=AB004922S1 Homo sapiens gene for
	Sma	
30	Metagene 296	
	34791_at	Cluster Incl. X52882:Human t-complex polypeptide 1 gene /cds=(21,1691)
	35364_at	Cluster Incl. U50939:Human amyloid precursor protein-binding protein 1
35	36197_at	Cluster Incl. Y08374:H.sapiens gene encoding cartilage GP-39 protein, e
	39808_at	Cluster Incl. Y12692:Homo sapiens mRNA for WNT11 gene /cds=(123,1187) /
	41530_at	Cluster Incl. D16294:Human mRNA for mitochondrial 3-oxoacyl-CoA thiolas
	1410_at	J03258 /FEATURE=mRNA /DEFINITION=HUMVDR Human vitamin D receptor mRNA,
	c	

471_f_atU47634 /FEATURE= /DEFINITION=HSU47634 Human beta-tubulin class III isot

Metagene 297

- 5** 31600_s_at Cluster Incl. D38435:Homo sapiens hPMS3 mRNA, partial cds /cds=(0,772
36778_at Cluster Incl. Z48804:H.sapiens mRNA (ocular albinism type 1 related) /c
35631_at Cluster Incl. U37689:Human RNA polymerase II subunit (hsRPB8) mRNA, com
35657_at Cluster Incl. U08998:Human TAR RNA binding protein 2 (TRBP2) mRNA, comp
37955_at Cluster Incl. AB015631:Homo sapiens mRNA for type II membrane protein,
10 38703_at Cluster Incl. AF005050:Homo sapiens aspartyl aminopeptidase mRNA, compl
33861_at Cluster Incl. AI123426:qa49c09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
38751_i_at Cluster Incl. AA426364:zv61b06.s1 Homo sapiens cDNA, 3 end /clone=IM
39089_at Cluster Incl. Y07604:H.sapiens mRNA for nucleoside-diphosphate kinase /
1248_at U37689 /FEATURE= /DEFINITION=HSU37689 Human RNA polymerase II subunit (h
15 1187_at X84740 /FEATURE=mRNA /DEFINITION=HSDNALIG3 H.sapiens mRNA for DNA
ligase
958_s_at Rna Polymerase II, 14.5 Kda Subunit

Metagene 298

- 20**
31706_at Cluster Incl. L13283:Homo sapiens (clone MG2-5-12) mucin (MG2) mRNA, co
32909_at Cluster Incl. U46569:Human aquaporin-5 (AQP5) gene /cds=(0,797) /gb=U46
35178_at Cluster Incl. W27944:39g8 Homo sapiens cDNA /gb=W27944 /gi=1307892 /ug=
36018_at Cluster Incl. AJ001183:Homo sapiens mRNA for Sox10 protein /cds=(120,15
25 36024_at Cluster Incl. S79048:LPRP=pHL E1F1 [human, lacrimal gland, mRNA Partial
38280_s_at Cluster Incl. W28432:47f2 Homo sapiens cDNA /gb=W28432 /gi=1308443 /u
40434_at Cluster Incl. U97519:Homo sapiens podocalyxin-like protein mRNA, comple
32780_at Cluster Incl. AB018271:Homo sapiens mRNA for KIAA0728 protein, partial
34354_at Cluster Incl. M80634:Human keratinocyte growth factor receptor mRNA, co
30 1970_s_at Z71929 /FEATURE=cds /DEFINITION=HSFGFR2MR H.sapiens FGFR2 mRNA
1438_at X75208 /FEATURE=cds /DEFINITION=HSPTKR H.sapiens HEK2 mRNA for protein t
1364_at M93426 /FEATURE= /DEFINITION=HUMPTPRZ Human protein tyrosine phosphatase
234_s_at M57399 /FEATURE= /DEFINITION=HUMHBNF1 Human nerve growth factor
(HBNF-1

35

Metagene 299

- 31851_at Cluster Incl. AJ224819:Homo sapiens mRNA for candidate tumor suppressor
33289_f_at Cluster Incl. D88827:Homo sapiens mRNA for zinc finger protein FPM315

	33305_at	Cluster Incl. M93056:Human monocyte/neutrophil elastase inhibitor mRNA
	33746_at	Cluster Incl. D88208:Homo sapiens hSGT1 mRNA for hSgt1p, complete cds /
	33749_at	Cluster Incl. AB007455:Homo sapiens mRNA for P53TG1-A, complete cds /cd
	34758_at	Cluster Incl. U23028:Human eukaryotic initiation factor 2B-epsilon mRNA
5	36830_at	Cluster Incl. U80034:Human mitochondrial intermediate peptidase precurs
	39687_at	Cluster Incl. AI524873:promrna-10.C03.r Homo sapiens cDNA, 5 end /clon
	40801_at	Cluster Incl. AA643063:nr95e11.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	40854_at	Cluster Incl. J04973:Human cytochrome bc-1 complex core protein II mRNA
	32196_at	Cluster Incl. AB020636:Homo sapiens mRNA for KIAA0829 protein, partial
10	33342_at	Cluster Incl. AF039029:Homo sapiens snurportin1 mRNA, complete cds /cds
	33918_s_at	Cluster Incl. AJ223349:Homo sapiens mRNA for HIRIP3 protein, clone pH
	34391_at	Cluster Incl. Y08915:H.sapiens mRNA for alpha 4 protein /cds=(8,1027) /
	34404_at	Cluster Incl. W28167:43a1 Homo sapiens cDNA /gb=W28167 /gi=1308115 /ug=
	35349_at	Cluster Incl. AF031647:Homo sapiens JAB1-containing signalosome subunit
15	35791_at	Cluster Incl. AF038961:Homo sapiens SL15 protein mRNA, complete cds /cd
	37029_at	Cluster Incl. X83218:H.sapiens mRNA for ATP synthase /cds=(36,677) /gb=
	37315_f_at	Cluster Incl. AI057607:oy31e07.x1 Homo sapiens cDNA, 3 end /clone=IM
	37321_at	Cluster Incl. U46570:Human tetratricopeptide repeat protein (tpr1) mRNA
	37709_at	Cluster Incl. M86934:Human GS1 (protein of unknown function) mRNA, comp
20	38477_at	Cluster Incl. S81752:DPH2L=candidate tumor suppressor gene {ovarian can
	39133_at	Cluster Incl. AI525379:PT1.1_06_H01.r Homo sapiens cDNA, 5 end /clone_
	40274_at	Cluster Incl. U48213:Human D-site binding protein gene, promoter region
	33133_at	Cluster Incl. U80184:Homo sapiens FLII gene, complete cds /cds=(35,3844
25	Metagene 300	
	38501_s_at	Cluster Incl. U37139:Human beta 3-endonexin mRNA, long form and short
	39984_g_at	Cluster Incl. U73704:Homo sapiens 48 kDa FKBP-associated protein FAP4
	31794_at	Cluster Incl. D38524:Human mRNA for 5-nucleotidase /cds=(83,1768) /gb=D
30	32096_at	Cluster Incl. AC005546:Homo sapiens chromosome 19, cosmid R29425 /cds=(
	33322_i_at	Cluster Incl. X57348:H.sapiens mRNA (clone 9112) /cds=(165,911) /gb=X
	33323_r_at	Cluster Incl. X57348:H.sapiens mRNA (clone 9112) /cds=(165,911) /gb=X
	33797_at	Cluster Incl. X98494:H.sapiens mRNA for M phase phosphoprotein 10 /cds=
	34177_at	Cluster Incl. AF038660:Homo sapiens chromosome 1p33-p34 beta-1,4-galact
35	35246_at	Cluster Incl. U18934:Human receptor tyrosine kinase (DTK) mRNA, complet
	35683_at	Cluster Incl. AB020659:Homo sapiens mRNA for KIAA0852 protein, complete
	35688_g_at	Cluster Incl. Z24459:H.sapiens MTCP1 gene, exons 2A to 7 (and joined
	36930_at	Cluster Incl. L05425:Homo sapiens autoantigen mRNA, complete cds /cds=(
	39795_at	Cluster Incl. D63475:Human mRNA for KIAA0109 gene, complete cds /cds=(8

- 41143_at Cluster Incl. U12022:Human calmodulin (CALM1) gene /cds=(199,648) /gb=U
 41172_at Cluster Incl. AA126515:zn85c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 41773_at Cluster Incl. U58048:Human metalloproteinase PRSM1 mRNA, complete cds /c
 32784_at Cluster Incl. AB011108:Homo sapiens mRNA for KIAA0536 protein, partial
 5 34787_at Cluster Incl. X93209:H.sapiens mRNA for NRD1 convertase /cds=UNKNOWN /g
 35795_at Cluster Incl. AJ011972:Homo sapiens mRNA for histone deacetylase-like p
 38060_at Cluster Incl. AI541336:pec1.2-7.A07.r Homo sapiens cDNA, 5 end /clone_
 40182_s_at Cluster Incl. AF055027:Homo sapiens clone 24658 mRNA sequence /cds=UN
 40593_at Cluster Incl. X66975:H.sapiens mRNA for heterogeneous nuclear ribonucle
 10 40979_at Cluster Incl. AJ243310:Homo sapiens mRNA for C14orf3 protein /cds=(131,
 41259_at Cluster Incl. AI553745:tn28c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41838_at Cluster Incl. X99270:H.sapiens Xq28, 2000bp sequence contg. ORF /cds=(5
 2086_s_at D17517 /FEATURE= /DEFINITION=HUMSKY Human sky mRNA for Sky,
 complete c
 15 1373_at M31523 /FEATURE= /DEFINITION=HUMTFAA Human transcription factor (E2A) mR

Metagene 301

- 35130_at Cluster Incl. X15722:Human mRNA for glutathione reductase (EC 1.6.4.2)
 20 36414_s_at Cluster Incl. AF032119:Homo sapiens hCASK (CASK) mRNA, complete cds /
 32954_at Cluster Incl. U79263:Human clone 23760 mRNA, partial cds /cds=(0,1021)
 34484_at Cluster Incl. AI961669:wt65e11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 36743_at Cluster Incl. AL096739:Homo sapiens mRNA; cDNA DKFZp586H0623 (from
 clon
 25 40691_at Cluster Incl. U71598:Human zinc finger protein zfp2 (zlf2) mRNA, partial
 34666_at Cluster Incl. X07834:Human mRNA for manganese superoxide dismutase (EC
 34683_at Cluster Incl. U63289:Human RNA-binding protein CUG-BP/hNab50 (NAB50) mR
 37913_at Cluster Incl. J00140:Human dihydrofolate reductase gene /cds=(42,605) /
 40447_at Cluster Incl. D87436:Human mRNA for KIAA0249 gene, complete cds /cds=(2
 30 40784_at Cluster Incl. Z69030:H.sapiens mRNA for gamma 1 isoform of 61kDa regula
 40785_g_at Cluster Incl. Z69030:H.sapiens mRNA for gamma 1 isoform of 61kDa regu
 40798_s_at Cluster Incl. Z48579:H.sapiens mRNA for disintegrin-metalloprotease (
 41176_at Cluster Incl. AF052162:Homo sapiens clone 24655 mRNA sequence /cds=UNKN
 32790_at Cluster Incl. D59253:Human mRNA for NCBP interacting protein 1, complet
 35 33385_g_at Cluster Incl. U31346:Human calpastatin mRNA, partial cds, long 3UTR /
 33823_at Cluster Incl. D12676:Human mRNA for lysosomal sialoglycoprotein, comple
 36101_s_at Cluster Incl. M63978:Human vascular endothelial growth factor gene /c
 37738_g_at Cluster Incl. D25547:Homo sapiens mRNA for PIMT isozyme I, complete c
 40555_at Cluster Incl. AL043108:DKFZp434C0823_r1 Homo sapiens cDNA, 5 end /clon

	41517_g_at	Cluster Incl. U95735:Human SNARE protein Ykt6 (YKT6) mRNA, complete c
	1560_g_at	U24153 /FEATURE= /DEFINITION=HSU24153 Human p21-activated protein kina
	1453_at	U68018 /FEATURE= /DEFINITION=HSU68018 Human mad protein homolog (hMAD-2)
5	1094_g_at	M65254 /FEATURE= /DEFINITION=HUMP2B Protein phosphatase 2A 65 kDa regu
	981_at	X74794 /FEATURE=cds /DEFINITION=HSP1CDC21 H.sapiens P1-Cdc21 mRNA
	968_i_at	X98296 /FEATURE=cds /DEFINITION=HSUBIQHYD H.sapiens mRNA for ubiquitin
10	969_s_at	X98296 /FEATURE=cds /DEFINITION=HSUBIQHYD H.sapiens mRNA for ubiquitin
	642_s_at	L76528 /FEATURE=expanded_cds /DEFINITION=HUMPS1A11 Homo sapiens preseni
	467_at	U63717 /FEATURE= /DEFINITION=HSU63717 Homo sapiens osteoclast stimulating
15	369_s_at	Z29331 /FEATURE=cds /DEFINITION=HSUCEH3 H.sapiens (23k/3) mRNA for ubiq
	263_g_at	M21154 /FEATURE=mRNA /DEFINITION=HUMAMD Human S-adenosylmethionine deca
	167_at	U49436 /FEATURE= /DEFINITION=HSU49436 Human translation initiation factor
20	160027_s_at	Y00285 /FEATURE=cds /DEFINITION=HSIGFIIR Human mRNA for insuline-lik
	Metagene 302	
	37451_at	Cluster Incl. AL109695:Homo sapiens mRNA full length insert cDNA clone
25	33809_at	Cluster Incl. AL049933:Homo sapiens mRNA; cDNA DKFZp564K1216 (from clon
	40475_at	Cluster Incl. AJ000388:Homo sapiens mRNA for calpain-like protease CANP
	38797_at	Cluster Incl. D31887:Human mRNA for KIAA0062 gene, partial cds /cds=(0,
30	Metagene 303	
	37442_at	Cluster Incl. AL050378:Homo sapiens mRNA; cDNA DKFZp586I1420 (from clon
	39261_at	Cluster Incl. L16896:Human zinc finger protein mRNA, complete cds /cds=
	35151_at	Cluster Incl. AF089814:Homo sapiens growth suppressor related (DOC-1R)
35	40154_at	Cluster Incl. AL096725:Homo sapiens mRNA; cDNA DKFZp434B103 (from clone
	40829_at	Cluster Incl. AB028960:Homo sapiens mRNA for KIAA1037 protein, partial
	40875_s_at	Cluster Incl. X06815:Human mRNA for hU1-70K small nuclear RNP protein
	41161_at	Cluster Incl. AB015051:Homo sapiens mRNA for Daxx, complete cds /cds=(1

	33360_at	Cluster Incl. AB023221:Homo sapiens mRNA for KIAA1004 protein, partial
	34369_at	Cluster Incl. D86987:Homo sapiens mRNA for KIAA0214 protein, complete c
	34874_at	Cluster Incl. AJ004832:Homo sapiens mRNA for neuropathy target esterase
	37379_at	Cluster Incl. X81789:H.sapiens mRNA for splicing factor SF3a60 /cds=(56
5	38020_at	Cluster Incl. AB014552:Homo sapiens mRNA for KIAA0652 protein, complete
	38828_s_at	Cluster Incl. AA628946:af28f05.s1 Homo sapiens cDNA, 3' end /clone=IM
	40562_at	Cluster Incl. M69013:Human guanine nucleotide-binding regulatory protei
	1277_at	D89016 /FEATURE= /DEFINITION=D89016 Homo sapiens mRNA for Neuroblastoma,
10	1251_g_at	M64788 /FEATURE= /DEFINITION=HUMRAP1GAP Human GTPase activating protei
	Metagene 304	
	33781_s_at	Cluster Incl. AF075599:Homo sapiens ubiquitin conjugating enzyme 12 (
15	38966_at	Cluster Incl. AF038958:Homo sapiens synaptic glycoprotein SC2 spliced v
	40089_at	Cluster Incl. AJ224442:Homo sapiens mRNA for putative methyltransferase
	40821_at	Cluster Incl. M61832:Human S-adenosylhomocysteine hydrolase (AHCY) mRNA
	33931_at	Cluster Incl. X71973:H.sapiens GPx-4 mRNA for phospholipid hydroperoxid
	35844_at	Cluster Incl. D79206:Homo sapiens gene for ryudocan core protein, exon1
20	37690_at	Cluster Incl. U61263:Human acetolactate synthase homolog mRNA, complete
	40549_at	Cluster Incl. L04658:Homo sapiens gene sequence /cds=UNKNOWN /gb=L04658
	1206_at	X66364 /FEATURE=cds /DEFINITION=HSSTHPKE H.sapiens mRNA PSSALRE for seri
	Metagene 305	
25	35094_f_at	Cluster Incl. AF025527:Homo sapiens leucocyte immunoglobulin-like rec
	38163_at	Cluster Incl. AB018294:Homo sapiens mRNA for KIAA0751 protein, complete
	38225_at	Cluster Incl. AF052728:Homo sapiens HERG-USO (HERG) mRNA, alternatively
	41423_at	Cluster Incl. AB018269:Homo sapiens mRNA for KIAA0726 protein, complete
30	41435_at	Cluster Incl. AB014554:Homo sapiens mRNA for KIAA0654 protein, partial
	33707_at	Cluster Incl. AF058921:Homo sapiens cytosolic phospholipase A2-gamma mR
	38671_at	Cluster Incl. AB014520:Homo sapiens mRNA for KIAA0620 protein, partial
	32837_at	Cluster Incl. U56418:Human lysophosphatidic acid acyltransferase-beta m
35	41496_at	Cluster Incl. AL050189:Homo sapiens mRNA; cDNA DKFZp586B0323 (from clon
	Metagene 306	
	39283_at	Cluster Incl. X83543:H.sapiens APXL mRNA /cds=(90,4940) /gb=X83543 /gi=

	35212_at	Cluster Incl. AF064801:Homo sapiens multiple membrane spanning receptor
	40764_at	Cluster Incl. M22632:Human mitochondrial aspartate aminotransferase mRNA
	32174_at	Cluster Incl. AF015926:Homo sapiens ezrin-radixin-moesin binding phosph
	32822_at	Cluster Incl. J02966:Human mitochondrial ADP/ADT translocator mRNA, com
5	33917_at	Cluster Incl. AB002336:Human mRNA for KIAA0338 gene, partial cds /cds=(
	34788_at	Cluster Incl. AL049365:Homo sapiens mRNA; cDNA DKFZp586A0618 (from
	clon	
	36959_at	Cluster Incl. U49278:Homo sapiens UEV-1 (UBE2V) mRNA, partial cds /cds=
	38729_at	Cluster Incl. M88279:Human immunophilin (FKBP52) mRNA, complete cds /cd
10	40631_at	Cluster Incl. D38305:Human mRNA for Tob, complete cds /cds=(43,1080) /g
Metagene 307		
	32928_at	Cluster Incl. AJ012214:Homo sapiens mRNA for PLA-1 protein /cds=(0,1310
15	36710_at	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds
	34238_at	Cluster Incl. AB002362:Human mRNA for KIAA0364 gene, complete cds /cds=
	36479_at	Cluster Incl. AF050078:untitled /cds=(122,1558) /gb=AF050078 /gi=381846
	34812_at	Cluster Incl. W26099:22f11 Homo sapiens cDNA /gb=W26099 /gi=1306645 /ug
	34847_s_at	Cluster Incl. AF112471:Homo sapiens calcium/calmodulin-dependent prot
20		
Metagene 308		
	35936_g_at	Cluster Incl. Y08683:H.sapiens mRNA for carnitine palmitoyltransferas
	36810_at	Cluster Incl. AB007954:Homo sapiens mRNA, chromosome 1 specific transcr
25	38523_f_at	Cluster Incl. D49677:Human U2AF1-RS2 mRNA, complete cds /cds=(24,1472
	39650_s_at	Cluster Incl. AB007895:Homo sapiens KIAA0435 mRNA, complete cds /cds=
	39925_at	Cluster Incl. M95610:Human alpha 2 type IX collagen (COL9A2) mRNA, part
	41645_at	Cluster Incl. AF064594:Homo sapiens calcium-independent phospholipase A
	31839_at	Cluster Incl. AC004475:Homo sapiens chromosome 19, cosmid F23858 /cds=(
30	35135_at	Cluster Incl. X13956:Human 12S RNA induced by poly(rI), poly(rC) and Ne
	35228_at	Cluster Incl. Y08682:H.sapiens mRNA for carnitine palmitoyltransferase
	36005_at	Cluster Incl. AF042800:Homo sapiens suppressor of white apricot homolog
	36068_at	Cluster Incl. AF002210:Homo sapiens copper chaperone for superoxide dis
	36545_s_at	Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, comple
35	37254_at	Cluster Incl. U09366:Human zinc finger protein ZNF133 /cds=(445,2409) /
	40869_at	Cluster Incl. AF069517:Homo sapiens RNA binding protein DEF-3 mRNA, com
	40870_g_at	Cluster Incl. AF069517:Homo sapiens RNA binding protein DEF-3 mRNA, c
	33406_at	Cluster Incl. AL050345:Novel human gene mapping to chromosome 22 /cds=(1
	35273_at	Cluster Incl. AF007151:Homo sapiens clone 23967 unknown mRNA, partial c

- 39551_at Cluster Incl. N98667:yy66d05.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-
 39861_at Cluster Incl. M98343:Homo sapiens amplexin (EMS1) mRNA, complete cds /c
 39876_at Cluster Incl. AL035252:Human DNA sequence from clone 738P15 on chromoso
 32554_s_at Cluster Incl. Y12781:Homo sapiens mRNA for transducin (beta) like 1 p
- 5**
- Metagene 309
- 31668_f_at Cluster Incl. W28193:43d12 Homo sapiens cDNA /gb=W28193 /gi=1308141 /
 35571_at Cluster Incl. AF055917:Homo sapiens protease-activated receptor 4 mRNA,
10 36762_at Cluster Incl. X15376:Human mRNA for GABA-A receptor, gamma 2 subunit /c
 37793_r_at Cluster Incl. AF034956:Homo sapiens RAD51D mRNA, complete cds /cds=(1
 32646_at Cluster Incl. AB007918:Homo sapiens mRNA for KIAA0449 protein, partial
 33220_at Cluster Incl. Z11773:Homo sapiens mRNA for SRE-ZBP /cds=(0,1226) /gb=Z1
 35208_at Cluster Incl. AB020681:Homo sapiens mRNA for KIAA0874 protein, partial
15 40484_g_at Cluster Incl. U49857:Human transcriptional activator mRNA, complete c
 33857_at Cluster Incl. N25122:yx19d10.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-
 1852_at X02910 /FEATURE=expanded_cds /DEFINITION=HSTNFA Human gene for tumor nec
 1671_s_at L35253 /FEATURE= /DEFINITION=HUMMAPKNS Human p38 mitogen
 activated pro
20 1464_at S73149 /FEATURE=mRNA /DEFINITION=S73149 insulin-like growth factor II {i
 917_g_at L18983 /FEATURE=mRNA /DEFINITION=HUMTYROPHO Homo sapiens
 tyrosine phosph
- Metagene 310
- 25**
- 40310_at Cluster Incl. AF051152:Homo sapiens Toll/interleukin-1 receptor-like pr
 35172_at Cluster Incl. AF049891:Homo sapiens tyrosylprotein sulfotransferase-2 m
 36591_at Cluster Incl. X06956:Human HALPHA44 gene for alpha-tubulin, exons 1-3 /
 36622_at Cluster Incl. AI989422:ws25a09.x1 Homo sapiens cDNA, 3' end /clone=IMAG
30 36983_f_at Cluster Incl. X00442:Human mRNA for haptoglobin alpha(2FS)-beta precu
 37019_at Cluster Incl. J00129:Human fibrinogen beta-chain mRNA, partial cds /cds
 39175_at Cluster Incl. D25328:Human mRNA for platelet-type phosphofructokinase,
 1713_s_at U26727 /FEATURE= /DEFINITION=HSU26727 Human p16INK4/MTS1 mRNA,
 complet
35 1388_g_at J03258 /FEATURE=mRNA /DEFINITION=HUMVDR Human vitamin D receptor
 mRNA,
 330_s_at Tubulin, Alpha 1, Isoform 44
- Metagene 311

- 31688_at Cluster Incl. AF005080:Homo sapiens skin-specific protein (xp5) mRNA, c
 32114_s_at Cluster Incl. S46950:adenosine A2 receptor [human, hippocampal, mRNA,
 32673_at Cluster Incl. U90543:Human butyrophilin (BTF1) mRNA, complete cds /cds=
5 35634_at Cluster Incl. U49928:Homo sapiens TAK1 binding protein (TAB1) mRNA, com
 34837_at Cluster Incl. AB002374:Human mRNA for KIAA0376 gene, partial cds /cds=(
 423_at X66899 /FEATURE=cds /DEFINITION=HSEWS H.sapiens EWS mRNA
- Metagene 312
- 10**
- 37855_at Cluster Incl. M95767:Homo sapiens di-N-acetylchitobiase mRNA, complete
 40399_r_at Cluster Incl. AI743406:wg92g12.x1 Homo sapiens cDNA, 3 end /clone=IM
 40665_at Cluster Incl. M83772:Human flavin-containing monooxygenase form II (FMO
 41405_at Cluster Incl. AF026692:Homo sapiens frizzled related protein frpHE mRNA
15 37397_at Cluster Incl. L34657:Homo sapiens platelet/endothelial cell adhesion mo
 38113_at Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial
 33122_at Cluster Incl. N95393:zb68c09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
- Metagene 313
- 20**
- 33991_g_at Cluster Incl. U22961:Human mRNA clone with similarity to L-glycerol-3
 33992_at Cluster Incl. M12523:Human serum albumin (ALB) gene, complete cds /cds=
 40114_at Cluster Incl. J00077:Human alpha-fetoprotein (AFP) mRNA, complete cds /
 41845_at Cluster Incl. W29036:55d12 Homo sapiens cDNA /gb=W29036 /gi=1308993 /ug
- 25**
- Metagene 314
- 33632_g_at Cluster Incl. AF023612:Homo sapiens Dim1p homolog mRNA, complete cds
 32065_at Cluster Incl. S68134:CREM=cyclic AMP-responsive element modulator beta
30 37581_at Cluster Incl. X92972:H.sapiens mRNA for protein phosphatase 6 /cds=(21,
 41733_at Cluster Incl. AC003007:Human Chromosome 16 BAC clone CIT987SK-A-61E3 /c
 1211_s_at U84388 /FEATURE= /DEFINITION=HSU84388 Human death domain containing
 pr
 688_at L02426 /FEATURE= /DEFINITION=HUM26SPSIV Human 26S protease (S4) regulator
- 35**
- Metagene 315
- 33052_at Cluster Incl. U95301:Human calcium-dependent group X phospholipase A2 m
 32046_at Cluster Incl. D10495:Homo sapiens mRNA for protein kinase C delta-type,

	36544_at	Cluster Incl. AF038193:Homo sapiens clone 23608 mRNA sequence /cds=UNKN
	39725_at	Cluster Incl. L10910:Homo sapiens splicing factor (CC1.3) mRNA, complet
	40045_g_at	Cluster Incl. AF009425:Homo sapiens clone 22 mRNA, alternative splici
	35350_at	Cluster Incl. AB011170:Homo sapiens mRNA for KIAA0598 protein, complete
5	37370_i_at	Cluster Incl. L41066:Homo sapiens NF-AT3 mRNA, complete cds /cds=(141
	38733_at	Cluster Incl. M30938:Human Ku (p70/p80) subunit mRNA, complete cds /cds
	40193_at	Cluster Incl. X51956:Human ENO2 gene for neuron specific (gamma) enolas
	1810_s_at	D10495 /FEATURE= /DEFINITION=HUMPKSCD Homo sapiens mRNA for protein ki
10	1138_at	L20859 /FEATURE= /DEFINITION=HUMGLVR1X Human leukemia virus receptor 1 (
	585_at	M30938 /FEATURE=mRNA#2 /DEFINITION=HUMKUP Human Ku (p70/p80) subunit mRNA
	Metagene 316	
15		
	34169_s_at	Cluster Incl. U57627:Human fetal brain oculocerebrorenal syndrome (OC
	38491_at	Cluster Incl. U11732:Human ets-like gene (tel) mRNA, complete cds /cds=
	36023_at	Cluster Incl. AI864120:wg64a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41806_at	Cluster Incl. J04513:Human basic fibroblast growth factor (bFGF) 22.5 k
20		
	Metagene 317	
	33576_at	Cluster Incl. AB020725:Homo sapiens mRNA for KIAA0918 protein, partial
	39267_at	Cluster Incl. AF102265:Homo sapiens N-acetylglucosamine-phosphate mutas
25	41040_at	Cluster Incl. U77664:Human RNaseP protein p38 (RPP38) mRNA, complete cd
	41415_at	Cluster Incl. L36720:Homo sapiens bystin mRNA, complete cds /cds=(64,98
	38709_at	Cluster Incl. D80009:Human mRNA for KIAA0187 gene, complete cds /cds=(2
	39767_at	Cluster Incl. D13627:Human mRNA for KIAA0002 gene, complete cds /cds=(2
	40417_at	Cluster Incl. D43950:Human mRNA for KIAA0098 gene, partial cds /cds=(0,
30	40774_at	Cluster Incl. X74801:H.sapiens Cctg mRNA for chaperonin /cds=(0,1634) /
	34882_at	Cluster Incl. Y12065:Homo sapiens mRNA for nucleolar protein hNop56 /cd
	36201_at	Cluster Incl. D13315:Human mRNA for lactoyl glutathione lyase /cds=(87,
	37326_at	Cluster Incl. U93305:Homo sapiens A4 differentiation-dependent protein
	32579_at	Cluster Incl. U29175:Human transcriptional activator (BRG1) mRNA, compl
35		
	Metagene 318	
	31692_at	Cluster Incl. M59830:Human MHC class III HSP70-2 gene (HLA), complete c
	34133_at	Cluster Incl. AL049685:Human gene from PAC 37M17, chromosome X, similar

- 36039_s_at Cluster Incl. X93498:H.sapiens mRNA for 21-Glutamic Acid-Rich Protein
 36040_at Cluster Incl. AI337192:qx88h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41233_at Cluster Incl. AB014888:Homo sapiens mRNA for MRJ, complete cds /cds=(10
 33901_at Cluster Incl. U81375:Human placental equilibrative nucleoside transport
5 1104_s_at M11717 /FEATURE=mRNA /DEFINITION=HUMHSP70D Human heat shock
 protein (h
 977_s_at Z35402 /FEATURE=mRNA /DEFINITION=HSECAD3 H.sapiens gene encoding
 E-cadh
- 10** Metagene 319
- 31353_f_at Cluster Incl. X94553:H.sapiens HFKH4 mRNA for fork head like protein
 31738_at Cluster Incl. W28912:53f11 Homo sapiens cDNA /gb=W28912 /gi=1308860 /ug
 32482_at Cluster Incl. L42563:Homo sapiens (clone ISW34) non-gastric H,K-ATPase
15 36706_at Cluster Incl. Y15057:Homo sapiens mRNA for STK9 protein /cds=(221,3313)
 34241_at Cluster Incl. L34357:Homo sapiens GATA-4 mRNA, complete cds /cds=(240,1
 37648_at Cluster Incl. D63487:Human mRNA for KIAA0153 gene, partial cds /cds=(0,
 36613_at Cluster Incl. U09585:Homo sapiens putative interferon-related protein (
 39459_at Cluster Incl. W28765:51d2 Homo sapiens cDNA /gb=W28765 /gi=1308713 /ug=
20 39870_at Cluster Incl. AI377866:te63h04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 1153_f_at J00117 /FEATURE=mRNA /DEFINITION=HUMCGB Human chorionic
 gonadotropin (
 887_at M62302 /FEATURE= /DEFINITION=HUMGDF1 Human growth/differentiation factor
 315_at D45132 /FEATURE= /DEFINITION=HUMHOXY1 Homo sapiens mRNA for zinc-finger
25 D
- Metagene 320
- 36376_at Cluster Incl. AF030880:Homo sapiens pendrin (PDS) mRNA, complete cds /c
30 41424_at Cluster Incl. L48516:Homo sapiens paraoxonase 3 (PON3) mRNA, 3 end of
 37268_at Cluster Incl. U43368:Human VEGF related factor isoform VRF186 precursor
 38315_at Cluster Incl. AB015228:Homo sapiens mRNA for RALDH2-T, complete cds /cd
 33203_s_at Cluster Incl. U59831:Human transcription factor, forkhead related act
- 35** Metagene 321
- 33613_at Cluster Incl. AA806239:oc21e02.s1 Homo sapiens cDNA /clone=IMAGE-134153
 37835_at Cluster Incl. M28827:Human thymocyte antigen CD1c mRNA, complete cds /c
 38862_at Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149

- 39582_at Cluster Incl. AL050166:Homo sapiens mRNA; cDNA DKFZp586D1122 (from
clon
- 39971_at Cluster Incl. M22637:Human LYL-1 protein mRNA, complete cds
/cds=UNKNOWN
- 5 40688_at Cluster Incl. AJ223280:Homo sapiens mRNA for 36 kDa phosphotyrosine pr
41100_at Cluster Incl. AB023172:Homo sapiens mRNA for KIAA0955 protein, complete
32033_at Cluster Incl. AL096780:Novel human gene mapping to chromosome 22p13.33 s
32649_at Cluster Incl. X59871:Human TCF-1 mRNA for T cell factor 1 (splice form
36843_at Cluster Incl. AB005666:Homo sapiens mRNA for GTPase-activating protein,
10 37579_at Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds
34871_at Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
35341_at Cluster Incl. U90547:Human Ro/SSA ribonucleoprotein homolog (RoRet) mRN
39835_at Cluster Incl. U93181:Homo sapiens nuclear dual-specificity phosphatase
506_s_at U43185 /FEATURE= /DEFINITION=HSU43185 Human signal transducer and
15 activ
216_at M98539 /FEATURE=exon /DEFINITION=HUMPDS03 Human prostaglandin D2 synthase
174_s_at U61167 /FEATURE= /DEFINITION=HSU61167 Human SH3 domain-containing;
prote
- 20 Metagene 322
- 32434_at Cluster Incl. D10522:Homo sapiens mRNA for 80K-L protein, complete cds
32318_s_at Cluster Incl. X63432:H.sapiens ACTB mRNA for mutant beta-actin (beta-
34761_r_at Cluster Incl. U41766:Human metalloprotease/disintegrin/cysteine-rich
25 35140_at Cluster Incl. R59697:yh11b03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
35692_at Cluster Incl. AL080235:Homo sapiens mRNA; cDNA DKFZp586E1621 (from
clon
40813_at Cluster Incl. AI768188:wg82b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
40879_at Cluster Incl. AB014599:Homo sapiens mRNA for KIAA0699 protein, partial
30 32808_at Cluster Incl. X07979:Human mRNA for integrin beta 1 subunit /cds=(103,2
33447_at Cluster Incl. X54304:Human mRNA for myosin regulatory light chain /cds=
33866_at Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /c
33891_at Cluster Incl. AL080061:Homo sapiens mRNA; cDNA DKFZp564H182 (from
clone
35 34342_s_at Cluster Incl. AF052124:Homo sapiens clone 23810 osteopontin mRNA, com
34793_s_at Cluster Incl. M22299:Human T-plastin polypeptide mRNA, complete cds,
35271_at Cluster Incl. AF006083:Homo sapiens actin-related protein Arp3 (ARP3) m
36190_at Cluster Incl. M63256:Human major Yo paraneoplastic antigen (CDR2) mRNA,
37345_at Cluster Incl. AF013759:Homo sapiens calumein (Calu) mRNA, complete cds

- 37747_at Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U0
 38041_at Cluster Incl. U41514:Human UDP-GalNAc-polypeptide N-acetylgalactosaminy
 38074_at Cluster Incl. U91932:Homo sapiens AP-3 complex sigma3A subunit mRNA, co
 39099_at Cluster Incl. X97064:H.sapiens mRNA for Sec23A isoform, 2748bp /cds=(15
 5 41485_at Cluster Incl. X02152:Human mRNA for lactate dehydrogenase-A (LDH-A, EC
 32544_s_at Cluster Incl. L12535:Human RSU-1/RSP-1 mRNA, complete cds /cds=(827,1
 32545_r_at Cluster Incl. L12535:Human RSU-1/RSP-1 mRNA, complete cds /cds=(827,1
 32563_at Cluster Incl. U51478:Human sodium/potassium-transporting ATPase beta-3
 2092_s_at J04765 /FEATURE= /DEFINITION=HUMOSTRO Human osteopontin mRNA,
 10 complete
 1659_s_at D78132 /FEATURE= /DEFINITION=D78132 Homo sapiens mRNA for ras-
 related
 1039_s_at U22431 /FEATURE= /DEFINITION=HSU22431 Human hypoxia-inducible factor
 1
 15 760_at Y09216 /FEATURE= /DEFINITION=HSDYRK2 H.sapiens mRNA for protein kinase, D
 Metagene 323
 32352_at Cluster Incl. X52730:Human gene for phenylethanolamine N-methylase (PNM
 20 37772_at Cluster Incl. AB020711:Homo sapiens mRNA for KIAA0904 protein, partial
 39668_at Cluster Incl. X95694:H.sapiens mRNA for AP-2 beta transcription factor
 41715_at Cluster Incl. Y11312:H.sapiens mRNA for phosphoinositide 3-kinase /cds=
 33218_at Cluster Incl. M11730:Human tyrosine kinase-type receptor (HER2) mRNA, c
 38261_at Cluster Incl. AF085692:Homo sapiens multidrug resistance-associated pro
 25 38672_at Cluster Incl. Y13247:Homo sapiens fb19 mRNA /cds=(539,3361) /gb=Y13247
 40113_at Cluster Incl. D87119:Homo sapiens mRNA for GS3955, complete cds /cds=(1
 41193_at Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(
 33399_at Cluster Incl. AA142942:zl43c04.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 37330_at Cluster Incl. U24266:Human pyrroline-5-carboxylate dehydrogenase (P5CDh
 30 37355_at Cluster Incl. D38255:Homo sapiens mRNA for CAB1, complete cds /cds=(121
 1930_at U83659 /FEATURE= /DEFINITION=HSU83659 Human multidrug resistance-associa
 1901_s_at M12036 /FEATURE=cds /DEFINITION=HUMHER2B Human tyrosine kinase-
 type re
 1802_s_at X03363 /FEATURE=cds /DEFINITION=HSERB2R Human c-erb-B-2 mRNA
 35 1680_at D43772 /FEATURE= /DEFINITION=HUMGRB7 Human squamous cell carcinoma of es
 881_at M35198 /FEATURE= /DEFINITION=HUMINTB6A Human integrin B-6 mRNA,
 complete
 717_at D87119 /FEATURE= /DEFINITION=D87119 Homo sapiens mRNA for GS3955, complet

Metagene 324

- 31622_f_at Cluster Incl. M10943:Human metallothionein-I ϵ gene (hMT-I ϵ) /cds=(0,1
 31623_f_at Cluster Incl. K01383:Human metallothionein-I-A gene, complete coding
5 39594_f_at Cluster Incl. R93527:yq35f10.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 41446_f_at Cluster Incl. H68340:yr82b10.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 32092_at Cluster Incl. AB007937:Homo sapiens mRNA for KIAA0468 protein, complete
 36130_f_at Cluster Incl. R92331:yq03h03.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 926_at J03910 /FEATURE=mRNA /DEFINITION=HUMMT2A Human (clone 14VS)
10 metallothione
 870_f_atM93311 /FEATURE=cds /DEFINITION=HUMMETIII Human metallothionein-III gen
 609_f_atM13485 /FEATURE=cds /DEFINITION=HUMMT1B2 Human metallothionein I-B gene

Metagene 325

- 15**
 35588_at Cluster Incl. AB011414:Homo sapiens ZK1 mRNA for Kruppel-type zinc fing
 36261_at Cluster Incl. AC003003:Human Chromosome 16 BAC clone CIT987SK-254P9 /cd
 31884_at Cluster Incl. L40399:Homo sapiens (clone S240ii117/zap112) mRNA, comple
 31903_at Cluster Incl. AB014593:Homo sapiens mRNA for KIAA0693 protein, partial
20 33753_at Cluster Incl. AB014566:Homo sapiens mRNA for KIAA0666 protein, partial
 34225_at Cluster Incl. AF101434:Homo sapiens Wolf-Hirschhorn syndrome candidate
 37533_r_at Cluster Incl. D86980:Human mRNA for KIAA0227 gene, partial cds /cds=(
 37561_at Cluster Incl. AL031778:dJ34B21.4.1 (nuclear transcription factor Y, alp
 38277_at Cluster Incl. M29550:Human calcineurin A1 mRNA, complete cds /cds=(107,
25 38988_at Cluster Incl. AJ007042:Homo sapiens mRNA for TRX5 protein /cds=(762,485
 39715_at Cluster Incl. W28214:45f7 Homo sapiens cDNA /gb=W28214 /gi=1308297 /ug=
 40103_at Cluster Incl. X51521:Human mRNA for ezrin /cds=(117,1877) /gb=X51521 /g
 32217_at Cluster Incl. AF052105:Homo sapiens clone 23965 mRNA sequence /cds=UNKN
 35306_at Cluster Incl. AB001636:Homo sapiens mRNA for ATP-dependent RNA helicase
30 38086_at Cluster Incl. AB007935:Homo sapiens mRNA for KIAA0466 protein, partial
 32602_at Cluster Incl. X63465:H.sapiens hGDS mRNA for smg GDS /cds=(0,1676) /gb=

Metagene 326

- 35** 39764_at Cluster Incl. Z22534:H.sapiens ALK-2 mRNA /cds=(103,1632) /gb=Z22534 /g
 35816_at Cluster Incl. U46692:Human cystatin B gene, complete cds /cds=(96,392)

Metagene 327

- 31495_at Cluster Incl. D63789:Homo sapiens DNA for SCM-1beta precursor, complete
 37085_g_at Cluster Incl. AF088219:Homo sapiens CC chemokine gene cluster, comple
 31830_s_at Cluster Incl. Y13492:Homo sapiens mRNA for smoothelin-B /cds=(219,297
 33758_f_at Cluster Incl. U25988:Human pregnancy-specific glycoprotein 13 (PSG13)
 5 36462_at Cluster Incl. U50383:Human retinoic acid-responsive protein (NN8-4AG) m
 37916_at Cluster Incl. AI086057:oz44f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 38622_at Cluster Incl. W28953:54b7 Homo sapiens cDNA /gb=W28953 /gi=1308901 /ug=
 36199_at Cluster Incl. X76105:H.sapiens DAP-1 mRNA /cds=(159,467) /gb=X76105 /gi
 38029_at Cluster Incl. J02939:Human membrane glycoprotein 4F2 antigen heavy chai
 10 38055_at Cluster Incl. AI683748:tw53e07.x1 Homo sapiens cDNA, 3 end /clone=IMAG

Metagene 328

- 33693_at Cluster Incl. M76482:Human 130-kD pemphigus vulgaris antigen mRNA, comp
 15 37131_at Cluster Incl. AB008390:Homo sapiens mRNA for neuropsin type1, complete
 38202_at Cluster Incl. AB011535:Homo sapiens mRNA for MEGF1, partial cds /cds=(0
 39271_at Cluster Incl. AA461365:zx70e07.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 39577_at Cluster Incl. AL050024:Homo sapiens mRNA; cDNA DKFZp564D206 (from
 clone
 20 40339_at Cluster Incl. U95367:Human GABA-A receptor pi subunit mRNA, complete cd
 33272_at Cluster Incl. AA829286:of08a01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 35726_at Cluster Incl. AI539439:te51e07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 36838_at Cluster Incl. AF055481:Homo sapiens normal epithelial cell-specific 1 (
 37582_at Cluster Incl. X07696:Human mRNA for cytokeratin 15 /cds=(61,1431) /gb=X
 25 37954_at Cluster Incl. X16662:Human mRNA for vascular anticoagulant-beta (VAC-be
 38608_at Cluster Incl. AA010777:ze22f06.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 39052_at Cluster Incl. J00124:Homo sapiens 50 kDa type I epidermal keratin gene,
 34301_r_at Cluster Incl. Z19574:H.sapiens gene for cytokeratin 17 /cds=(64,1362)
 34395_at Cluster Incl. AB002352:Human mRNA for KIAA0354 gene, complete cds /cds=
 30 35280_at Cluster Incl. Z15008:H.sapiens mRNA for laminin /cds=(117,3698) /gb=Z15
 2084_s_at D12765 /FEATURE= /DEFINITION=HUME1AF Human mRNA for E1A-F
 2027_at M87068 /FEATURE= /DEFINITION=HUMCAN H.sapiens CaN19 mRNA sequence
 1898_at L24203 /FEATURE= /DEFINITION=HUMDK Homo sapiens ataxia-telangiectasia gr
 862_at U04313 /FEATURE= /DEFINITION=HSU04313 Human maspin mRNA, complete cds
 35 863_g_at U04313 /FEATURE= /DEFINITION=HSU04313 Human maspin mRNA,
 complete cds
 668_s_at L22524 /FEATURE=expanded_cds /DEFINITION=HUMMATRY06 Human
 matrilysin ge

613_at M21389 /FEATURE=mRNA /DEFINITION=HUMKER2A Human keratin type II (58 kD)
m

Metagene 329

5

31661_at Cluster Incl. AJ243936:Homo sapiens mRNA for G16 protein (G16 gene loca
34151_at Cluster Incl. AL050284:Homo sapiens mRNA; cDNA DKFZp586M1019 (from
clon

10

37424_at Cluster Incl. AB029343:Homo sapiens HCR (a-helix coiled-coil rod homolo
41463_at Cluster Incl. AL042729:DKFZp434B0222_s1 Homo sapiens cDNA, 3 end /clon
32137_at Cluster Incl. AF029778:Homo sapiens Jagged2 (JAG2) mRNA, complete cds /
36076_g_at Cluster Incl. AL037167:DKFZp564P1564_s1 Homo sapiens cDNA, 3 end /cl
38665_at Cluster Incl. D85939:Homo sapiens mRNA for p97 homologous protein, comp
39020_at Cluster Incl. U82938:Human CD27BP (Siva) mRNA, complete cds /cds=(252,8
15 39339_at Cluster Incl. AB018335:Homo sapiens mRNA for KIAA0792 protein, complete
37365_at Cluster Incl. X63368:H.sapiens HSJ1 mRNA /cds=(25,1080) /gb=X63368 /gi=
40926_at Cluster Incl. U36341:Human Xq28 cosmid, creatine transporter (SLC6A8) g
40997_at Cluster Incl. AI660963:wf20e04.x1 Homo sapiens cDNA, 3 end /clone=IMAG

20 Metagene 330

35099_at Cluster Incl. AF019225:Homo sapiens apolipoprotein L mRNA, complete cds
35583_at Cluster Incl. X99699:H.sapiens mRNA for XIAP associated factor-1 /cds=(
36412_s_at Cluster Incl. U53831:Homo sapiens interferon regulatory factor 7B mRN
25 34491_at Cluster Incl. AJ225089:Homo sapiens mRNA for 2-5 oligoadenylate synthe
38517_at Cluster Incl. M87503:Human IFN-responsive transcription factor subunit
38549_at Cluster Incl. AF026941:Homo sapiens cig5 mRNA, partial sequence /cds=UN
39263_at Cluster Incl. M87434:Human 71 kDa 25 oligoadenylate synthetase (p69 2-
39264_at Cluster Incl. M87284:Human 69 kDa 25 oligoadenylate synthetase (P69 2-
30 33236_at Cluster Incl. AF060228:Homo sapiens retinoic acid receptor responder 3
36927_at Cluster Incl. AB000115:Homo sapiens mRNA expressed in osteoblast, compl
38662_at Cluster Incl. AL047596:DKFZp586G0421_s1 Homo sapiens cDNA
/clone=DKFZp5
39061_at Cluster Incl. D28137:Human mRNA for BST-2, complete cds /cds=(9,551) /g
35 40505_at Cluster Incl. AA883502:am25h07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
41745_at Cluster Incl. X57352:Human 1-8U gene from interferon-inducible gene fam
32814_at Cluster Incl. M24594:Human interferon-inducible 56 Kd protein mRNA, com
32860_g_at Cluster Incl. M97935:Homo sapiens transcription factor ISGF-3 mRNA, c
37014_at Cluster Incl. M33882:Human p78 protein mRNA, complete cds /cds=(345,233

- 37754_at Cluster Incl. L13210:Human Mac-2 binding protein mRNA, complete cds /cd
 38388_at Cluster Incl. M11810:Human (2-5) oligo A synthetase E gene /cds=(0,120
 38389_at Cluster Incl. X04371:Human 1.6Kb mRNA for 2-5A synthetase induced by in
 38432_at Cluster Incl. AA203213:zx57e04.r1 Homo sapiens cDNA, 5 end /clone=IMAG
5 1358_s_at U22970 /FEATURE=mRNA#1 /DEFINITION=HSU22970 Human interferon-
 inducible
 1107_s_at M13755 /FEATURE=mRNA /DEFINITION=HUMIFN15K Human interferon-
 induced 17
 915_at M24594 /FEATURE=mRNA /DEFINITION=HUMII56KD Human interferon-inducible 56
10 879_at M30818 /FEATURE=mRNA /DEFINITION=HUMMXB Human interferon-induced
 cellular
 675_at J04164 /FEATURE= /DEFINITION=HUM927A Human interferon-inducible protein 9
 626_s_at L78833 /FEATURE=cds#5 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7
 and vatI g
15 464_s_at U72882 /FEATURE= /DEFINITION=HSU72882 Human interferon-induced
 leucine
 425_at X67325 /FEATURE=cds /DEFINITION=HSP27 H.sapiens p27 mRNA
 269_at L40387 /FEATURE=cds /DEFINITION=HUMTRIP14G Homo sapiens thyroid receptor

20 Metagene 331

 36711_at Cluster Incl. AL021977:bK447C4.1 (novel MAFF (v-maf musculoaponeurotic
 38935_at Cluster Incl. X72790:Human endogenous retrovirus mRNA for ORF /cds=(524
 37544_at Cluster Incl. X64318:H.sapiens E4BP4 gene /cds=(213,1601) /gb=X64318 /g
25 39081_at Cluster Incl. AI547258:PN001_AH_H08.r Homo sapiens cDNA, 5 end /clone_
 32168_s_at Cluster Incl. U85267:Homo sapiens down syndrome candidate region 1 (D
 39839_at Cluster Incl. M24069:Human DNA-binding protein A (dbpA) gene, 3 end /c
 1733_at M60315 /FEATURE= /DEFINITION=HUMTGFBC Human transforming growth factor-b
 1379_at M59371 /FEATURE=mRNA /DEFINITION=HUMECK Human protein tyrosine kinase mR
30
 Metagene 332

 31690_at Cluster Incl. U08997:Human glutamate dehydrogenase gene, complete cds /
 33989_f_at Cluster Incl. W28869:53h2 Homo sapiens cDNA /gb=W28869 /gi=1308880 /u
35 38581_at Cluster Incl. U40038:Human GTP-binding protein alpha q subunit (GNAQ) m
 34735_at Cluster Incl. U43195:Human Rho-associated, coiled-coil containing prote
 37250_at Cluster Incl. AB007191:Homo sapiens mRNA for AMY-1, complete cds /cds=(
 39376_at Cluster Incl. AB014530:Homo sapiens mRNA for KIAA0630 protein, partial
 39790_at Cluster Incl. M23115:Homo sapiens calcium-ATPase (HK2) mRNA, complete c

	40473_at	Cluster Incl. AF024636:Homo sapiens STE20-like kinase 3 (mst-3) mRNA, c
	40487_at	Cluster Incl. W26634:34b10 Homo sapiens cDNA /gb=W26634 /gi=1307477 /ug
	40874_at	Cluster Incl. AJ005259:Homo sapiens mRNA for EDF-1 protein /cds=(34,480
	32765_f_at	Cluster Incl. W28330:45d4 Homo sapiens cDNA /gb=W28330 /gi=1308278 /u
5	34350_at	Cluster Incl. X64838:H.sapiens mRNA for restin /cds=(132,4415) /gb=X648
	35363_at	Cluster Incl. AL080113:Homo sapiens mRNA; cDNA DKFZp586K2322 (from clon
	35784_at	Cluster Incl. U64520:Human synaptobrevin-3 mRNA, complete cds /cds=(24,
	35788_at	Cluster Incl. W28994:54b7 Homo sapiens cDNA /gb=W28994 /gi=1308960 /ug=
10	36146_at	Cluster Incl. AF057297:Homo sapiens ornithine decarboxylase antizyme 2
	36971_at	Cluster Incl. D87446:Human mRNA for KIAA0257 gene, partial cds /cds=(0,
	37318_at	Cluster Incl. X81625:H.sapiens mRNA for C11 protein /cds=(135,1448) /gb
	38446_at	Cluster Incl. X56199:Human XIST, coding sequence a mRNA (locus DXS399
	38476_at	Cluster Incl. L13434:Human chromosome 3p21.1 gene sequence, complete cd
15	39118_at	Cluster Incl. L08069:Human heat shock protein, E. coli DnaJ homologue m
	39560_at	Cluster Incl. H10776:ym07h11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
	39873_at	Cluster Incl. X66360:H.sapiens mRNA PCTAIRE-2 for serine/threonine prot
	40618_at	Cluster Incl. H15872:ym22b12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
	40634_at	Cluster Incl. M86667:H.sapiens NAP (nucleosome assembly protein) mRNA,
20	40962_s_at	Cluster Incl. D26155:Human mRNA for transcriptional activator hSNF2a,
	41244_f_at	Cluster Incl. X80910:H.sapiens PPP1CB mRNA /cds=(258,1241) /gb=X80910
	41300_s_at	Cluster Incl. AA477898:zu34f08.r1 Homo sapiens cDNA, 5 end /clone=IM
	41495_at	Cluster Incl. W37606:zc12a03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
	32569_at	Cluster Incl. L13385:Homo sapiens(clone 71) Miller-Dieker lissencephaly
25	2093_s_at	J04977 /FEATURE=mRNA /DEFINITION=HUMKUANT Human Ku autoimmune antigen
	1161_at	J04988 /FEATURE=cds /DEFINITION=HUMHSP90B Human 90 kD heat shock protein
	1119_at	J05249 /FEATURE= /DEFINITION=HUMREPA Human replication protein A 32-kDa
	755_at	D26070 /FEATURE=mRNA /DEFINITION=HUMINSP3R1 Human mRNA for type 1
30	inosito	
	756_at	D26350 /FEATURE= /DEFINITION=HUMHT2I Human mRNA for type 2 inositol 1,4,5
	630_at	L39874 /FEATURE=expanded_cds /DEFINITION=HUMDODDA Homo sapiens deoxycytid
	517_at	U07000 /FEATURE=cds#4 /DEFINITION=HSU07000 Human breakpoint cluster regio
35	457_s_at	U67122 /FEATURE= /DEFINITION=HSU67122 Human ubiquitin-related protein S
	312_s_at	Focal Adhesion Kinase
	226_at	M33336 /FEATURE= /DEFINITION=HUMCAMPPK Human cAMP-dependent protein kinas

227_g_at M33336 /FEATURE= /DEFINITION=HUMCAMPPK Human cAMP-dependent protein kin

115_at X14787 /FEATURE=cds /DEFINITION=HSTS Human mRNA for thrombospondin

5 Metagene 333

- 38923_at Cluster Incl. L76159:Homo sapiens FRG1 mRNA, complete cds /cds=(191,967
40375_at Cluster Incl. X63741:H.sapiens pilot mRNA /cds=(353,1516) /gb=X63741 /g
41638_at Cluster Incl. D38552:Human mRNA for KIAA0073 gene, partial cds /cds=(0,
10 31898_at Cluster Incl. D86967:Human mRNA for KIAA0212 gene, complete cds /cds=(5
35217_at Cluster Incl. AL049404:Homo sapiens mRNA; cDNA DKFZp586F0219 (from
clon
36852_at Cluster Incl. U42349:Human N33 mRNA, complete cds /cds=(157,1203) /gb=U
39405_at Cluster Incl. D87455:Human mRNA for KIAA0266 gene, complete cds /cds=(7
15 39441_at Cluster Incl. Y11395:H.sapiens mRNA for p40 /cds=(104,1303) /gb=Y11395
40078_at Cluster Incl. AF015287:Homo sapiens serine protease mRNA, complete cds
40137_at Cluster Incl. M31724:Human phosphotyrosyl-protein phosphatase (PTP-1B)
33343_at Cluster Incl. AB022663:Homo sapiens HFB30 mRNA, complete cds /cds=(236,
33347_at Cluster Incl. AA883868:am26el1.s1 Homo sapiens cDNA, 3 end /clone=IMAG
20 36171_at Cluster Incl. AI521453:th60h07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
39097_at Cluster Incl. X63753:H.sapiens son-a mRNA /cds=(414,4985) /gb=X63753 /g
588_at M31724 /FEATURE=mRNA /DEFINITION=HUMPTPBX Human phosphotyrosyl-protein
ph
218_at S74221 /FEATURE= /DEFINITION=S74221 IK=IK factor [human, leukemic cells K

25

Metagene 334

- 31691_g_at Cluster Incl. U08997:Human glutamate dehydrogenase gene, complete cds
32389_at Cluster Incl. W25892:17b9 Homo sapiens cDNA /gb=W25892 /gi=1306222 /ug=
30 33466_at Cluster Incl. AF038182:Homo sapiens clone 23860 mRNA sequence /cds=UNKN
33944_at Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, pla
33988_at Cluster Incl. X75861:H.sapiens TEGT gene /cds=(40,753) /gb=X75861 /gi=4
35450_s_at Cluster Incl. AF015553:Homo sapiens TFII-I protein (TFII-I) mRNA, com
41713_at Cluster Incl. U09848:Human zinc finger protein (ZNF139) mRNA, partial c
35 41127_at Cluster Incl. L14595:Human alanine/serine/cysteine/threonine transporte
32215_i_at Cluster Incl. AB020685:Homo sapiens mRNA for KIAA0878 protein, comple
32741_at Cluster Incl. X77723:H.sapiens mRNA for unknown protein of uterine endo
34863_s_at Cluster Incl. W29030:55c4 Homo sapiens cDNA /gb=W29030 /gi=1308987 /u
36211_at Cluster Incl. D87461:Human mRNA for KIAA0271 gene, complete cds /cds=(1

- 40545_at Cluster Incl. AB018566:Homo sapiens gene for Proline synthetase associa
2018_at M65188 /FEATURE= /DEFINITION=HUMCX43 Human connexin 43 (GJA1, Cx43)
mRNA
- 2025_s_at M80261 /FEATURE= /DEFINITION=HUMAPE Human apurinic endonuclease
5 (APE)
- 1850_at U07418 /FEATURE= /DEFINITION=HSHMLHI Human DNA mismatch repair (hmlh1) m
1473_s_at U22376 /FEATURE=cds#2 /DEFINITION=HSU22376 Human (c-myb) gene,
complet
- 1474_s_at U22376 /FEATURE=cds#3 /DEFINITION=HSU22376 Human (c-myb) gene,
10 complet
- 1475_s_at U22376 /FEATURE=cds#4 /DEFINITION=HSU22376 Human (c-myb) gene,
complet
- 1476_s_at U22376 /FEATURE=cds#5 /DEFINITION=HSU22376 Human (c-myb) gene,
complet
- 15 1383_at M64929 /FEATURE= /DEFINITION=HUMPROP2AA Human protein phosphatase 2A alp
1335_at X04434 /FEATURE=cds /DEFINITION=HSIGFIRR Human mRNA for insulin-like gro
368_at Z29083 /FEATURE=cds /DEFINITION=HS5T4OA H.sapiens 5T4 gene for 5T4 Oncofe
343_s_at D12485 /FEATURE=cds#1 /DEFINITION=HUMNPP Human mRNA for
nucleotide pyro
- 20 Metagene 335
- 31317_r_at Cluster Incl. M21388:Human unproductively rearranged Ig mu-chain mRNA
31531_g_at Cluster Incl. U89344:Human acetyl-CoA carboxylase (ACC2) mRNA, comple
- 25 31627_f_at Cluster Incl. AF047485:Homo sapiens amine oxidase pseudogene mRNA, sp
31667_r_at Cluster Incl. W27698:36f8 Homo sapiens cDNA /gb=W27698 /gi=1307664 /u
32003_at Cluster Incl. D49357:Human mRNA for S-adenosylmethionine synthetase, co
34154_at Cluster Incl. U62437:Human nicotinic acetylcholine receptor beta2 subun
34589_f_at Cluster Incl. AC002366:Human Xp22 BAC CT-285I15 (from CalTech/Researc
- 30 34602_at Cluster Incl. D63160:Homo sapiens DNA for lectin P35 /cds=(10,951) /gb=
32362_r_at Cluster Incl. D87012:Human (lambda) DNA for immunoglobulin light chain
32907_at Cluster Incl. L41147:Homo sapiens 5-HT6 serotonin receptor mRNA, comple
35420_r_at Cluster Incl. AB020720:Homo sapiens mRNA for KIAA0913 protein, partia
35448_at Cluster Incl. U37219:Human cyclophilin-like protein CyP-60 mRNA, comple
- 35 36226_r_at Cluster Incl. W27611:35b9 Homo sapiens cDNA /gb=W27611 /gi=1307559 /u
38190_r_at Cluster Incl. AB014545:Homo sapiens mRNA for KIAA0645 protein, comple
40298_at Cluster Incl. AB014603:Homo sapiens mRNA for KIAA0703 protein, complete
40342_at Cluster Incl. U66077:Human DAZ mRNA, 3UTR /cds=UNKNOWN /gb=U66077
/gi=1

	40650_r_at	Cluster Incl. X72304:H.sapiens mRNA for corticotrophin releasing fact
	41383_at	Cluster Incl. AJ001403:Homo sapiens mRNA for MUC5AC protein (placental)
	41720_r_at	Cluster Incl. AF009767:AF009767 Homo sapiens cDNA /clone=C97A-12 /gb=
	31789_at	Cluster Incl. M14564:Human cytochrome P450c17 (steroid 17-alpha-hydroxy
5	32677_at	Cluster Incl. AF000979:Homo sapiens testis-specific Basic Protein Y 1 (
	33231_at	Cluster Incl. AI761148:wh97h07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	33738_r_at	Cluster Incl. AI871359:wl81b11.x1 Homo sapiens cDNA, 3 end /clone=IM
	34692_r_at	Cluster Incl. AF006087:Homo sapiens Arp2/3 protein complex subunit p2
	36464_at	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb
10	36547_r_at	Cluster Incl. AA521233:aa79a12.s1 Homo sapiens cDNA, 3 end /clone=IM
	37239_r_at	Cluster Incl. AF014118:Homo sapiens membrane-associated kinase (Myt1)
	40163_r_at	Cluster Incl. AC003107:Human DNA from chromosome 19-specific cosmid R
	40481_r_at	Cluster Incl. M14333:Homo sapiens c-syn protooncogene mRNA, complete
	40499_r_at	Cluster Incl. AF040708:Homo sapiens candidate tumor suppressor gene 2
15	40769_r_at	Cluster Incl. D14689:Human mRNA for KIAA0023 gene, complete cds /cds=
	40776_at	Cluster Incl. M63391:Human desmin gene, complete cds /cds=(80,1489) /gb
	32831_at	Cluster Incl. AA453183:zx46b09.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	33841_at	Cluster Incl. R48209:yj63d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	37744_r_at	Cluster Incl. U60062:Human FEZ1-T mRNA, alternatively spliced form, c
20	39113_at	Cluster Incl. AI262789:qk35e02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39177_r_at	Cluster Incl. M54994:Human bile salt-activated lipase (BAL) mRNA, com
	39482_at	Cluster Incl. W26787:15d8 Homo sapiens cDNA /gb=W26787 /gi=1306078 /ug=
	40176_at	Cluster Incl. J03407:Human rfp transforming protein mRNA, complete cds
	40594_r_at	Cluster Incl. Z22533:H.sapiens ALK-1 mRNA /cds=(282,1793) /gb=W22533
25	40883_at	Cluster Incl. W28230:43h12 Homo sapiens cDNA /gb=W28230 /gi=1308178 /ug
	41312_r_at	Cluster Incl. AI189624:qd32h08.x1 Homo sapiens cDNA, 3 end /clone=IM
	1998_i_at	U19599 /FEATURE= /DEFINITION=HSU19599 Human (BAX delta) mRNA, complete
	1904_at	D50692 /FEATURE= /DEFINITION=HUMAMY1 Homo sapiens mRNA for c-myc
30	binding	
	1569_r_at	L42243 /FEATURE=exon#3 /DEFINITION=HUMIFNAM08 Homo sapiens (clone 51H8
	1553_r_at	U22028 /FEATURE=expanded_cds /DEFINITION=HSU22028 Human cytochrome P45
35	586_s_at	M31153 /FEATURE=cds /DEFINITION=HUMCYP178 Human steroid 17-alpha-hydrox
	293_at	Homeotic Protein Hpx-42
	301_at	Mucin 6, Gastric

242_at M64571 /FEATURE=mRNA /DEFINITION=HUMMAP4 Human microtubule-associated pro

114_r_atX14474 /FEATURE=cds /DEFINITION=HSTAU1 Human mRNA for microtubule-assoc

5 Metagene 336

37781_at Cluster Incl. AB023138:Homo sapiens mRNA for KIAA0921 protein, partial

37865_at Cluster Incl. J05081:Human endothelin 3 (EDN3) mRNA, complete cds /cds=

38508_s_at Cluster Incl. U89337:Human HLA class III region containing cAMP respo

10 40366_at Cluster Incl. M25322:Human granule membrane protein-140 mRNA, complete

32109_at Cluster Incl. AA524547:ng45h04.s1 Homo sapiens cDNA, 3 end /clone=IMAG

33295_at Cluster Incl. X85785:H.sapiens DARC gene /cds=(494,1510) /gb=X85785 /gi

33790_at Cluster Incl. AI720438:as81g04.x1 Homo sapiens cDNA, 3 end /clone=IMAG

36569_at Cluster Incl. X64559:H.sapiens mRNA for tetranectin /cds=(93,701) /gb=X

15 36892_at Cluster Incl. AF032108:Homo sapiens integrin alpha-7 mRNA, complete cds

38995_at Cluster Incl. AF000959:Homo sapiens transmembrane protein mRNA, complet

41137_at Cluster Incl. AB007972:Homo sapiens mRNA, chromosome 1 specific transcr

34797_at Cluster Incl. AF014402:Homo sapiens type-2 phosphatidic acid phosphatas

36156_at Cluster Incl. U41518:Human channel-like integral membrane protein (AQP-

20 36617_at Cluster Incl. X77956:H.sapiens Id1 mRNA /cds=(35,499) /gb=X77956 /gi=45

36681_at Cluster Incl. J02611:Human apolipoprotein D mRNA, complete cds /cds=(61

37407_s_at Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain

38408_at Cluster Incl. L10373:Human (clone CCG-B7) mRNA sequence /cds=UNKNOWN /g

25 39545_at Cluster Incl. U22398:Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete

39561_at Cluster Incl. AL008583:dJ327J16.3 (novel CHROMObox family protein) /cds

32582_at Cluster Incl. AF001548:Human Chromosome 16 BAC clone CIT987SK-A-815A9 /

1736_at M62402 /FEATURE= /DEFINITION=HUMIGFBP4 Human insulin-like growth factor

1673_at M14764 /FEATURE=mRNA /DEFINITION=HUMNGFR Human nerve growth factor

30 recep

1596_g_at L06139 /FEATURE= /DEFINITION=HUMTEKRPTK Homo sapiens receptor protein-

767_at AF001548 /FEATURE=mRNA /DEFINITION=HUA001548 Human Chromosome 16 BAC clo

35 774_g_at D10667 /FEATURE= /DEFINITION=HUMMHCAA Homo sapiens mRNA for smooth mus

Metagene 337

	32097_at	Cluster Incl. AB007862:Homo sapiens KIAA0402 mRNA, partial cds /cds=(0,
	34287_at	Cluster Incl. AB023175:Homo sapiens mRNA for KIAA0958 protein, partial
	37555_at	Cluster Incl. X95263:H.sapiens mRNA for PWP2 protein /cds=(31,2790) /gb
	33824_at	Cluster Incl. X74929:H.sapiens KRT8 mRNA for keratin 8 /cds=(59,1510) /
5	490_g_at	U63329 /FEATURE=cds /DEFINITION=HSU63329 Human mutY homolog (hMYH) gene
	382_at	X70218 /FEATURE= /DEFINITION=HSPPX Homo sapiens mRNA for protein phosphat
	141_s_at	U75276 /FEATURE= /DEFINITION=HSU75276 Human TFIIB related factor hBRF (
10		Metagene 338
	35016_at	Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cd
	35926_s_at	Cluster Incl. AF004230:Homo sapiens monocyte/macrophage Ig-related re
15	36773_f_at	Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2),
	37493_at	Cluster Incl. H04668:yj49e08.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-
	38213_at	Cluster Incl. U78027:Homo sapiens Brutons tyrosine kinase (BTK), alpha-
	38547_at	Cluster Incl. Y00796:Human mRNA for leukocyte-associated molecule-1 alp
	39319_at	Cluster Incl. U20158:Human 76 kDa tyrosine phosphoprotein SLP-76 mRNA,
20	39591_s_at	Cluster Incl. Z36531:H.sapiens mRNA for fibrinogen-like protein (pT49
	40019_at	Cluster Incl. M60830:Human EVI2B3P gene, exon and complete cds /cds=(21
	40296_at	Cluster Incl. AL023653:Human DNA sequence from clone 753P9 on chromosom
	40699_at	Cluster Incl. M12824:Human T-cell differentiation antigen Leu-2/T8 mRNA
	40738_at	Cluster Incl. M16336:Human T-cell surface antigen CD2 (T11) mRNA, compl
25	40757_at	Cluster Incl. M18737:Human Hanukah factor serine protease (HuHF) mRNA,
	41433_at	Cluster Incl. M73255:Human vascular cell adhesion molecule-1 (VCAM1) ge
	41468_at	Cluster Incl. M30894:Human T-cell receptor Ti rearranged gamma-chain mR
	41609_at	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /
	31820_at	Cluster Incl. X16663:Human HS1 gene for heamatopoietic lineage cell spe
30	32035_at	Cluster Incl. M16942:Human MHC class II HLA-DRw53-associated glycoprote
	32704_at	Cluster Incl. D86964:Human mRNA for KIAA0209 gene, partial cds /cds=(0,
	33261_at	Cluster Incl. M16941:Human MHC class II HLA-DR7-associated glycoprotein
	34210_at	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-
	34268_at	Cluster Incl. X91809:H.sapiens mRNA for GAIP protein /cds=(288,941) /gb
35	36878_f_at	Cluster Incl. M60028:Human MHC class II HLA-DQ-beta (DQB1,DQw9), comp
	37918_at	Cluster Incl. M15395:Human leukocyte adhesion protein (LFA-1/Mac-1/p150
	37975_at	Cluster Incl. X04011:Human mRNA of X-CGD gene involved in chronic granu
	38006_at	Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds /cds
	40518_at	Cluster Incl. Y00062:Human mRNA for T200 leukocyte common antigen (CD45

- 40519_at Cluster Incl. Y00638:Human mRNA for leukocyte common antigen (T200) /cd
 40520_g_at Cluster Incl. Y00638:Human mRNA for leukocyte common antigen (T200) /
 41723_s_at Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5
 32227_at Cluster Incl. X17042:Human mRNA for hematopoietic proteoglycan core prot
 5 32747_at Cluster Incl. X05409:Human RNA for mitochondrial aldehyde dehydrogenase
 32773_at Cluster Incl. AA868382:ak41e04.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 32794_g_at Cluster Incl. X00437:Human mRNA for T-cell specific protein /cds=(37,
 34375_at Cluster Incl. M28225:Human JE gene encoding a monocyte secretory protei
 37023_at Cluster Incl. J02923:Human 65-kilodalton phosphoprotein (p65) mRNA, com
 10 37039_at Cluster Incl. J00194:human hla-dr antigen alpha-chain mrna & ivs fragme
 37328_at Cluster Incl. X07743:Human mRNA for pleckstrin (P47) /cds=(60,1112) /gb
 37344_at Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like
 37759_at Cluster Incl. U51240:Human lysosomal-associated multitransmembrane prot
 38095_i_at Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) b
 15 38096_f_at Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) b
 38378_at Cluster Incl. M37033:Human CD53 glycoprotein mRNA, complete cds /cds=(9
 38833_at Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antig
 40585_at Cluster Incl. D25538:Human mRNA for KIAA0037 gene, complete cds /cds=(2
 41352_at Cluster Incl. X62822:H.sapiens gene encoding beta-galactoside alpha-2,6
 20 2045_s_at M16592 /FEATURE=mRNA /DEFINITION=HUMHCKB Human hemopoietic
 cell protei
 1919_at X16316 /FEATURE=cds /DEFINITION=HSVAVPO Human mRNA for vav oncogene
 1506_at D11086 /FEATURE= /DEFINITION=HUMIL2RG Human mRNA for interleukin 2 recep
 1426_at D89077 /FEATURE= /DEFINITION=D89077 Homo sapiens mRNA for Src-like adapt
 25 1403_s_at M21121 /FEATURE= /DEFINITION=HUMTCSM Human T cell-specific protein
 (RA
 1061_at U00672 /FEATURE= /DEFINITION=U00672 Human interleukin-10 receptor mRNA,
 875_g_at M26683 /FEATURE= /DEFINITION=HUMIFNIND Human interferon gamma
 treatment
 30 432_s_at X02883 /FEATURE=cds /DEFINITION=HSTCRAC Human gene for T-cell
 receptor
 Metagene 339
 35 34512_at Cluster Incl. J03853:Human kidney alpha-2-adrenergic receptor mRNA, com
 39350_at Cluster Incl. U50410:Human heparan sulphate proteoglycan (OC15) mRNA, c
 1822_at Oncogene Ret/Ptc2, Fusion Activated
 1823_g_at Oncogene Ret/Ptc2, Fusion Activated
 1745_at Oncogene Ret/Ptc2, Fusion Activated

Metagene 340

- 33437_at Cluster Incl. AJ005892:Homo sapiens mRNA for JM23 protein, complete cod
- 5** 41516_at Cluster Incl. U95735:Human SNARE protein Ykt6 (YKT6) mRNA, complete cds
- 1715_at U37518 /FEATURE= /DEFINITION=HSU37518 Human TNF-related apoptosis induci
- 1463_at M93425 /FEATURE= /DEFINITION=HUMPTPPEST Human protein tyrosine phosphata
- 1378_g_at M58603 /FEATURE= /DEFINITION=HUMNFKB Human nuclear factor kappa-B DNA
- 10** 946_at D50663 /FEATURE= /DEFINITION=D50663 Human mRNA for TCTEL1 gene, complete;
- 855_at S78085 /FEATURE= /DEFINITION=S78085 PDCD2=programmed cell death-2/Rp8 hom

Metagene 341

- 15** 37106_at Cluster Incl. D89928:Homo sapiens HKL1 mRNA, complete cds /cds=(152,196
- 39964_at Cluster Incl. AJ007590:Homo sapiens mRNA for XRP2 protein /cds=(172,122
- 32674_at Cluster Incl. D83032:Homo sapiens mRNA for nuclear protein, NP220, comp
- 32734_at Cluster Incl. L76703:Homo sapiens protein phosphatase 2A B56-epsilon (P
- 36474_at Cluster Incl. AB018319:Homo sapiens mRNA for KIAA0776 protein, partial
- 20** 36845_at Cluster Incl. D50926:Human mRNA for KIAA0136 gene, partial cds /cds=(0,
- 38357_at Cluster Incl. AL049321:Homo sapiens mRNA; cDNA DKFZp564D156 (from clone
- 40146_at Cluster Incl. AL080212:Homo sapiens mRNA; cDNA DKFZp586H0723 (from clon
- 25** 40878_f_at Cluster Incl. AF041081:Homo sapiens D15F37 pseudogene, S4 allele, mRN
- 40881_at Cluster Incl. X64330:H.sapiens mRNA for ATP-citrate lyase /cds=(84,3401
- 41179_at Cluster Incl. AB029023:Homo sapiens mRNA for KIAA1100 protein, complete
- 33893_r_at Cluster Incl. AB007939:Homo sapiens mRNA for KIAA0470 protein, comple
- 35734_at Cluster Incl. AI935551:wo97g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 30** 36110_at Cluster Incl. M28215:Homo sapiens GTP-binding protein (RAB5) mRNA, comp
- 36576_at Cluster Incl. AF054174:Homo sapiens histone macroH2A1.2 mRNA, complete
- 36946_at Cluster Incl. D86550:Human mRNA for serine/threonine protein kinase, co
- 37336_at Cluster Incl. D87684:Human mRNA for KIAA0242 gene, partial cds /cds=(0,
- 37338_at Cluster Incl. D61391:Human mRNA for phosphoribosypyrophosphate syntheta
- 35** 37670_at Cluster Incl. J04543:Human synexin mRNA, complete cds /cds=(60,1460) /g
- 37729_at Cluster Incl. Y08614:Homo sapiens mRNA for CRM1 protein /cds=(38,3253)
- 37735_at Cluster Incl. U31383:Human G protein gamma-10 subunit mRNA, complete cd
- 38093_at Cluster Incl. U90909:Human clone 23722 mRNA sequence /cds=UNKNOWN
- /gb=U

- 38443_at Cluster Incl. U79291:Human clone 23721 mRNA sequence /cds=UNKNOWN
/gb=U
- 38814_at Cluster Incl. AF038954:Homo sapiens vacuolar H(+)-ATPase subunit mRNA,
1512_at D86550 /FEATURE= /DEFINITION=D86550 Human mRNA for serine/threonine prot
- 5** 891_at M77698 /FEATURE= /DEFINITION=HUMKRP Homo sapiens GLI-Krupple related prot
- Metagene 342
- 38237_at Cluster Incl. M64099:Human gamma-glutamyl transpeptidase-related protein
- 10** 32123_at Cluster Incl. L02870:Human alpha-1 type VII collagen (COL7A1) mRNA, com
- 34281_at Cluster Incl. AF039555:Homo sapiens visinin-like protein 1 (VSNL1) mRNA
- 37248_at Cluster Incl. U83411:Homo sapiens carboxypeptidase Z precursor, mRNA, c
- 38673_s_at Cluster Incl. D64137:Human KIP2 gene for Cdk-inhibitor p57KIP2, compl
- 39026_r_at Cluster Incl. AF052114:Homo sapiens clone 23887 mRNA sequence /cds=UN
- 15** 37022_at Cluster Incl. U41344:Human prolargin (PRELP) gene, 5 flanking sequence
- 37658_at Cluster Incl. L13720:Homo sapiens growth-arrest-specific protein (gas)
- 37765_at Cluster Incl. X54162:Human mRNA for a 64 Kd autoantigen expressed in th
- 38800_at Cluster Incl. D45352:HUMHG17416 Homo sapiens cDNA /gb=D45352
/gi=113667
- 20** 1597_at L13720 /FEATURE= /DEFINITION=HUMGAS Homo sapiens growth-arrest-specific
1598_g_at L13720 /FEATURE= /DEFINITION=HUMGAS Homo sapiens growth-arrest-specifi
- Metagene 343
- 25**
- 31480_f_at Cluster Incl. L18877:Human MAGE-12 protein gene, complete cds /cds=(7
- 40024_at Cluster Incl. D86640:Homo sapiens mRNA for stac, complete cds /cds=(39,
- 34218_at Cluster Incl. U57099:Human APEG-1 mRNA, complete cds /cds=(125,466) /gb
- 37603_at Cluster Incl. X52015:H.sapiens mRNA for interleukin-1 receptor antagoni
- 30** 38691_s_at Cluster Incl. J03553:Human pulmonary surfactant protein (SP5) mRNA, c
- 36676_at Cluster Incl. AL031659:dJ343K2.2.1 (ribophorin II (isoform 1)) /cds=(28
- 32506_at Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial
- Metagene 344
- 35**
- 41087_at Cluster Incl. AC004774:Homo sapiens BAC clone RG300E22 from 7q21-q31.1
- 36880_at Cluster Incl. U07736:Human quinone oxidoreductase2 (NQO2) gene /cds=(27
- 37558_at Cluster Incl. U97188:Homo sapiens putative RNA binding protein KOC (koc
- 39721_at Cluster Incl. U09303:Human T cell leukemia LERK-2 (EPLG2) mRNA, complet

- 40843_at Cluster Incl. AF012023:Homo sapiens integrin cytoplasmic domain associa
39468_r_at Cluster Incl. W27081:22g5 Homo sapiens cDNA /gb=W27081 /gi=1306660 /u
- Metagene 345
- 5**
- 38191_at Cluster Incl. AI040181:ox42d12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
39272_g_at Cluster Incl. AA461365:zx70e07.r1 Homo sapiens cDNA, 5 end /clone=IM
40302_at Cluster Incl. AL031186:bK984G1.1 (PUTATIVE C-terminal end of a novel pr
41856_at Cluster Incl. AL049370:Homo sapiens mRNA; cDNA DKFZp586D0918 (from
10 clon
1041_at U26403 /FEATURE= /DEFINITION=HSU26403 Human receptor tyrosine kinase lig
- Metagene 346
- 15** 37178_at Cluster Incl. M74089:Human TB1 gene mRNA, 3 end /cds=(0,1305) /gb=M740
- Metagene 347
- 20** 32314_g_at Cluster Incl. M12125:Human fibroblast muscle-type tropomyosin mRNA, c
37809_at Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial c
40017_at Cluster Incl. AL050214:Homo sapiens mRNA; cDNA DKFZp586H2123 (from
clon
- 25** 33222_at Cluster Incl. AB017365:Homo sapiens mRNA for frizzled-7, complete cds /
34203_at Cluster Incl. D17408:Homo sapiens mRNA for calponin, complete cds /cds=
35703_at Cluster Incl. X06374:Human mRNA for platelet-derived growth factor PDGF
36061_at Cluster Incl. AF009314:Homo sapiens clone TUA8 Cri-du-chat region mRNA
36929_at Cluster Incl. U17760:Human laminin S B3 chain (LAMB3) gene /cds=(399,39
37906_at Cluster Incl. Z37976:H.sapiens mRNA for latent transforming growth fact
38298_at Cluster Incl. U25138:Human MaxiK potassium channel beta subunit mRNA, c
30 38700_at Cluster Incl. M33146:Human cysteine-rich peptide mRNA, complete cds /cd
39750_at Cluster Incl. W61005:zd29a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
32755_at Cluster Incl. X13839:Human mRNA for vascular smooth muscle alpha-actin
32847_at Cluster Incl. U48959:Homo sapiens myosin light chain kinase (MLCK) mRNA
34403_at Cluster Incl. U58516:Human breast epithelial antigen BA46 mRNA, complet
35 35785_at Cluster Incl. W28281:47e7 Homo sapiens cDNA /gb=W28281 /gi=1308436 /ug=
37745_s_at Cluster Incl. U15780:Human p82 (ST5) mRNA, alternatively spliced, com
39170_at Cluster Incl. AL049957:Homo sapiens mRNA; cDNA DKFZp564J0323 (from clon
39544_at Cluster Incl. AB002351:Human mRNA for KIAA0353 gene, partial cds /cds=(
40279_at Cluster Incl. D50911:Human mRNA for KIAA0121 gene, complete cds /cds=(4

- 1787_at U22398 /FEATURE= /DEFINITION=HSU22398 Human Cdk-inhibitor p57KIP2 (KIP2)
- 1197_at D00654 /FEATURE=cds /DEFINITION=HUMACTSG7 Homo sapiens gene for enteric
- 996_at X59065 /FEATURE=exon /DEFINITION=HSFGFEX3 H.sapiens FGF gene, exon 3
- 873_at M26679 /FEATURE=expanded_cds /DEFINITION=HUMHOX13G Homo sapiens
- 5** homeobox
- Metagene 348
- 31739_at Cluster Incl. AA977513:on60e11.s1 Homo sapiens cDNA, 3' end /clone=IMAG
- 10** 33062_at Cluster Incl. AL096729:Homo sapiens mRNA; cDNA DKFZp434D044 (from clone
- 35019_at Cluster Incl. AF054180:Homo sapiens hematopoietic cell derived zinc fin
- 37538_at Cluster Incl. AL049354:Homo sapiens mRNA; cDNA DKFZp566E183 (from clone
- 15** 39030_at Cluster Incl. AJ133534:Homo sapiens mRNA for prenylated Rab acceptor 1
- 38423_at Cluster Incl. L38935:Homo sapiens GT212 mRNA /cds=UNKNOWN /gb=L38935 /g
- 38439_at Cluster Incl. L24123:Homo sapiens NRF1 protein (NRF1) mRNA /cds=UNKNOWN
- 20**
- Metagene 349
- 37432_g_at Cluster Incl. AF077953:Homo sapiens protein inhibitor of activated ST
- 39991_at Cluster Incl. L20815:Human S protein mRNA, complete cds /cds=(62,1522)
- 25** 40755_at Cluster Incl. X92841:H.sapiens MICA gene /cds=(39,1196) /gb=X92841 /gi=
- 36562_at Cluster Incl. AB007887:Homo sapiens KIAA0427 mRNA, complete cds /cds=(2
- 41241_at Cluster Incl. D84273:Homo sapiens mRNA for Asparaginyl tRNA Synthetase,
- 32205_at Cluster Incl. AF072860:Homo sapiens protein activator of the interferon
- 30** Metagene 350
- 34162_at Cluster Incl. D84111:Homo sapiens mRNA for RBP-MS/type 5, partial cds /
- 34163_g_at Cluster Incl. D84111:Homo sapiens mRNA for RBP-MS/type 5, partial cds
- 38047_at Cluster Incl. D84109:Homo sapiens mRNA for RBP-MS/type 3, complete cds
- 35** 38049_g_at Cluster Incl. D84110:Homo sapiens mRNA for RBP-MS/type 4, complete cd
- 1276_g_at D84110 /FEATURE= /DEFINITION=D84110 Homo sapiens mRNA for RBP-MS/type
- Metagene 351

- 34541_at Cluster Incl. L02867:Homo sapiens 62 kDa paraneoplastic antigen mRNA, 3
 35027_at Cluster Incl. X14830:Human mRNA for muscle acetylcholine receptor beta-
 39274_at Cluster Incl. X58521:Human mRNA for p62 nucleoporin /cds=(151,1719) /gb
5 34694_at Cluster Incl. U66618:Human SWI/SNF complex 60 KDa subunit (BAF60b) mRNA
 38726_at Cluster Incl. W80399:zh49e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 32750_r_at Cluster Incl. X53416:Human mRNA for actin-binding protein (filamin) (
 32844_at Cluster Incl. AF104913:Homo sapiens eukaryotic protein synthesis initia
 33818_at Cluster Incl. AC004472:Homo sapiens chromosome 9, P1 clone 11659 /cds=(
10 33879_at Cluster Incl. U79528:Human SR31747 binding protein 1 mRNA, complete cds
 40275_at Cluster Incl. AL046322:DKFZp434I087_r1 Homo sapiens cDNA, 5 end /clone
 1936_s_at Proto-Oncogene C-Myc, Alt. Splice 3, Orf 114
 1362_s_at M84820 /FEATURE= /DEFINITION=HUMRXRB Human retinoid X receptor
 beta (R
15 1306_at D12686 /FEATURE= /DEFINITION=HUMEIF4G Human mRNA for eukaryotic initiati
 973_at Y10032 /FEATURE=cds /DEFINITION=HSRNASTPK H.sapiens mRNA for putative ser
 910_at M15205 /FEATURE=cds /DEFINITION=HUMTKRA Human thymidine kinase gene,
 comp
 727_at Ornithine Aminotransferase-Like 3
20 689_at L02867 /FEATURE= /DEFINITION=HUMPPA Homo sapiens 62 kDa paraneoplastic an
 625_at L78833 /FEATURE=cds#4 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and vafl
 gen
 455_at U66618 /FEATURE= /DEFINITION=HSU66618 Human SWI/SNF complex 60 KDa
 subuni
25 463_g_at U70862 /FEATURE= /DEFINITION=HSU70862 Human nuclear factor I B3
 mRNA, c
 391_at X89416 /FEATURE=cds /DEFINITION=HSRNAPPP5 H.sapiens mRNA for protein phos
 207_at M86752 /FEATURE= /DEFINITION=HUMIEF Human transformation-sensitive protei

30 Metagene 352

 34078_s_at Cluster Incl. M61854:Human cytochrome P4502C19 (CYP2C19) mRNA, clone
 38865_at Cluster Incl. AJ011736:Homo sapiens mRNA for growth factor receptor bin
 39245_at Cluster Incl. U72507:Human 40871 mRNA partial sequence /cds=UNKNOWN /gb
35 37580_at Cluster Incl. AF036271:Homo sapiens EEN-B2-L3 mRNA, complete cds /cds=(
 36984_f_at Cluster Incl. X89214:H.sapiens mRNA for haptoglobin related protein /
 40584_at Cluster Incl. Y08612:Homo sapiens mRNA for nuclear pore complex protein

Metagene 353

- 31906_at Cluster Incl. AF068754:Homo sapiens heat shock factor binding protein 1
- 39253_s_at Cluster Incl. M29893:Human low molecular mass GTP-binding protein (ra
- 33737_f_at Cluster Incl. AI871359:wl81b11.x1 Homo sapiens cDNA, 3 end /clone=IM
- 5 33815_at Cluster Incl. J03626:Human UMP synthase mRNA, complete cds
/cds=UNKNOWN
- 35697_at Cluster Incl. L76259:Homo sapiens PTS gene, complete cds /cds=(68,505)
- 36457_at Cluster Incl. U10860:Human guanosine 5-monophosphate synthase mRNA, com
- 40427_at Cluster Incl. AA149486:zl27g01.r1 Homo sapiens cDNA, 5 end /clone=IMAG
- 10 34795_at Cluster Incl. U84573:Homo sapiens lysyl hydroxylase isoform 2 (PLOD2) m
- 35342_at Cluster Incl. AF052159:Homo sapiens clone 24416 mRNA sequence /cds=UNKN
- 37726_at Cluster Incl. X06323:Human MRL3 mRNA for ribosomal protein L3 homologue
- 1877_g_at Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene Related
- 15 Metagene 354
- 31546_at Cluster Incl. L11566:Homo sapiens ribosomal protein L18 (RPL18) mRNA, c
- 32437_at Cluster Incl. U14970:Human ribosomal protein S5 mRNA, complete cds /cds
- 32440_at Cluster Incl. X53777:Human L23 mRNA for putative ribosomal protein /cds
- 20 34570_at Cluster Incl. S79522:ubiquitin carboxyl extension protein [human, mRNA,
- 34592_at Cluster Incl. M13932:Human ribosomal protein S17 mRNA, complete cds /cd
- 34609_g_at Cluster Incl. M24194:Human MHC protein homologous to chicken B comple
- 36358_at Cluster Incl. U09953:Human ribosomal protein L9 mRNA, complete cds /cds
- 32337_at Cluster Incl. U25789:Human ribosomal protein L21 mRNA, complete cds /cd
- 25 36786_at Cluster Incl. AL022721:dJ109F14.2 (60S Ribosomal Protein RPL10A) /cds=(
- 41449_at Cluster Incl. AJ000534:Homo sapiens mRNA for epsilon-sarcoglycan /cds=(
- 32843_s_at Cluster Incl. M30448:Human casein kinase II beta subunit mRNA, comple
- 34302_at Cluster Incl. U96074:Human translation initiation factor eIF3 p44 subun
- 34316_at Cluster Incl. W52024:zd13a03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
- 30 37364_at Cluster Incl. U72511:Human B-cell receptor associated protein (hBAP) mR
- 37724_at Cluster Incl. V00568:Human mRNA encoding the c-myc oncogene /cds=(558,1
- 32576_at Cluster Incl. U94855:Homo sapiens translation initiation factor 3 47 kD
- 33116_f_at Cluster Incl. AA977163:q25a04.s1 Homo sapiens cDNA, 3 end /clone=IM
- 33117_r_at Cluster Incl. AA977163:q25a04.s1 Homo sapiens cDNA, 3 end /clone=IM
- 35 1973_s_at V00568 /FEATURE=cds /DEFINITION=HSMYC1 Human mRNA encoding the
c-myc o
- 1653_at M84711 /FEATURE= /DEFINITION=HUMFTE1A Human v-fos transformation effecto

Metagene 355

- 39682_at Cluster Incl. X87159:H.sapiens mRNA for beta subunit of epithelial amil
 32632_g_at Cluster Incl. J03060:Human glucocerebrosidase (GCB) gene /cds=(229,17
 32715_at Cluster Incl. N90862:zb11b06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 5 33294_at Cluster Incl. D29958:Human mRNA for KIAA0116 gene, partial cds /cds=(0,
 35646_at Cluster Incl. Z35093:H.sapiens mRNA for SURF-1 /cds=(14,916) /gb=Z35093
 39747_at Cluster Incl. U52427:Human RNA polymerase II seventh subunit (rpb-7) ge
 40410_at Cluster Incl. W26651:34c5 Homo sapiens cDNA /gb=W26651 /gi=1307494 /ug=
 36954_at Cluster Incl. D86972:Human mRNA for KIAA0218 gene, complete cds /cds=(3
 10 37361_at Cluster Incl. AF010187:Homo sapiens FGF-1 intracellular binding protein
 1695_at D23662 /FEATURE= /DEFINITION=HUMULP Homo sapiens mRNA for ubiquitin-like
 1650_g_at U61836 /FEATURE=mRNA /DEFINITION=HSU61836 Human putative cyclin
 G1 int
 1470_at U21090 /FEATURE= /DEFINITION=HSU21090 Human DNA polymerase delta small s
 15 283_at L16842 /FEATURE= /DEFINITION=HUMMITCORA Human ubiquinol cytochrome-c
 redu

Metagene 356

- 20 39934_at Cluster Incl. AB023061:Homo sapiens mRNA for small GTP-binding protein
 33796_at Cluster Incl. U73960:Human ADP-ribosylation factor-like protein 4 mRNA,
 35993_s_at Cluster Incl. AI698103:we20h11.x1 Homo sapiens cDNA, 3 end /clone=IM
 40419_at Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X851
 41544_at Cluster Incl. AF059617:Homo sapiens serum-inducible kinase mRNA, comple

25

Metagene 357

- 32959_at Cluster Incl. M25809:Human endomembrane proton pump subunit mRNA, compl
 34006_s_at Cluster Incl. L26318:Human protein kinase (JNK1) mRNA, complete cds /
 30 39646_at Cluster Incl. S60415:myasthenic syndrome antigen B [human, fetal brain,
 41831_at Cluster Incl. AF077820:Homo sapiens LDL receptor member LR3 mRNA, compl
 2056_at M34641 /FEATURE= /DEFINITION=HUMFGF1A Human fibroblast growth factor (FG
 2057_g_at M34641 /FEATURE= /DEFINITION=HUMFGF1A Human fibroblast growth
 factor (
 35 424_s_at X66945 /FEATURE=cds /DEFINITION=HSNSAMTK H.sapiens N-sam mRNA
 for fibro

Metagene 358

	31604_at	Cluster Incl. AJ009849:Homo sapiens GNAS1 gene encoding NESP55 /cds=(38
	31620_at	Cluster Incl. AF033579:untitled /cds=(0,633) /gb=AF033579 /gi=3213224 /
	32401_at	Cluster Incl. U78110:Human prepro-neurturin mRNA, complete cds /cds=(0,
	32968_s_at	Cluster Incl. AL050253:H.sapiens mRNA similar to D29763 mouse mRNA fo
5	36784_at	Cluster Incl. J03071:Human growth hormone (GH-1 and GH-2) and chorionic
	37790_at	Cluster Incl. AF068006:Homo sapiens haemopoietic progenitor homeobox HP
	40668_s_at	Cluster Incl. U34624:Human T cell surface glycoprotein CD-6 mRNA, com
	41380_at	Cluster Incl. AF053003:Homo sapiens diphthamide biosynthesis protein-2
	34679_at	Cluster Incl. X02596:Human mRNA for bcr (breakpoint cluster region) gen
10	36052_at	Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced p
	37553_at	Cluster Incl. D50863:Human mRNA for TESK1, complete cds /cds=(272,2152)
	38973_at	Cluster Incl. AB028943:Homo sapiens mRNA for KIAA1020 protein, partial
	41181_r_at	Cluster Incl. U49785:Human D-dopachrome tautomerase mRNA, complete cd
	36094_at	Cluster Incl. M21984:Human (clone PWH1nT16) skeletal muscle Troponin T
15	36195_at	Cluster Incl. U07681:Human NAD(H)-specific isocitrate dehydrogenase alp
	36640_at	Cluster Incl. X66141:H.sapiens mRNA for cardiac ventricular myosin ligh
	37033_s_at	Cluster Incl. X13710:H.sapiens unspliced mRNA for glutathione peroxid
	37323_r_at	Cluster Incl. X82460:H.sapiens mRNA for 15-hydroxy prostaglandin dehy
	39845_at	Cluster Incl. AF020760:Homo sapiens serine protease (Omi) mRNA, complet
20	41566_at	Cluster Incl. AI218364:qh21h01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
Metagene 359		
	31521_f_at	Cluster Incl. X60484:H.sapiens H4/e gene for H4 histone /cds=(0,311)
25	36422_s_at	Cluster Incl. AF038198:Homo sapiens clone 23928 mRNA sequence /cds=UN
	34027_f_at	Cluster Incl. AA010078:ze16d01.s1 Homo sapiens cDNA, 3 end /clone=IM
	36751_at	Cluster Incl. AF035154:Homo sapiens regulator of G-protein signalling 1
	37785_at	Cluster Incl. U69563:U69563 Homo sapiens cDNA /clone=25050 /gb=U69563 /
	37811_at	Cluster Incl. AF042792:Homo sapiens alpha 2 delta calcium channel subun
30	38531_at	Cluster Incl. AA428150:zw57c05.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	38960_at	Cluster Incl. U45975:Human phosphatidylinositol (4,5)bisphosphate 5-pho
	39623_at	Cluster Incl. X65724:H.sapiens DNA for ORF1 and ORF2 from chromosome X
	39669_at	Cluster Incl. AJ009985:Homo sapiens mRNA for annexin 31 /cds=(436,1452)
	39992_at	Cluster Incl. AF030302:Homo sapiens p45-BWR1A (BWR1-A) mRNA, complete
35	c	
	32108_at	Cluster Incl. M76231:Human sepiapterin reductase mRNA, complete cds /cd
	33785_at	Cluster Incl. AB005298:Homo sapiens BAI 2 mRNA, complete cds /cds=(378,
	35164_at	Cluster Incl. AF084481:Homo sapiens transmembrane protein (WFS1) mRNA,
	35174_i_at	Cluster Incl. X70940:H.sapiens mRNA for elongation factor 1 alpha-2 /

	35183_at	Cluster Incl. U78735:Human ABC3 mRNA, complete cds /cds=(559,5673) /gb=
	35207_at	Cluster Incl. X76180:H.sapiens mRNA for lung amiloride sensitive Na ⁺ ch
	35666_at	Cluster Incl. U38276:Human semaphorin III family homolog mRNA, complete
	36454_at	Cluster Incl. AF037335:Homo sapiens carbonic anhydrase precursor (CA 12
5	36495_at	Cluster Incl. U21931:Human fructose-1,6-biphosphatase (FBP1) gene /cds=
	37205_at	Cluster Incl. AB020647:Homo sapiens mRNA for KIAA0840 protein, partial
	37562_at	Cluster Incl. L11370:Human protocadherin 42 mRNA, complete cds for abbr
	37600_at	Cluster Incl. U68186:Human extracellular matrix protein 1 mRNA, complet
	37602_at	Cluster Incl. Z49878:H.sapiens mRNA for guanidinoacetate N-methyltransf
10	37614_g_at	Cluster Incl. X63578:H.sapiens gene for parvalbumin /cds=(77,403) /gb
	40093_at	Cluster Incl. X83425:H.sapiens LU gene for Lutheran blood group glycopr
	40148_at	Cluster Incl. U62325:Human FE65-like protein (hFE65L) mRNA, partial cds
	40497_at	Cluster Incl. AF040707:Homo sapiens candidate tumor suppressor gene 21
	32156_at	Cluster Incl. AF044968:untitled /cds=(0,1351) /gb=AF044968 /gi=3941380
15	32251_at	Cluster Incl. AA149307:z125h05.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	34408_at	Cluster Incl. AF004222:Homo sapiens RTN2-A (RTN2) mRNA, complete cds /c
	34859_at	Cluster Incl. Z98046:dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) /
	34860_g_at	Cluster Incl. Z98046:dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE)
	35275_at	Cluster Incl. AL050025:Homo sapiens mRNA; cDNA DKFZp564D066 (from
20	clone	
	35329_at	Cluster Incl. AF091084:Homo sapiens clone 638 unknown mRNA, complete se
	35766_at	Cluster Incl. M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343)
	37405_at	Cluster Incl. U29091:Human selenium-binding protein (hSBP) mRNA, comple
	39154_at	Cluster Incl. AI952982:wp98b06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
25	39837_s_at	Cluster Incl. AC004877:Homo sapiens PAC clone DJ0751H13 from 7q35-qte
	40546_s_at	Cluster Incl. AF047185:Homo sapiens NADH-ubiquinone oxidoreductase su
	40569_at	Cluster Incl. M58297:Human zinc finger protein 42 (MZF-1) mRNA, complet
	40902_at	Cluster Incl. AL050082:Homo sapiens mRNA; cDNA DKFZp566J2446 (from clon
	32527_at	Cluster Incl. AI381790:te41h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
30	33118_at	Cluster Incl. U73167:Homo sapiens cosmid clone LUCA14 from 3p21.3 /cds=
	1890_at	AB000584 /FEATURE= /DEFINITION=AB000584 Homo sapiens mRNA for TGF-beta s
	1723_g_at	S61953 /FEATURE= /DEFINITION=S61953 c-erbB3= receptor tyrosine kinase {
	1371_s_at	M29874 /FEATURE= /DEFINITION=HUMCYP2BB Human cytochrome P450-
	IIB (hIIB	
35	342_at	D12485 /FEATURE= /DEFINITION=HUMNPP Human mRNA for nucleotide
	pyrophospha	
	181_g_at	S82470 /FEATURE= /DEFINITION=S82470 BB1=malignant cell expression-
	enhan	

Metagene 360

- 34148_at Cluster Incl. AJ012611:Homo sapiens mRNA for SIX3 protein /cds=(207,120
 34438_at Cluster Incl. U71364:Human serine proteinase inhibitor (P19) mRNA, comp
5 39315_at Cluster Incl. D13628:Human mRNA for KIAA0003 gene, complete cds /cds=(9
 32739_at Cluster Incl. AA001791:zh86c04.r1 Homo sapiens cDNA, 5 end /clone=IMAG

Metagene 361

- 10** 31315_at Cluster Incl. D84143:Human immunoglobulin (mAb59) light chain V region
 31319_at Cluster Incl. M20707:Human kappa-immunoglobulin germline pseudogene (Ch
 31344_at Cluster Incl. AF063725:Homo sapiens clone BCSynL38 immunoglobulin lambd
 31347_at Cluster Incl. AF058075:Homo sapiens clone ASPBLL54 immunoglobulin lambd
 31460_f_at Cluster Incl. AF043586:Homo sapiens clone CPRF1-T2 immunoglobulin lam
15 31512_at Cluster Incl. Z00010:H.sapiens germ line pseudogene for immunoglobulin
 31596_f_at Cluster Incl. L02326:Homo sapiens (clone Hu lambda-17) lambda-like ge
 34094_i_at Cluster Incl. U80114:Human immunoglobulin heavy chain variable region
 34095_f_at Cluster Incl. U80114:Human immunoglobulin heavy chain variable region
 34098_f_at Cluster Incl. AI799757:wc37g12.x1 Homo sapiens cDNA, 3 end /clone=IM
20 35017_f_at Cluster Incl. M80469:Human MHC class I HLA-J gene, exons 1-8 and comp
 35530_f_at Cluster Incl. X92997:H.sapiens mRNA for IgG lambda light chain V-J-C
 35566_f_at Cluster Incl. AF015128:Homo sapiens IgG heavy chain variable region (
 35607_at Cluster Incl. AA934573:oo67b04.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 34947_at Cluster Incl. AA442560:zv75g07.r1 Homo sapiens cDNA, 5 end /clone=IMAG
25 36293_at Cluster Incl. U73531:Human G protein-coupled receptor STRL33.3 (STRL33)
 37421_f_at Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex,
 39936_at Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr
 40323_at Cluster Incl. D84276:Homo sapiens mRNA for CD38, complete cds /cds=(103
 40369_f_at Cluster Incl. AL022723:dJ377H14.1 (major histocompatibility complex,
30 40370_f_at Cluster Incl. M90683:Human lymphocyte antigen (HLA-G1) mRNA, complete
 41064_at Cluster Incl. AL049296:Homo sapiens mRNA; cDNA DKFZp564P013 (from
 clone
 32640_at Cluster Incl. M24283:Human major group rhinovirus receptor (HRV) mRNA,
 32737_at Cluster Incl. M64595:Human small G protein (Gx) mRNA, 3 end /cds=(0,54
35 36564_at Cluster Incl. W27419:31a10 Homo sapiens cDNA /gb=W27419 /gi=1307241 /ug
 1652_at U77735 /FEATURE= /DEFINITION=HSU77735 Human pim-2 protooncogene homolog
 1633_g_at U77735 /FEATURE= /DEFINITION=HSU77735 Human pim-2 protooncogene
 homolo
 1534_at U64198 /FEATURE= /DEFINITION=HSU64198 Human IL-12 receptor beta2 mRNA, c

1081_at M33764 /FEATURE=cds /DEFINITION=HUMSODB Human ornithine decarboxylase ge
703_at Immunoglobulin Heavy Chain, Vdjrc Regions

428_s_at V00567 /FEATURE=cds /DEFINITION=HSMGLO Human messenger RNA
fragment for

5 133_at X87212 /FEATURE=cds /DEFINITION=HSCATHCGE H.sapiens mRNA for cathepsin C

Metagene 362

36264_at Cluster Incl. S75168:Matk=megakaryocyte-associated tyrosine kinase [hum
10 38533_s_at Cluster Incl. J03925:Human Mac-1 gene encoding complement receptor ty
40742_at Cluster Incl. M16591:Human hemopoietic cell protein-tyrosine.kinase (HC
31859_at Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=
36856_at Cluster Incl. W28743:51a9 Homo sapiens cDNA /gb=W28743 /gi=1308691 /ug=
37967_at Cluster Incl. AF000424:Homo sapiens LST1 mRNA, cLST1/C splice variant,
15 39062_at Cluster Incl. AL008726:dJ337O18.2 (Lysosomal Protective Protein precurs
32176_at Cluster Incl. AB011110:Homo sapiens mRNA for KIAA0538 protein, partial
38487_at Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,
39182_at Cluster Incl. U87947:Human hematopoietic neural membrane protein (HNMP-
1693_s_at D11139 /FEATURE=exons#1-4 /DEFINITION=HUMTIMP Human gene for
20 tissue in
402_s_at X69819 /FEATURE=cds /DEFINITION=HSICAM3RN H.sapiens ICAM-3
mRNA

Metagene 363

25
35054_at Cluster Incl. AF035278:Homo sapiens clone 23676 mRNA sequence /cds=UNKN
35508_at Cluster Incl. X79781:H.sapiens ray mRNA /cds=(81,686) /gb=X79781 /gi=76
36368_at Cluster Incl. AF054998:Homo sapiens clone 24479 mRNA sequence /cds=UNKN
36271_at Cluster Incl. AB028947:Homo sapiens mRNA for KIAA1024 protein, partial
30 33907_at Cluster Incl. AF012072:Homo sapiens eIF4GII mRNA, complete cds /cds=(25
37299_at Cluster Incl. J04501:Human muscle glycogen synthase mRNA, complete cds
37386_i_at Cluster Incl. X55885:Human mRNA for a presumptive KDEL receptor /cds=
39127_f_at Cluster Incl. X73478:H.sapiens hPTPA mRNA /cds=(189,1160) /gb=X73478
41545_at Cluster Incl. X66365:H.sapiens mRNA PLSTIRE for serine/threonine protei
35 41821_at Cluster Incl. AA203246:zx54h03.r1 Homo sapiens cDNA, 5 end /clone=IMAG
41822_at Cluster Incl. AF060503:Homo sapiens zinc finger protein (ZF5128) mRNA,

Metagene 364

- 33559_at Cluster Incl. U61412:Human non-receptor type protein tyrosine kinase (P
 34939_r_at Cluster Incl. AF070536:Homo sapiens clone 24566 mRNA sequence /cds=UN
 37426_at Cluster Incl. U80736:Homo sapiens CAGF9 mRNA, partial cds /cds=(0,995)
 37821_at Cluster Incl. AF041260:Homo sapiens AIBC1 (AIBC1) mRNA, complete cds /c
5 34700_at Cluster Incl. AF045239:Homo sapiens brain expressed ring finger protein
 39763_at Cluster Incl. M36803:Human hemopexin gene /cds=(28,1416) /gb=M36803 /gi
 33448_at Cluster Incl. AB000095:Homo sapiens mRNA for hepatocyte growth factor a
 34319_at Cluster Incl. AA131149:zo16d05.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 36105_at Cluster Incl. M18728:Human nonspecific crossreacting antigen mRNA, comp
10 36193_at Cluster Incl. U52522:Human arfaptin 2, putative target protein of ADP-r
 1582_at M29540 /FEATURE= /DEFINITION=HUMCEAF Human carcinoembryonic antigen
 mRNA
 896_at L21998 /FEATURE= /DEFINITION=HUMMUC2X Homo sapiens intestinal mucin
 (MUC2
15
 Metagene 365
- 35545_at Cluster Incl. AB018282:Homo sapiens mRNA for KIAA0739 protein, partial
 37529_at Cluster Incl. AF051946:Homo sapiens T-type calcium channel alpha-1 subu
20 40677_at Cluster Incl. AF054984:Homo sapiens clone 23709 mRNA sequence /cds=UNKN
 33814_at Cluster Incl. AF005046:Homo sapiens serine/threonine kinase mRNA, compl
 34693_at Cluster Incl. U14550:Human sialyltransferase SThM (sthm) mRNA, complete
 38655_at Cluster Incl. AI525633:PT1.3_04_A08.r Homo sapiens cDNA, 5 end /clone_
 35800_at Cluster Incl. D63391:Human mRNA for platelet activating factor acetylhy
25 35841_at Cluster Incl. N24355:yx14b01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 36995_at Cluster Incl. M88249:Human inter-alpha-trypsin inhibitor light chain (I
 37761_at Cluster Incl. AB015020:Homo sapiens mRNA for BAP2-beta protein, complet
 1057_at M97815 /FEATURE=expanded_cds /DEFINITION=HUMCRABP02 Human retinoic acid-
 503_at U37690 /FEATURE= /DEFINITION=HSU37690 Human RNA polymerase II subunit (hs
30
 Metagene 366
- 36449_s_at Cluster Incl. D13897:Human DNA for peptide YY, complete cds /cds=(91,
 39305_at Cluster Incl. AI191826:qd47g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35 40312_at Cluster Incl. AJ005670:Homo sapiens mRNA for dachshund protein /cds=(24
 33221_at Cluster Incl. U80735:Homo sapiens CAGF28 mRNA, partial cds /cds=(0,2235
 34718_at Cluster Incl. X04434:Human mRNA for insulin-like growth factor I recept
 35252_at Cluster Incl. AB011100:Homo sapiens mRNA for KIAA0528 protein, complete
 38317_at Cluster Incl. M99701:Homo sapiens (pp21) mRNA, complete cds /cds=(164,6

- 40075_at Cluster Incl. M55047:Human synaptotagmin mRNA, complete cds /cds=(27,12
 40088_at Cluster Incl. X84373:H.sapiens mRNA for nuclear factor RIP140 /cds=(287
 40522_at Cluster Incl. X59834:Human rearranged mRNA for glutamine synthase /cds=
 40790_at Cluster Incl. AB004066:Homo sapiens mRNA for DEC1, complete cds /cds=(1
5 35283_at Cluster Incl. H05692:yl76b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 36165_at Cluster Incl. W51774:zc48b04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 38415_at Cluster Incl. U14603:Human protein-tyrosine phosphatase (HU-PP-1) mRNA,
 39161_at Cluster Incl. AF052093:Homo sapiens clone 23685 mRNA sequence /cds=UNKN
 39841_at Cluster Incl. U79745:Homo sapiens monocarboxylate transporter homologue
10 40215_at Cluster Incl. D50840:Homo sapiens mRNA for ceramide glucosyltransferase
 41328_s_at Cluster Incl. AL096717:Homo sapiens mRNA; cDNA DKFZp564P0662 (from cl
 41348_at Cluster Incl. U90304:Human iroquois-class homeodomain protein IRX-2a mR
 41354_at Cluster Incl. U25997:Homo sapiens stanniocalcin precursor (STC) mRNA, c
 2017_s_at M64349 /FEATURE= /DEFINITION=HUMCYCD1 Human cyclin D (cyclin D1)
15 mRNA,
 1681_at X03635 /FEATURE=cds /DEFINITION=HSERR Human mRNA for oestrogen receptor
 1252_at M73547 /FEATURE= /DEFINITION=HUMPOLLA Human polyposis locus (DP1 gene) m
 783_at U96113 /FEATURE= /DEFINITION=HSU96113 Homo sapiens Nedd-4-like ubiquitin-
 784_g_at U96113 /FEATURE= /DEFINITION=HSU96113 Homo sapiens Nedd-4-like
20 ubiquiti
 520_at U07358 /FEATURE= /DEFINITION=HSU07358 Human protein kinase (zpk) mRNA, co
 160028_s_at X12949 /FEATURE=cds /DEFINITION=HSRETPON Human ret proto-oncogene
 mR
25 Metagene 367
 31608_g_at Cluster Incl. AJ002428:Homo sapiens VDAC1 pseudogene /cds=(0,853) /gb
 31951_s_at Cluster Incl. Z48501:H.sapiens mRNA for polyadenylate binding protein
 34642_at Cluster Incl. U28964:Homo sapiens 14-3-3 protein mRNA, complete cds /cd
30 37770_at Cluster Incl. AF026445:Homo sapiens cofactor of initiator function (CIF
 32034_at Cluster Incl. AF041259:Homo sapiens breast cancer putative transcriptio
 34753_at Cluster Incl. X92396:H.sapiens mRNA for novel gene in Xq28 region /cds=
 39425_at Cluster Incl. X91247:H.sapiens mRNA for thioredoxin reductase /cds=(439
 39724_s_at Cluster Incl. U58087:Human Hs-cul-1 mRNA, complete cds /cds=(124,2382
35 40122_at Cluster Incl. AF037448:Homo sapiens RRM RNA binding protein Gry-rbp (GR
 41188_at Cluster Incl. W28186:43c2 Homo sapiens cDNA /gb=W28186 /gi=1308134 /ug=
 33367_s_at Cluster Incl. D88674:Homo sapiens mRNA for antizyme inhibitor, comple
 34814_at Cluster Incl. AL041443:DKFZp434D0717_s1 Homo sapiens cDNA, 3 end /clon
 36111_s_at Cluster Incl. X75755:H.sapiens PR264 gene /cds=(98,763) /gb=X75755 /g

- 36992_at Cluster Incl. AI653621:tz21b11.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 37757_at Cluster Incl. L23959:Homo sapiens E2F-related transcription factor (DP-
- 40638_at Cluster Incl. X70944:H.sapiens mRNA for PTB-associated splicing factor
- 32615_at Cluster Incl. J05032:Human aspartyl-tRNA synthetase alpha-2 subunit mRNA
- 5 2012_s_at U34994 /FEATURE= /DEFINITION=HSU34994 Homo sapiens DNA dependent prote
- 1959_at D88674 /FEATURE= /DEFINITION=D88674 Homo sapiens mRNA for antizyme inhib
- 1660_at D83004 /FEATURE= /DEFINITION=D83004 Human epidermoid carcinoma mRNA for
- 1592_at J04088 /FEATURE= /DEFINITION=HUMTOPII Human DNA topoisomerase II (top2)
- 10 1565_s_at M96995 /FEATURE= /DEFINITION=HUMEGFGRBA Homo sapiens epidermal growth
- 1449_at D00763 /FEATURE= /DEFINITION=HUMPSC9 Human mRNA for proteasome subunit H
- 1235_at M86400 /FEATURE= /DEFINITION=HUMPHPLA2 Human phospholipase A2 mRNA, comp
- 15 1031_at U09564 /FEATURE= /DEFINITION=HSU09564 Human serine kinase mRNA, complete
- 623_s_at M28213 /FEATURE= /DEFINITION=HUMRAB2A Homo sapiens GTP-binding protein
- Metagene 368
- 20
- 32264_at Cluster Incl. L23134:Homo sapiens metase (MET-1) mRNA, complete cds /cd
- 32904_at Cluster Incl. M28393:Human perforin mRNA, complete cds /cds=(0,1667) /g
- 34432_at Cluster Incl. AF051325:Homo sapiens SH3 domain containing adaptor prote
- 34481_at Cluster Incl. AF030227:untitled /cds=(97,2634) /gb=AF030227 /gi=3282618
- 25 34965_at Cluster Incl. AF031824:Homo sapiens leukocystatin mRNA, complete cds /c
- 37479_at Cluster Incl. M54992:Human B cell differentiation antigen mRNA, complet
- 37774_at Cluster Incl. AI819942:wj88e02.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 37845_at Cluster Incl. M58285:Human membrane-associated protein (HEM-1) mRNA, co
- 39672_at Cluster Incl. M64322:Human protein tyrosine phosphatase (LPTase) mRNA,
- 30 40702_at Cluster Incl. X13274:Human mRNA for interferon IFN-gamma /cds=(108,608)
- 40715_at Cluster Incl. D83597:Homo sapiens mRNA for RP105, complete cds /cds=(14
- 40720_at Cluster Incl. AL022398:dJ434O14.3.1 (putative protein) (isoform 1) /cds
- 32736_at Cluster Incl. W68830:zd37g06.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-
- 33283_at Cluster Incl. AF106941:Homo sapiens beta-arrestin 2 mRNA, complete cds
- 35 33748_at Cluster Incl. D86976:Human mRNA for KIAA0223 gene, partial cds /cds=(0,
- 33774_at Cluster Incl. X98172:H.sapiens mRNA for MACH-alpha-1 protein /cds=(291,
- 33804_at Cluster Incl. U43522:Human cell adhesion kinase beta (CAKbeta) mRNA, co
- 33812_at Cluster Incl. AL049415:Homo sapiens mRNA; cDNA DKFZp586N2119 (from clon

	35659_at	Cluster Incl. U00672:Human interleukin-10 receptor mRNA, complete cds /
	35974_at	Cluster Incl. U10485:Human lymphoid-restricted membrane protein (Jaw1)
	37180_at	Cluster Incl. X14034:Human mRNA for phospholipase C /cds=(152,3910) /gb
	37598_at	Cluster Incl. D79990:Human mRNA for KIAA0168 gene, complete cds /cds=(1
5	38319_at	Cluster Incl. AA919102:ol84h02.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	38631_at	Cluster Incl. M92357:Homo sapiens B94 protein mRNA, complete cds /cds=(
	38976_at	Cluster Incl. D44497:Human mRNA for actin binding protein p57, complete
	34830_at	Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=
	35261_at	Cluster Incl. W07033:za93f08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
10	35786_at	Cluster Incl. AB007945:Homo sapiens mRNA for KIAA0476 protein, complete
	37352_at	Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA, complete
	38454_g_at	Cluster Incl. X15606:Human mRNA for ICAM-2, cell adhesion ligand for
	39533_at	Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(2
	41585_at	Cluster Incl. AB018289:Homo sapiens mRNA for KIAA0746 protein, partial
15	41592_at	Cluster Incl. AB000734:Homo sapiens mRNA for TIP3, complete cds /cds=(1
	1867_at	AF005775 /FEATURE= /DEFINITION=AF005775 Homo sapiens caspase-like apopto
	1779_s_at	M16750 /FEATURE= /DEFINITION=HUMPIM1 Human pim-1 oncogene
	mRNA, comple	
	1427_g_at	D89077 /FEATURE= /DEFINITION=D89077 Homo sapiens mRNA for Src-like
20	ada	
	1062_g_at	U00672 /FEATURE= /DEFINITION=U00672 Human interleukin-10 receptor
	mRNA	
	649_s_at	L06797 /FEATURE= /DEFINITION=HUMGPCR Human (clone L5) orphan G
	protein-	
25	288_s_at	L25931 /FEATURE= /DEFINITION=HUMLBR Human lamin B receptor (LBR)
	mRNA,	
	Metagene 369	
30	32874_at	Cluster Incl. M65214:Human (HeLa) helix-loop-helix protein HE47 (E2A) m
	35434_at	Cluster Incl. L16794:Human transcription factor (MEF2) mRNA, complete c
	38138_at	Cluster Incl. D38583:Human mRNA for calgizzarin, complete cds /cds=(120
	41454_at	Cluster Incl. W27949:39h3 Homo sapiens cDNA /gb=W27949 /gi=1307897 /ug=
	36139_at	Cluster Incl. AL050289:Homo sapiens mRNA; cDNA DKFZp586G0522 (from
35	clon	
	37001_at	Cluster Incl. M23254:Human Ca2-activated neutral protease large subunit
	39126_at	Cluster Incl. AL080101:Homo sapiens mRNA; cDNA DKFZp564L0472 (from
	clon	
	32546_at	Cluster Incl. U59309:Human fumarase precursor (FH) mRNA, nuclear gene e

Metagene 370

- 39611_at Cluster Incl. AI557322:PT2.1_16_F11.r Homo sapiens cDNA, 3' end /clone_
- 5** 35720_at Cluster Incl. AB020700:Homo sapiens mRNA for KIAA0893 protein, complete
- 36526_at Cluster Incl. AF000416:Homo sapiens EXT-like protein 2 (EXTL2) mRNA, co
- 37642_at Cluster Incl. D63877:Human mRNA for KIAA0157 gene, partial cds /cds=(0,
- 37895_at Cluster Incl. D87969:Homo sapiens mRNA for CMP-sialic acid transporter,
- 38365_at Cluster Incl. AF026086:Homo sapiens peroxisome biogenesis disorder prot
- 10** 38684_at Cluster Incl. AJ010953:Homo sapiens mRNA for putative Ca²⁺-transporting
- 39351_at Cluster Incl. M84349:Human transmembrane protein (CD59) gene /cds=(18,4
- 40069_at Cluster Incl. AF051850:Homo sapiens supervillin mRNA, complete cds /cds
- 40091_at Cluster Incl. U00115:Human zinc-finger protein (bcl-6) mRNA, complete c
- 40805_at Cluster Incl. AB007900:Homo sapiens KIAA0440 mRNA, partial cds /cds=(0,
- 15** 40810_at Cluster Incl. U66615:Human SWI/SNF complex 155 KDa subunit (BAF155) mRN
- 41136_s_at Cluster Incl. Y00264:Human mRNA for amyloid A4 precursor of Alzheimer
- 33827_at Cluster Incl. AL049783:Novel human gene mapping to chromosome 13 /cds=(1
- 33895_at Cluster Incl. AL050373:Homo sapiens mRNA; cDNA DKFZp586F1318 (from
- clon
- 20** 35764_at Cluster Incl. Y15164:Homo sapiens mRNA for protein encoded by cxorf5 (7
- 37755_at Cluster Incl. AB023169:Homo sapiens mRNA for KIAA0952 protein, complete
- 38816_at Cluster Incl. AF095791:Homo sapiens TACC2 protein (TACC2) mRNA, partial
- 38842_at Cluster Incl. AB023206:Homo sapiens mRNA for KIAA0989 protein, partial
- 860_at U03911 /FEATURE= /DEFINITION=HSU03911 Human mutator gene (hMSH2) mRNA,
- 25** co
- 525_g_at U13695 /FEATURE=cds /DEFINITION=HSU13695 Human homolog of yeast
- mutL (h

Metagene 371

- 30**
- 31396_r_at Cluster Incl. AB012851:Homo sapiens mRNA for Musashi, complete cds /c
- 33587_f_at Cluster Incl. AI369146:qy74f11.x1 Homo sapiens cDNA, 3' end /clone=IM
- 40006_at Cluster Incl. U63090:Human Gal beta-1,3 GalNAc alpha-2,3 sialyltransfer
- 31807_at Cluster Incl. U69190:U69190 Homo sapiens cDNA /clone=27655 /gb=U69190 /
- 35** 1026_s_at U41068 /FEATURE=cds /DEFINITION=HSCOLLA5 Human collagen alpha2(XI)
- (CO
- 441_s_at X13967 /FEATURE=cds /DEFINITION=HSLIF Human mRNA for leukaemia
- inhibito

Metagene 372

- 33034_at Cluster Incl. Y17108:Homo sapiens mRNA for rhomboid-related protein, co
 38221_at Cluster Incl. AF100153:Homo sapiens connector enhancer of KSR-like prot
5 34769_at Cluster Incl. U82535:Human fatty acid amide hydrolase mRNA, complete cd
 37996_s_at Cluster Incl. L08835:Homo sapiens DMR-N9, partial cds; and myotonic d
 38307_at Cluster Incl. AB011179:Homo sapiens mRNA for KIAA0607 protein, partial
 38308_g_at Cluster Incl. AB011179:Homo sapiens mRNA for KIAA0607 protein, partia
 38314_at Cluster Incl. AB002304:Human mRNA for KIAA0306 gene, partial cds /cds=(
10 41134_at Cluster Incl. AB023181:Homo sapiens mRNA for KIAA0964 protein, complete
 33454_at Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /
 35749_at Cluster Incl. AF069733:Homo sapiens ADA3-like protein mRNA, complete cd
 38117_at Cluster Incl. D38555:Human mRNA for KIAA0079 gene, complete cds /cds=(1
 38766_at Cluster Incl. AB002307:Human mRNA for KIAA0309 gene, partial cds /cds=(
15 39128_r_at Cluster Incl. X73478:H.sapiens hPTPA mRNA /cds=(189,1160) /gb=X73478
 41565_at Cluster Incl. AF034373:Homo sapiens ataxin-2-like protein A2LP (A2LG) m
 1700_at U82987 /FEATURE= /DEFINITION=HSU82987 Human Bcl-2 binding component 3 (b
 1270_at M64788 /FEATURE= /DEFINITION=HUMRAP1GAP Human GTPase activating protein
 454_at U66617 /FEATURE= /DEFINITION=HSU66617 Human SWI/SNF complex 60 KDa
20 subuni

Metagene 373

- 35118_at Cluster Incl. M12625:Human lecithin-cholesterol acyltransferase mRNA, c
25 36248_at Cluster Incl. AF070572:Homo sapiens clone 24778 unknown mRNA /cds=(0,17
 37138_at Cluster Incl. AB018352:Homo sapiens mRNA for KIAA0809 protein, partial
 37489_s_at Cluster Incl. U05596:Human anion exchanger 3 brain isoform (bAE3) mRN
 38916_at Cluster Incl. U46023:Human Xq28 mRNA, complete cds /cds=(283,2388) /gb=
 40365_at Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(
30 33242_at Cluster Incl. U92980:Homo sapiens clone DT1P1A10 mRNA, CAG repeat regio
 35165_at Cluster Incl. AF070582:Homo sapiens clone 24766 mRNA sequence /cds=UNKN
 38615_at Cluster Incl. AF097021:Homo sapiens GW112 protein (GW112) mRNA, complet
 38634_at Cluster Incl. M11433:Human cellular retinol-binding protein mRNA, compl
 39387_at Cluster Incl. U34044:Human selenium donor protein (selD) mRNA, complete
35 40472_at Cluster Incl. AF007155:Homo sapiens clone 23763 unknown mRNA, partial c
 32753_at Cluster Incl. D13642:Human mRNA for KIAA0017 gene, complete cds /cds=(1
 33392_at Cluster Incl. AL080155:Homo sapiens mRNA; cDNA DKFZp434J154 (from clone
 38396_at Cluster Incl. Y09836:H.sapiens mRNA for 3UTR of unknown protein /cds=UN
 39842_at Cluster Incl. AF059293:Homo sapiens cytokine-like factor-1 precursor (C

39865_at Cluster Incl. AI890903:wm91f10.x1 Homo sapiens cDNA, 3' end /clone=IMAG
 40224_s_at Cluster Incl. AB014585:Homo sapiens mRNA for KIAA0685 protein, complete
 1497_at L04270 /FEATURE= /DEFINITION=HUMTNFRP Homo sapiens (clone CD18) tumor n

5 Metagene 374

34945_at Cluster Incl. AF070526:Homo sapiens clone 24787 mRNA sequence /cds=UNKN
 39634_at Cluster Incl. AB017168:Homo sapiens mRNA for Slit-2 protein, complete c
 40687_at Cluster Incl. M96789:Homo sapiens connexin 37 (GJA4) mRNA, complete cds
 10 33328_at Cluster Incl. W28612:49b3 Homo sapiens cDNA /gb=W28612 /gi=1308560 /ug=
 34719_at Cluster Incl. AB020645:Homo sapiens mRNA for KIAA0838 protein, complete
 32184_at Cluster Incl. X61118:Human TTG-2 mRNA for a cysteine rich protein with
 36659_at Cluster Incl. X05610:Human mRNA for type IV collagen alpha (2) chain /c
 38101_at Cluster Incl. AB011151:Homo sapiens mRNA for KIAA0579 protein, partial
 15 38427_at Cluster Incl. L25286:Homo sapiens alpha-1 type XV collagen mRNA, comple
 40560_at Cluster Incl. U28049:Human TBX2 (TXB2) mRNA, complete cds /cds=(47,2155
 40913_at Cluster Incl. W28589:48h12 Homo sapiens cDNA /gb=W28589 /gi=1308537 /ug
 41274_at Cluster Incl. AA908993:ol10d03.s1 Homo sapiens cDNA, 3' end /clone=IMAG
 41504_s_at Cluster Incl. AF055376:Homo sapiens short form transcription factor C
 20 1535_at U68723 /FEATURE= /DEFINITION=HSU68723 Human checkpoint suppressor 1 mRNA

Metagene 375

40112_at Cluster Incl. AA522698:ni39d03.s1 Homo sapiens cDNA, 3' end /clone=IMAG
 25 34782_at Cluster Incl. AL021938:Homo sapiens DNA sequence from PAC 232K4 on chro
 36664_at Cluster Incl. M60091:Homo sapiens galactose-1-phosphate uridyl transfer
 36974_at Cluster Incl. D88378:Homo sapiens mRNA for proteasome inhibitor hPI31 s
 38425_at Cluster Incl. U49719:Human hydroxymethylglutaryl-CoA lyase (HMGCL) gene
 38455_at Cluster Incl. AL049650:dJ734P14.2.1 (snRNP (small nuclear ribonucleopro
 30 41343_at Cluster Incl. Y16521:Homo sapiens mRNA for CDS2 protein /cds=(258,1595)
 1394_at L25080 /FEATURE= /DEFINITION=HUMRHOAA Homo sapiens GTP-binding protein (

Metagene 376

35 31586_f_at Cluster Incl. X72475:H.sapiens mRNA for rearranged Ig kappa light cha
 34105_f_at Cluster Incl. AI147237:qb36f02.x1 Homo sapiens cDNA, 3' end /clone=IM
 36239_at Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,12
 37864_s_at Cluster Incl. Y14737:Homo sapiens mRNA for immunoglobulin lambda heav
 38194_s_at Cluster Incl. M63438:Human Ig rearranged gamma chain mRNA, V-J-C regi

- 33273_f_at Cluster Incl. X57809:Human rearranged immunoglobulin lambda light cha
 33274_f_at Cluster Incl. M18645:Human Ig rearranged lambda-chain mRNA VJC-region
 37625_at Cluster Incl. U52682:Human lymphocyte specific interferon regulatory fa
 41164_at Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region
5 41165_g_at Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant regi
 41827_f_at Cluster Incl. AI932613:wo05c02.x1 Homo sapiens cDNA, 3 end /clone=IM

Metagene 377

- 10** 35511_at Cluster Incl. AB014559:Homo sapiens mRNA for KIAA0659 protein, partial
 34200_at Cluster Incl. X83378:H.sapiens mRNA for putative chloride channel /cds=
 34222_at Cluster Incl. AL035289:H.sapiens gene from PAC 1026E2, partial /cds=(1,
 35216_at Cluster Incl. X79440:H.sapiens mRNA for NADP+-dependent malic enzyme /c
 38970_s_at Cluster Incl. AJ011896:Homo sapiens mRNA for HIV-1, Nef-associated fa
15 32768_at Cluster Incl. AL048308:DKFZp586A2224_s1 Homo sapiens cDNA
 /clone=DKFZp5
 32804_at Cluster Incl. AF091263:Homo sapiens RNA binding motif protein 5 (RBM5)
 33916_at Cluster Incl. AB023192:Homo sapiens mRNA for KIAA0975 protein, partial
 34365_at Cluster Incl. AF042386:Homo sapiens cyclophilin-33B (CYP-33) mRNA, comp
20 36154_at Cluster Incl. D87452:Human mRNA for KIAA0263 gene, complete cds /cds=(3
 36945_at Cluster Incl. X94910:Homo sapiens mRNA for ERp28 protein /cds=(11,796)
 36964_at Cluster Incl. D42053:Human mRNA for KIAA0091 gene, complete cds /cds=(4
 37767_at Cluster Incl. L12392:Homo sapiens Huntingtons Disease (HD) mRNA, comple
 33140_at Cluster Incl. AF029893:Homo sapiens i-beta-1,3-N-acetylglucosaminyltran
25 484_at U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-

Metagene 378

- 31927_s_at Cluster Incl. D86062:Human mRNA for KNP-Ib, complete cds /cds=(18,731
30 39663_at Cluster Incl. D63998:Human mRNA for golgi alpha-mannosidaseII, complete
 41102_at Cluster Incl. U66359:Human T54 protein (T54) mRNA, complete cds /cds=(6
 41622_r_at Cluster Incl. AA868898:ak55b08.s1 Homo sapiens cDNA, 3 end /clone=IM
 33716_at Cluster Incl. N95443:zb81c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 35994_at Cluster Incl. AC002398:Human DNA from chromosome 19-specific cosmid F25
35 35351_at Cluster Incl. U89505:Human Hlark mRNA, complete cds /cds=(55,1155) /gb=
 36955_at Cluster Incl. U10362:Human GP36b glycoprotein mRNA, complete cds /cds=(
 37041_at Cluster Incl. AB023160:Homo sapiens mRNA for KIAA0943 protein, partial
 39810_at Cluster Incl. AC005253:Homo sapiens chromosome 19, cosmid R26445 /cds=(
 39896_at Cluster Incl. AB011149:Homo sapiens mRNA for KIAA0577 protein, complete

- 41528_at Cluster Incl. W72239:zd62h08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 41810_at Cluster Incl. AA203545:zx59a05.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 2051_at M31767 /FEATURE=mRNA /DEFINITION=HUMDNAMET Human O6-methylguanine-
 DNA me
- 5** 1825_at L33075 /FEATURE= /DEFINITION=HUMIQGA Homo sapiens ras GTPase-activating-
 1137_at L20852 /FEATURE= /DEFINITION=HUMGLVR2X Human leukemia virus receptor 2 (
 999_at X59812 /FEATURE=cds /DEFINITION=HSVD3HYD H.sapiens CYP 27 mRNA for
 vitami
- 465_at U74667 /FEATURE= /DEFINITION=HSU74667 Human tat interactive protein (TIP6
- 10** 405_at X52773 /FEATURE=cds /DEFINITION=HSRARLP Human mRNA for retinoic acid rece
 399_at X99325 /FEATURE=cds /DEFINITION=HSSTE20 H.sapiens mRNA for Ste20-like kin

Metagene 379

- 15** 39420_at Cluster Incl. S62138:TLS/CHOP=hybrid gene {translocation breakpoint} [h
 33393_at Cluster Incl. AJ237946:Homo sapiens mRNA for DEAD Box Protein 5 /cds=(0
 34803_at Cluster Incl. AF022789:Homo sapiens ubiquitin hydrolyzing enzyme I (UBH

Metagene 380

- 20**
- 33602_at Cluster Incl. AJ000479:Homo sapiens mRNA for putative G-protein coupled
 34077_at Cluster Incl. X95876:H.sapiens mRNA for G-protein coupled receptor /cds
 36334_at Cluster Incl. L42621:Homo sapiens Ly-9 mRNA, complete cds /cds=(0,1832)
 32953_at Cluster Incl. X04391:Human mRNA for lymphocyte glycoprotein T1/Leu-1 /c
- 25** 32967_at Cluster Incl. AF057557:Homo sapiens anti-Fas-induced apoptosis (TOSO) m
 32977_at Cluster Incl. U49187:Human placenta (Diff48) mRNA, complete cds /cds=(4
 33555_at Cluster Incl. AF041261:Homo sapiens immunoglobulin-like transcript 7 mR
 33569_at Cluster Incl. D50532:Homo sapiens mRNA for macrophage lectin 2, complet
 34959_at Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, com
- 30** 34960_g_at Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, c
 35883_at Cluster Incl. X66079:H.sapiens Spi-B mRNA /cds=(5,793) /gb=X66079 /gi=3
 36227_at Cluster Incl. AF043129:untitled /cds=(0,1379) /gb=AF043129 /gi=3978161
 36277_at Cluster Incl. M23323:Human membrane protein (CD3-epsilon) gene /cds=(59
 37411_at Cluster Incl. D30758:Human mRNA for KIAA0050 gene, complete cds /cds=(1
- 35** 37417_at Cluster Incl. M36542:Human lymphoid-specific transcription factor mRNA,
 37419_g_at Cluster Incl. M36653:Human Oct-2 factor mRNA, complete cds /cds=UNKNO
 38149_at Cluster Incl. D29642:Human mRNA for KIAA0053 gene, complete cds /cds=(1
 38570_at Cluster Incl. X03066:Human mRNA for HLA-D class II antigen DO beta chai
 38963_i_at Cluster Incl. U12707:Human Wiskott-Aldrich syndrome protein (WASP) mR

	38964_r_at	Cluster Incl. U12707:Human Wiskott-Aldrich syndrome protein (WASP) mR
	39318_at	Cluster Incl. X82240:H.sapiens mRNA for Tcell leukemia/lymphoma 1 /cds=
	40396_at	Cluster Incl. U49395:Human ionotropic ATP receptor P2X5a mRNA, complete
	40667_at	Cluster Incl. X60992:H.sapiens CD6 mRNA for T cell glycoprotein CD6 /cd
5	40700_at	Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B)
	40718_at	Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=
	40721_g_at	Cluster Incl. AL022398:dJ434O14.3.1 (putative protein) (isoform 1) /c
	40723_at	Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010
	40729_s_at	Cluster Incl. Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /c
10	40749_at	Cluster Incl. X07203:Human mRNA for CD20 receptor (S7) /cds=(90,983) /g
	41104_at	Cluster Incl. AF044197:Homo sapiens B lymphocyte chemoattractant BLC mR
	31870_at	Cluster Incl. X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908
	32070_at	Cluster Incl. X97267:H.sapiens LPAP gene /cds=(63,683) /gb=X97267 /gi=1
	32629_f_at	Cluster Incl. U90552:Human butyrophilin (BTF5) mRNA, complete cds /cd
15	32716_at	Cluster Incl. X62535:H.sapiens mRNA for diacylglycerol kinase /cds=(103
	33243_at	Cluster Incl. AF099935:Homo sapiens MDC-3.13 isoform 2 mRNA, complete c
	34183_at	Cluster Incl. AL080169:Homo sapiens mRNA; cDNA DKFZp434C171 (from
	clone	
	36482_s_at	Cluster Incl. Y15724:Homo sapiens SERCA3 gene, exons 1-7 (and joined
20	36874_at	Cluster Incl. M26004:Human CR2/CD21/C3d/Epstein-Barr virus receptor mRN
	37272_at	Cluster Incl. X57206:H.sapiens mRNA for 1D-myo-inositol-trisphosphate 3
	37645_at	Cluster Incl. Z22576:H.sapiens CD69 gene /cds=(81,680) /gb=Z22576 /gi=3
	37988_at	Cluster Incl. M89957:Human immunoglobulin superfamily member B cell rec
	38269_at	Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from
25	clon	
	38359_at	Cluster Incl. Y12336:H.sapiens mRNA for F25B3.3 kinase like protein fro
	40159_r_at	Cluster Incl. M55067:Human 47-kD autosomal chronic granulomatous dise
	40420_at	Cluster Incl. AB015718:Homo sapiens lok mRNA for protein kinase, comple
	40480_s_at	Cluster Incl. M14333:Homo sapiens c-syn protooncogene mRNA, complete
30	41166_at	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy
	32224_at	Cluster Incl. AB018312:Homo sapiens mRNA for KIAA0769 protein, complete
	32793_at	Cluster Incl. X00437:Human mRNA for T-cell specific protein /cds=(37,97
	36155_at	Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(3
	37021_at	Cluster Incl. X16832:Human mRNA for cathepsin H (EC 3.4.22.16) /cds=(34
35	38017_at	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U0
	38018_g_at	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=
	38119_at	Cluster Incl. X12496:Human mRNA for erythrocyte membrane sialoglycoprot
	38406_f_at	Cluster Incl. AI207842:ao89h09.x1 Homo sapiens cDNA, 3 end /clone=IM

- 2039_s_at M14333 /FEATURE= /DEFINITION=HUMCSYNA Homo sapiens c-syn protooncogene
- 2059_s_at M36881 /FEATURE=mRNA /DEFINITION=HUMLCKAA Human lymphocyte-specific pr
- 5 1768_s_at X59932 /FEATURE=mRNA /DEFINITION=HSCSRCKIN Human mRNA for C-SRC-kinase
- 1760_s_at D11327 /FEATURE= /DEFINITION=HUMLCPTP Human mRNA for protein-tyrosine
- 1498_at L05148 /FEATURE= /DEFINITION=HUMTYRKIN Human protein tyrosine kinase rel
- 10 1370_at M29696 /FEATURE= /DEFINITION=HUMIL7AA Human interleukin-7 receptor (IL-7
- 1336_s_at X06318 /FEATURE=cds /DEFINITION=HSPKCB1A Human mRNA for protein kinase
- 1097_s_at L31584 /FEATURE=exon /DEFINITION=HUMEBI103 Human G protein-coupled rec
- 15 1105_s_at M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active bet
- 1106_s_at M12959 /FEATURE= /DEFINITION=HUMTCAXB Human T-cell receptor active alp
- 1110_at M21624 /FEATURE=mRNA /DEFINITION=HUMTCRGC Human T-cell receptor delta ch
- 20 1096_g_at M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (
- 1085_s_at M37238 /FEATURE=mRNA /DEFINITION=HUMPLC Human phospholipase C mRNA, co
- 1004_at X68149 /FEATURE=exon#2 /DEFINITION=HSBLR1A Homo sapiens BLR1 gene for Bu
- 25 906_at L78440 /FEATURE=mRNA /DEFINITION=HUMSTAT4R Homo sapiens STAT4 mRNA, compl
- 854_at S76617 /FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B
- 848_at U19261 /FEATURE= /DEFINITION=HSU19261 Homo sapiens Epstein-Barr virus-ind
- 849_g_at U19261 /FEATURE= /DEFINITION=HSU19261 Homo sapiens Epstein-Barr
- 30 virus-i
- 810_at U64105 /FEATURE= /DEFINITION=HSU64105 Human guanine nucleotide exchange f
- 619_s_at M27394 /FEATURE=cds /DEFINITION=HUMB1LYM Human B-lymphocyte cell-surfac
- 590_at M32334 /FEATURE=cds /DEFINITION=HUMICAM4 Homo sapiens intercellular adhes
- 35 253_g_at L42324 /FEATURE=cds /DEFINITION=HUMFRCG Homo sapiens (clone GPCR W) G p
- 245_at M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRN
- 172_at U57650 /FEATURE= /DEFINITION=HSU57650 Human SH2-containing inositol 5-pho

138_at U66464 /FEATURE= /DEFINITION=HSU66464 Human hematopoietic progenitor kina
 160029_at X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein
 kinase

5 Metagene 381

38924_s_at Cluster Incl. AF001628:Homo sapiens interactor protein AblBP4 (AblBP4
 40115_at Cluster Incl. D16562:Human mRNA for ATP synthase gamma-subunit (L-type)
 36599_at Cluster Incl. M55905:Human mitochondrial NAD(P)+ dependent malic enzyme
 10 1236_s_at M89914 /FEATURE= /DEFINITION=HUMNF1B Human neurofibromin (NF1)
 gene, c

Metagene 382

15 31701_r_at Cluster Incl. X83412:H.sapiens B1 mRNA for mucin /cds=(0,515) /gb=X83
 40249_at Cluster Incl. M55040:Human acetylcholinesterase (ACHE) mRNA, complete c
 1875_f_at D38498 /FEATURE= /DEFINITION=HUMPMS1A Human PMS5 mRNA (yeast
 mismatch
 1331_s_at U83598 /FEATURE= /DEFINITION=HSU83598 Human death domain receptor 3
 20 so

Metagene 383

31836_at Cluster Incl. L34600:Human nuclear-encoded mitochondrial initiation fac
 25 32661_s_at Cluster Incl. D79992:Human mRNA for KIAA0170 gene, complete cds /cds=
 32662_at Cluster Incl. AL041663:DKFZp434M0217_s1 Homo sapiens cDNA, 3 end /clon
 33810_at Cluster Incl. AF110377:Homo sapiens PCAF-associated factor 400 (PAF400)
 34176_at Cluster Incl. AF091087:Homo sapiens clone 643 unknown mRNA, complete se
 34659_at Cluster Incl. AB018334:Homo sapiens mRNA for KIAA0791 protein, complete
 30 35226_at Cluster Incl. U71207:Human eyes absent homolog (Eab1) mRNA, complete cd
 35722_at Cluster Incl. AL080198:Homo sapiens mRNA; cDNA DKFZp434D222 (from
 clone
 38720_at Cluster Incl. AF026292:Homo sapiens chaperonin containing t-complex pol
 39357_at Cluster Incl. U72514:Human C2f mRNA, complete cds /cds=(0,720) /gb=U725
 35 40090_at Cluster Incl. AI797997:wh80b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40816_at Cluster Incl. L07758:Human IEF SSP 9502 mRNA, complete cds /cds=(87,159
 41754_at Cluster Incl. M92439:Human leucine-rich protein mRNA, complete cds /cds
 41756_at Cluster Incl. AJ010842:Homo sapiens mRNA for putative ATP(GTP)-binding
 34839_at Cluster Incl. AB029027:Homo sapiens mRNA for KIAA1104 protein, complete

- 35305_at Cluster Incl. X95762:H.sapiens mRNA for aminopeptidase P-like /cds=(0,1
 36186_at Cluster Incl. L37368:Human (clone E5.1) RNA-binding protein mRNA, compl
 36685_at Cluster Incl. W63793:zc55a10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 37739_at Cluster Incl. M86737:Human high mobility group box (SSRP1) mRNA, comple
 5 38384_at Cluster Incl. X54199:Human mRNA for GARS-AIRS-GART /cds=UNKNOWN
 /gb=X54
 38416_at Cluster Incl. L27706:Human chaperonin protein (Tcp20) gene complete cds
 38824_at Cluster Incl. AF039103:Homo sapiens Tat-interacting protein TIP30 mRNA,
 40269_at Cluster Incl. U51990:Human hPrp18 mRNA, complete cds /cds=(72,1100) /gb
 10 1942_s_at U37022 /FEATURE=mRNA /DEFINITION=HSU37022 Human cyclin-dependent
 kinas
 1313_at D38048 /FEATURE= /DEFINITION=D38048 Human mRNA for proteasome subunit z,
 1044_s_at U31556 /FEATURE= /DEFINITION=HSU31556 Human transcription factor E2F-
 5
 15 229_at M37197 /FEATURE=mRNA /DEFINITION=HUMCBF Human CCAAT-box-binding
 factor (C

Metagene 384

- 20 35937_at Cluster Incl. U65416:Human MHC class I molecule (MICB) gene, complete c
 37435_s_at Cluster Incl. U52153:Human inwardly rectifying potassium channel Kir3
 38270_at Cluster Incl. AF005043:Homo sapiens poly(ADP-ribose) glycohydrolase (hP
 38985_at Cluster Incl. AF063605:Homo sapiens brain my047 protein mRNA, complete
 40818_at Cluster Incl. D14041:Homo sapiens mRNA for H-2K binding factor-2, compl
 25 41763_g_at Cluster Incl. D64015:Homo sapiens mRNA for T-cluster binding protein,
 34386_at Cluster Incl. AF072250:Homo sapiens methyl-CpG binding protein MBD4 (MB
 35847_at Cluster Incl. AB028980:Homo sapiens mRNA for KIAA1057 protein, partial
 37295_at Cluster Incl. X63469:H.sapiens mRNA for transcription factor TFIIIE beta
 32607_at Cluster Incl. AF039656:Homo sapiens neuronal tissue-enriched acidic pro

30

Metagene 385

- 41480_at Cluster Incl. AF029669:Homo sapiens Rad51C (RAD51C) mRNA, complete cds
 38670_at Cluster Incl. AL031685:dJ963K23.2 (novel protein) /cds=(2,688) /gb=AL03
 35 40102_at Cluster Incl. AB018315:Homo sapiens mRNA for KIAA0772 protein, complete
 41823_at Cluster Incl. AJ132258:Homo sapiens mRNA for staufer protein, partial /
 157_at U65011 /FEATURE= /DEFINITION=HSU65011 Human preferentially expressed anti

Metagene 386

- 35506_s_at Cluster Incl. J03870:Human cystatin SA-I mRNA, complete cds /cds=(70,
38676_at Cluster Incl. AA059408:z196e07.r1 Homo sapiens cDNA, 5 end /clone=IMAG
824_at U90313 /FEATURE= /DEFINITION=HSU90313 Human glutathione-S-transferase hom
- 5**
Metagene 387
- 34003_at Cluster Incl. U47924:Human chromosome 12p13 sequence /cds=(373,1122) /g
41400_at Cluster Incl. K02581:Human thymidine kinase mRNA, complete cds /cds=(57
10 41670_at Cluster Incl. R38263:yc92c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
41719_i_at Cluster Incl. AF009767:AF009767 Homo sapiens cDNA /clone=C97A-12 /gb=
32702_at Cluster Incl. U04810:Human tastin mRNA, complete cds /cds=(110,2446) /g
34715_at Cluster Incl. U74612:Human hepatocyte nuclear factor-3/fork head homolo
35714_at Cluster Incl. U89606:Human pyridoxal kinase mRNA, complete cds /cds=(6,
15 35723_at Cluster Incl. D16581:Human mRNA for 8-oxo-dGTPase, complete cds /cds=(2
36837_at Cluster Incl. U63743:Homo sapiens mitotic centromere-associated kinesin
38618_at Cluster Incl. AC002073:Human PAC clone DJ515N1 from 22q11.2-q22 /cds=(0
40412_at Cluster Incl. AA203476:zx55e01.r1 Homo sapiens cDNA, 5 end /clone=IMAG
32263_at Cluster Incl. AL080146:Homo sapiens mRNA; cDNA DKFZp434B174 (from
20 clone
34852_g_at Cluster Incl. AF011468:Homo sapiens serine/threonine kinase (BTAK) mR
36205_at Cluster Incl. L04490:Homo sapiens (clone CC6) NADH-ubiquinone oxidoredu
38414_at Cluster Incl. U05340:Human p53CDC mRNA, complete cds /cds=(110,1609) /g
41296_s_at Cluster Incl. W27761:37c5 Homo sapiens cDNA /gb=W27761 /gi=1307709 /u
25 41583_at Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (B
32536_at Cluster Incl. Z37986:H.sapiens mRNA for phenylalkylamine binding protei
32589_at Cluster Incl. U20979:Human chromatin assembly factor-I p150 subunit mRN
1979_s_at X55504 /FEATURE=cds /DEFINITION=HSP120A H.sapiens mRNA for P120
antige
- 30** 1599_at L25876 /FEATURE= /DEFINITION=HUMPTPB Homo sapiens protein tyrosine phosph
1516_g_at Rad2
1347_at S78187 /FEATURE= /DEFINITION=S78187 CDC25Hu2=cdc25+ homolog [human,
mRNA
149_at U90426 /FEATURE= /DEFINITION=HSU90426 Human nuclear RNA helicase, complet
- 35**
Metagene 388
- 31860_at Cluster Incl. X51804:Human PMI gene for a putative receptor protein /cd

Metagene 389

- 36225_s_at Cluster Incl. W27611:35b9 Homo sapiens cDNA /gb=W27611 /gi=1307559 /u
- 38545_at Cluster Incl. M31682:Human testicular inhibin beta-B-subunit mRNA, 3 e
- 5 41644_at Cluster Incl. AB018333:Homo sapiens mRNA for KIAA0790 protein, partial
- 32648_at Cluster Incl. U15979:Human (dlk) mRNA, complete cds /cds=(173,1321) /gb
- 33795_at Cluster Incl. AB006630:Homo sapiens mRNA for KIAA0292 gene, partial cds
- 35142_at Cluster Incl. AF070617:Homo sapiens clone 24812 mRNA sequence /cds=UNKN
- 39404_s_at Cluster Incl. D86988:Human mRNA for KIAA0221 gene, complete cds /cds=
- 10 41767_r_at Cluster Incl. AB020662:Homo sapiens mRNA for KIAA0855 protein, partial
- 36944_f_at Cluster Incl. U72621:Human LOT1 mRNA, complete cds /cds=(657,2048) /g

Metagene 390

- 15 32430_at Cluster Incl. M73481:Human gastrin releasing peptide receptor (GRPR) mR
- 41680_at Cluster Incl. AF007170:Homo sapiens DEME-6 mRNA, partial cds /cds=(0,17
- 37615_at Cluster Incl. D86962:Human mRNA for KIAA0207 gene, complete cds /cds=(7
- 32798_at Cluster Incl. AF043105:Homo sapiens glutathione S-transferase mu 3 (GST
- 33878_at Cluster Incl. W27472:31d4 Homo sapiens cDNA /gb=W27472 /gi=1307276 /ug=
- 20 1120_at J05459 /FEATURE=mRNA /DEFINITION=HUMGSTM3A Human glutathione transferase
- 1121_g_at J05459 /FEATURE=mRNA /DEFINITION=HUMGSTM3A Human glutathione transferase

Metagene 391

- 25 33505_at Cluster Incl. AI887421:wm05c01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 35879_at Cluster Incl. M77140:H.sapiens pro-galanin mRNA, 3 end /cds=(0,323) /g
- 36308_at Cluster Incl. D76435:Homo sapiens mRNA for Zic protein, complete cds /c
- 39302_at Cluster Incl. X56807:Human DSC2 mRNA for desmocollins type 2a and 2b /c
- 30 32072_at Cluster Incl. U40434:Human mesothelin or CAK1 antigen precursor mRNA, c
- 34282_at Cluster Incl. AB010812:Homo sapiens Nrf3 mRNA for NF-E2-related factor
- 35134_at Cluster Incl. U47054:Human putative mono-ADP-ribosyltransferase (htMART
- 35674_at Cluster Incl. AB023211:Homo sapiens mRNA for KIAA0994 protein, partial
- 36873_at Cluster Incl. D16532:Human gene for very low density lipoprotein recept
- 35 37177_at Cluster Incl. Y00636:Human mRNA for lymphocyte function associated anti
- 37218_at Cluster Incl. D64110:Homo sapiens mRNA for ANA, complete cds /cds=(94,8
- 37534_at Cluster Incl. Y07593:H.sapiens mRNA for 46 kDa coxsackievirus and adeno
- 38352_at Cluster Incl. AF016371:Homo sapiens U-snRNP-associated cyclophilin (USA
- 40049_at Cluster Incl. X76104:H.sapiens DAP-kinase mRNA /cds=(336,4631) /gb=X761

- 40454_at Cluster Incl. X87241:H.sapiens mRNA for hFat protein /cds=(186,13958) /
 40506_s_at Cluster Incl. U75686:Homo sapiens polyadenylate binding protein mRNA,
 40803_at Cluster Incl. AL050161:Homo sapiens mRNA; cDNA DKFZp586B0222 (from
 clon
- 5** 41742_s_at Cluster Incl. AF061034:Homo sapiens FIP2 alternatively translated mRN
 41743_i_at Cluster Incl. AF061034:Homo sapiens FIP2 alternatively translated mRN
 33396_at Cluster Incl. U12472:Human glutathione S-transferase (GST phi) gene, co
 34850_at Cluster Incl. AB017644:Homo sapiens mRNA for ubiquitin-conjugating enzy
 35362_at Cluster Incl. AB018342:Homo sapiens mRNA for KIAA0799 protein, partial
- 10** 36104_at Cluster Incl. AA526497:ni96d07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 36990_at Cluster Incl. X04741:Human mRNA for protein gene product (PGP) 9.5 /cds
 38819_at Cluster Incl. U33635:Human colon carcinoma kinase-4 (CCK4) mRNA, comple
 1490_at M19720 /FEATURE=mRNA#2 /DEFINITION=HUMMYC3L Human L-myc protein gene,
 co
- 15** 1452_at U24576 /FEATURE= /DEFINITION=U24576 Homo sapiens breast tumor autoantige
 1042_at U27185 /FEATURE= /DEFINITION=HSU27185 Human RAR-responsive (TIG1) mRNA,
 829_s_at U21689 /FEATURE=cds /DEFINITION=HSU21689 Human glutathione S-
 transferas
- 408_at X54489 /FEATURE=mRNA /DEFINITION=HSMGSAG Human gene for melanoma
20 growth s
 333_s_at Single-Stranded Dna-Binding Protein Mssp-1
- Metagene 392
- 25** 39658_at Cluster Incl. AB007901:Homo sapiens KIAA0441 mRNA, complete cds /cds=(1
 32112_s_at Cluster Incl. AI800499:tc11f11.x1 Homo sapiens cDNA, 3 end /clone=IM
 32113_at Cluster Incl. U83115:Human non-lens beta gamma-crystallin like protein
 37950_at Cluster Incl. X74496:H.sapiens mRNA for prolyl oligopeptidase /cds=(0,2
 39013_at Cluster Incl. Y11588:H.sapiens mRNA for apoptosis specific protein /cds
- 30** 39360_at Cluster Incl. AF034546:Homo sapiens sorting nexin 3 (SNX3) mRNA, comple
 34349_at Cluster Incl. AJ011779:Homo sapiens mRNA for SEC63 protein /cds=(98,238
 34368_at Cluster Incl. U31814:Human transcriptional regulator homolog RPD3 mRNA,
 34819_at Cluster Incl. D14043:Human mRNA for MGC-24, complete cds /cds=(79,648)
 41798_at Cluster Incl. AJ222801:Homo sapiens mRNA for neutral sphingomyelinase /
- 35** 266_s_at L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal
 transduc
- Metagene 393

- 32030_at Cluster Incl. X99459:H.sapiens mRNA for sigma 3B protein /cds=(30,611)
- 33751_at Cluster Incl. AL109702:Homo sapiens mRNA full length insert cDNA clone
- 37222_at Cluster Incl. X79389:H.sapiens GSTT1 mRNA /cds=(0,722) /gb=X79389 /gi=5
- 41163_at Cluster Incl. AL109672:Homo sapiens mRNA full length insert cDNA clone
- 5 39139_at Cluster Incl. AI357653:qy15c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 375_at Z84718 /FEATURE=mRNA#1 /DEFINITION=HS322B1 Human DNA sequence from clone
- Metagene 394
- 10
- 41366_at Cluster Incl. AB023219:Homo sapiens mRNA for KIAA1002 protein, complete
- 36870_at Cluster Incl. AB018347:Homo sapiens mRNA for KIAA0804 protein, partial
- 40120_at Cluster Incl. X90999:H.sapiens mRNA for Glyoxalase II /cds=(36,818) /gb
- 40123_at Cluster Incl. D87435:Human mRNA for KIAA0248 gene, partial cds /cds=(0,
- 15 40421_at Cluster Incl. U49070:Human peptidyl-prolyl isomerase and essential mito
- 34833_at Cluster Incl. AL050157:Homo sapiens mRNA; cDNA DKFZp586O0120 (from clon
- Metagene 395
- 20
- 33641_g_at Cluster Incl. Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /c
- 33956_at Cluster Incl. AB018549:Homo sapiens MD-2 mRNA, complete cds /cds=(125,6
- 35012_at Cluster Incl. M81750:H.sapiens myeloid cell nuclear differentiation ant
- 36795_at Cluster Incl. J03077:Human co-beta glucosidase (proactivator) mRNA, com
- 25 37099_at Cluster Incl. AI806222:wf26e10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 39593_at Cluster Incl. AI432401:tg73b09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 40698_at Cluster Incl. X96719:H.sapiens mRNA for AICL (activation-induced C-type
- 41620_at Cluster Incl. AB018259:Homo sapiens mRNA for KIAA0716 protein, complete
- 33777_at Cluster Incl. D34625:Human TBXAS1 gene for thromboxane synthase, promot
- 30 34660_at Cluster Incl. AI142565:qb47d08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 38323_at Cluster Incl. AC005162:Homo sapiens BAC clone RG113D17 from 7p14-p15 /c
- 39760_at Cluster Incl. AL031781:dJ51J12.1.3 (human ortholog of mouse KH Domain R
- 32193_at Cluster Incl. AF030339:Homo sapiens receptor for viral semaphorin prote
- 32207_at Cluster Incl. M64925:Human palmitoylated erythrocyte membrane protein (
- 35 36661_s_at Cluster Incl. X06882:Human gene for CD14 differentiation antigen /cds
- 36674_at Cluster Incl. J04130:Human activation (Act-2) mRNA, complete cds /cds=(
- 37011_at Cluster Incl. U49392:Human allograft inflammatory factor-1 (AIF-1) mRNA
- 37684_at Cluster Incl. AB020687:Homo sapiens mRNA for KIAA0880 protein, complete
- 32593_at Cluster Incl. D42043:Human mRNA for KIAA0084 gene, partial cds /cds=(0,

- 1520_s_at X04500 /FEATURE=expanded_cds /DEFINITION=HSIL1B Human gene for
propte
- 307_at J03600 /FEATURE= /DEFINITION=HUMLOX5 Human lipoxygenase mRNA, complete
cd
- 5**
- Metagene 396
- 33980_at Cluster Incl. X52638:Human mRNA for 6-phosphofructo-2-kinase/fructose-2
34740_at Cluster Incl. AF032886:Homo sapiens forkhead protein (FKHRL1) mRNA, com
- 10**
- 36515_at Cluster Incl. AJ238764:Homo sapiens mRNA for UDP-N-acetylglucosamine-2-
39693_at Cluster Incl. N53547:yv43b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
41200_at Cluster Incl. Z22555:H.sapiens encoding CLA-1 mRNA /cds=(69,1598) /gb=Z
35260_at Cluster Incl. AB020674:Homo sapiens mRNA for KIAA0867 protein, complete
- 15**
- Metagene 397
- 38361_g_at Cluster Incl. AI688812:wd41c03.x1 Homo sapiens cDNA, 3 end /clone=IM
33869_at Cluster Incl. AL080218:Homo sapiens mRNA; cDNA DKFZp586N1323 (from
clon
- 20**
- 38051_at Cluster Incl. X76220:H.sapiens MAL gene exon 1 (and joined CDS) /cds=(5
1460_g_at M68941 /FEATURE=mRNA /DEFINITION=HUMPTYPH Human protein-
tyrosine phosph
- Metagene 398
- 25**
- 33963_at Cluster Incl. M96326:Human azurocidin gene, complete cds /cds=(16,771)
35401_s_at Cluster Incl. AB021225:Homo sapiens mRNA for membrane-type-4 matrix m
36785_at Cluster Incl. Z23090:H.sapiens mRNA for 28 kDa heat shock protein /cds=
41079_at Cluster Incl. AB010575:Homo sapiens mRNA for sodium channel, complete c
- 30**
- 31846_at Cluster Incl. AW003733:ws16b04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
33224_at Cluster Incl. AB007965:Homo sapiens mRNA, chromosome 1 specific transcr
33251_at Cluster Incl. AB018322:Homo sapiens mRNA for KIAA0779 protein, partial
33783_at Cluster Incl. AB007867:Homo sapiens KIAA0407 mRNA, complete cds /cds=(2
35671_at Cluster Incl. U02619:Human TFIIC Box B-binding subunit mRNA, complete
- 35**
- 38628_at Cluster Incl. AF029777:Homo sapiens histone acetyltransferase (GCN5) mR
38725_s_at Cluster Incl. N36295:yx99b12.r1 Homo sapiens cDNA, 5 end /clone=IMAG
33929_at Cluster Incl. X54232:Human mRNA for heparan sulfate proteoglycan (glypi
34347_at Cluster Incl. AL049955:Homo sapiens mRNA; cDNA DKFZp564J0123 (from clon
34412_s_at Cluster Incl. U59632:Homo sapiens H5 mRNA, partial cds; and platelet

	36152_at	Cluster Incl. X79353:H.sapiens XAP-4 mRNA for GDP-dissociation inhibito
	36643_at	Cluster Incl. L20817:Homo sapiens tyrosine protein kinase (CAK) gene, c
	37368_at	Cluster Incl. AA292277:zt51a05.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	37369_s_at	Cluster Incl. L41066:Homo sapiens NF-AT3 mRNA, complete cds /cds=(141
5	40235_at	Cluster Incl. L13738:Human activated p21cdc42Hs kinase (ack) mRNA, comp
	40899_at	Cluster Incl. Y00503:Human mRNA for keratin 19 /cds=(32,1234) /gb=Y0050
	41306_at	Cluster Incl. AA004795:zh96a06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	41800_s_at	Cluster Incl. U46571:Human tetratricopeptide repeat protein (tpr2) mR
	2047_s_at	M23410 /FEATURE= /DEFINITION=HUMPLAKO Human plakoglobin (PLAK)
10	mRNA, c	
	1134_at	L13738 /FEATURE=mRNA /DEFINITION=HUMNRTYKIN Human activated
	p21cdc42Hs k	
	1007_s_at	U48705 /FEATURE=mRNA /DEFINITION=HSU48705 Human receptor tyrosine
	kina	
15	361_at	Y13620 /FEATURE= /DEFINITION=HSRNABCL9 Homo sapiens mRNA for BCL9 gene
	249_at	L41066 /FEATURE= /DEFINITION=HUMNFAT3A Homo sapiens NF-AT3 mRNA,
	complete	
	Metagene 399	
20		
	32321_at	Cluster Incl. X56841:H.sapiens HLA-E gene /cds=(0,363) /gb=X56841 /gi=4
	34934_at	Cluster Incl. L29376:Homo sapiens (clone 3.8-1) MHC class I mRNA fragme
	36280_at	Cluster Incl. U26174:Human pre-granzyme 3 mRNA, complete cds /cds=(40,8
	37078_at	Cluster Incl. J04132:Human T cell receptor zeta-chain mRNA, complete cd
25	37112_at	Cluster Incl. AB002384:Human mRNA for KIAA0386 gene, complete cds /cds=
	37127_at	Cluster Incl. AB023143:Homo sapiens mRNA for KIAA0926 protein, complete
	37456_at	Cluster Incl. AL022315:dJ1177I5.3 (Lectin, Galactose-binding, soluble,
	37775_at	Cluster Incl. W25951:17d10 Homo sapiens cDNA /gb=W25951 /gi=1306236 /ug
	37861_at	Cluster Incl. X14975:Human CD1 R2 gene for MHC-related antigen /cds=(0,
30	38160_at	Cluster Incl. AF011333:Homo sapiens DEC-205 mRNA, complete cds /cds=(53
	38488_s_at	Cluster Incl. AF031167:Homo sapiens interleukin 15 precursor (IL-15)
	38949_at	Cluster Incl. L01087:Human protein kinase C-theta (PRKCT) mRNA, complet
	40719_at	Cluster Incl. AL022398:dJ434O14.3.3 (novel protein) (isoform 3) /cds=(2
	33238_at	Cluster Incl. U23852:Human T-lymphocyte specific protein tyrosine kinas
35	33267_at	Cluster Incl. AF035315:Homo sapiens clone 23664 and 23905 mRNA sequence
	34748_at	Cluster Incl. AB020653:Homo sapiens mRNA for KIAA0846 protein, complete
	35625_at	Cluster Incl. X94630:H.sapiens CD97 gene exon 1 (and joined CDS) /cds=(
	36067_at	Cluster Incl. AB000887:Homo sapiens mRNA for EBI1-ligand chemokine, com
	36503_at	Cluster Incl. AB002409:Homo sapiens mRNA for SLC, complete cds /cds=(58

- 36825_at Cluster Incl. X82200:H.sapiens Staf50 mRNA /cds=(122,1450) /gb=X82200 /
- 36885_at Cluster Incl. L28824:Homo sapiens protein tyrosine kinase (Syk) mRNA, c
- 37960_at Cluster Incl. AB014679:Homo sapiens GN6ST mRNA for N-acetylglucosamine-
- 38666_at Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /
- 5 40143_at Cluster Incl. D50930:Human mRNA for KIAA0140 gene, complete cds /cds=(2
- 40468_at Cluster Incl. AB011126:Homo sapiens mRNA for KIAA0554 protein, partial
- 34306_at Cluster Incl. AB007888:Homo sapiens KIAA0428 mRNA, complete cds /cds=(1
- 35310_at Cluster Incl. D45288:HUMHG2121 Homo sapiens cDNA /gb=D45288
- /gi=1136684
- 10 36108_at Cluster Incl. M16276:Human MHC class II HLA-DR2-Dw12 mRNA DQw1-beta,
- co
- 36650_at Cluster Incl. D13639:Human mRNA for KIAK0002 gene, complete cds /cds=(2
- 38407_r_at Cluster Incl. AI207842:ao89h09.x1 Homo sapiens cDNA, 3 end /clone=IM
- 38453_at Cluster Incl. X15606:Human mRNA for ICAM-2, cell adhesion ligand for LF
- 15 38826_at Cluster Incl. D50918:Human mRNA for KIAA0128 gene, partial cds /cds=(0,
- 41577_at Cluster Incl. AB020630:Homo sapiens mRNA for KIAA0823 protein, partial
- 1717_s_at U45878 /FEATURE= /DEFINITION=HSU45878 Human inhibitor of apoptosis
- pro
- 1478_at L10717 /FEATURE= /DEFINITION=HUMTKTCS Homo sapiens T cell-specific tyros
- 20 1405_i_at M21121 /FEATURE= /DEFINITION=HUMTCSM Human T cell-specific protein
- (RA
- 1365_at M26062 /FEATURE= /DEFINITION=HUMIL2RBC Human interleukin 2 receptor beta
- 1292_at L11329 /FEATURE= /DEFINITION=HUMPAC1 Homo sapiens protein tyrosine phosph
- 595_at M59465 /FEATURE= /DEFINITION=HUMA20 Human tumor necrosis factor alpha ind
- 25 106_at Z35278 /FEATURE=mRNA /DEFINITION=HSAML1RN H.sapiens PEBP2aC1 acute
- myeloi

Metagene 400

- 30 32633_at Cluster Incl. U26591:Human clone IS10 diabetes mellitus type I autoanti
- 38969_at Cluster Incl. AI828168:wk32h09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 40849_s_at Cluster Incl. U88528:Human transcription factor LZIP mRNA, complete c
- 41778_at Cluster Incl. U53347:Human neutral amino acid transporter B mRNA, compl
- 35311_at Cluster Incl. AF084523:Homo sapiens cellular repressor of E1A-stimulate

35

Metagene 401

- 32975_g_at Cluster Incl. U07563:Human ABL gene, exon 1b and intron 1b, and putat
- 39614_at Cluster Incl. AB018345:Homo sapiens mRNA for KIAA0802 protein, partial

Metagene 402

- 41619_at Cluster Incl. AL022398:dJ434O14.4 (Interferon Regulatory Factor 6) /cds
- 5** 41641_at Cluster Incl. AJ223603:Homo sapiens mRNA encoding rat C4.4-like protein
- 32634_s_at Cluster Incl. U38260:Human islet cell autoantigen ICAp69 mRNA, comple
- 34709_r_at Cluster Incl. Z75331:H.sapiens mRNA for nuclear protein SA-2 /cds=(64
- 35175_f_at Cluster Incl. X70940:H.sapiens mRNA for elongation factor 1 alpha-2 /
- 38268_at Cluster Incl. U08989:Human glutamate transporter mRNA, complete cds /cd
- 10** 38482_at Cluster Incl. AJ011497:Homo sapiens mRNA for Claudin-7 /cds=(334,969) /
- 2089_s_at H06628 /FEATURE= /DEFINITION=H06628 yl82g03.r1 Soares infant brain 1NI
- 1641_s_at U32986 /FEATURE= /DEFINITION=HSU32986 Human xeroderma pigmentosum grou
- 1458_at M64572 /FEATURE= /DEFINITION=HUMCAP Human protein tyrosine phosphatase m

15

Metagene 403

- 36427_at Cluster Incl. W27129:22g8 Homo sapiens cDNA /gb=W27129 /gi=1306663 /ug=
- 31883_at Cluster Incl. AF025794:Homo sapiens methionine synthase reductase (MTRR
- 20** 38656_s_at Cluster Incl. W27939:39g3 Homo sapiens cDNA /gb=W27939 /gi=1307887 /u
- 32758_g_at Cluster Incl. U84720:Homo sapiens mRNA export protein (RAE1) mRNA, co
- 36592_at Cluster Incl. S85655:prohibitin [human, mRNA, 1043 nt] /cds=(50,868) /g
- 40229_at Cluster Incl. AJ010071:Homo sapiens for TOM1-like protein /cds=(30,1460
- 41322_s_at Cluster Incl. AI816034:au44e05.x1 Homo sapiens cDNA, 3 end /clone=IM
- 25** 1614_s_at X63546 /FEATURE=cds#2 /DEFINITION=HSTRE210 H.sapiens mRNA for tre
- onco
- 508_at U43923 /FEATURE= /DEFINITION=HSU43923 Human transcription factor SUPT4H m

Metagene 404

30

- 39705_at Cluster Incl. AB014600:Homo sapiens mRNA for KIAA0700 protein, partial

Metagene 405

- 35** 35425_at Cluster Incl. AJ243512:Homo sapiens mRNA for Barx2 protein (Barx2 gene)
- 35435_s_at Cluster Incl. AF001903:Human 3-hydroxyacyl-CoA dehydrogenase, isoform
- 40303_at Cluster Incl. U85658:Human transcription factor ERF-1 mRNA, complete cd
- 34292_at Cluster Incl. X92475:H.sapiens mRNA for ITBA1 protein /cds=(284,1069) /
- 35263_at Cluster Incl. N73769:za61g08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-

- 36965_at Cluster Incl. U13616:Human ankyrin G (ANK-3) mRNA, complete cds /cds=(1
 37749_at Cluster Incl. D78611:Human MEST mRNA, complete cds /cds=(223,1230) /gb=
 38768_at Cluster Incl. X96752:H.sapiens mRNA for L-3-hydroxyacyl-CoA dehydrogena
- 5** Metagene 406
- 35957_at Cluster Incl. AF030196:Homo sapiens stannin mRNA, complete cds /cds=(14
 37458_at Cluster Incl. AJ223728:Homo sapiens Porc-P1 gene similar to yeast CDC45
 38943_at Cluster Incl. U36787:Human putative holocytochrome c-type synthetase mR
10 33247_at Cluster Incl. U86782:Human 26S proteasome-associated pad1 homolog (POH1
 39432_at Cluster Incl. AF038662:Homo sapiens chromosome 3q13 beta-1,4-galactosyl
 40074_at Cluster Incl. X16396:Human mRNA for NAD-dependent methylene tetrahydrof
 36135_at Cluster Incl. U86602:Human nucleolar protein p40 mRNA, complete cds /cd
 40271_at Cluster Incl. D42085:Human mRNA for KIAA0095 gene, complete cds /cds=(6
15 40276_at Cluster Incl. D50063:Human mRNA for proteasome subunit p40_ / Mov34 prot
 32559_s_at Cluster Incl. AJ238096:Homo sapiens mRNA for Lsm4 protein /cds=(23,44
 2035_s_at M55914 /FEATURE= /DEFINITION=HUMCMYCQ Human c-myc binding
 protein (MBP
 1310_at D26599 /FEATURE= /DEFINITION=HUMPSH2 Human mRNA for proteasome subunit H
20 1314_at D44466 /FEATURE= /DEFINITION=D44466 Homo sapiens mRNA for proteasome sub
 Metagene 407
- 31605_at Cluster Incl. U72518:Human destrin-2 pseudogene mRNA, complete cds /cds
25 34648_at Cluster Incl. Z12830:H.sapiens mRNA for SSR alpha subunit /cds=(29,889)
 34649_at Cluster Incl. M14219:Human chondroitin/dermatan sulfate proteoglycan (P
 38226_at Cluster Incl. W27152:23h11 Homo sapiens cDNA /gb=W27152 /gi=1306731 /ug
 39277_at Cluster Incl. U60805:Human oncostatin-M specific receptor beta subunit
 34667_at Cluster Incl. U15306:Human cysteine-rich sequence-specific DNA-binding
30 38702_at Cluster Incl. AF070640:Homo sapiens clone 24781 mRNA sequence /cds=UNKN
 40096_at Cluster Incl. D14710:Human mRNA for ATP synthase alpha subunit, complet
 40132_g_at Cluster Incl. D89937:Homo sapiens mRNA for follistatin-related protei
 40440_at Cluster Incl. AL080119:Homo sapiens mRNA; cDNA DKFZp564M2423 (from
 clon
35 40441_g_at Cluster Incl. AL080119:Homo sapiens mRNA; cDNA DKFZp564M2423 (from cl
 41739_s_at Cluster Incl. M83216:Human aorta caldesmon mRNA, complete cds /cds=(2
 34305_at Cluster Incl. Z29505:H.sapiens mRNA for nucleic acid binding protein su
 34855_at Cluster Incl. X76770:H.sapiens PAP mRNA /cds=UNKNOWN /gb=X76770
 /gi=556

- 36684_at Cluster Incl. M21154:Human S-adenosylmethionine decarboxylase mRNA, com
 37024_at Cluster Incl. AF010312:Homo sapiens Pig7 (PIG7) mRNA, complete cds /cds
 38085_at Cluster Incl. AI740522:wg16b07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 38401_s_at Cluster Incl. W27594:34h4 Homo sapiens cDNA /gb=W27594 /gi=1307542 /u
5 39471_at Cluster Incl. Z48042:H.sapiens mRNA encoding GPI-anchored protein p137
 41594_at Cluster Incl. M64174:Human protein-tyrosine kinase (JAK1) mRNA, complet
 41842_at Cluster Incl. AI701156:we10f09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32548_at Cluster Incl. L24804:Human (p23) mRNA, complete cds /cds=(232,714) /gb=
 32571_at Cluster Incl. X68836:H.sapiens mRNA for S-adenosylmethionine synthetase
10 2033_s_at U10564 /FEATURE= /DEFINITION=HSU10564 Human CDK tyrosine 15-kinase
 WEE
 1928_s_at U78733 /FEATURE=mRNA#1 /DEFINITION=HSSMAD2S8 Homo sapiens mad
 protein
 1920_s_at X77794 /FEATURE=cds /DEFINITION=HSCYCG1 H.sapiens mRNA for cyclin
15 G1
 1903_at Ras-Related Protein Rap1b
 1839_at Ras-Like Protein Tc4
 1824_s_at J05614 /FEATURE=mRNA /DEFINITION=HUMPCNAPRM Human
 proliferating cell n
20 1670_at L23959 /FEATURE= /DEFINITION=HUMDP1A Homo sapiens E2F-related transcript
 1318_at X74262 /FEATURE=cds /DEFINITION=HSRBAP48 H.sapiens RbAp48 mRNA encoding
 1272_at L19161 /FEATURE= /DEFINITION=HUMIEF2G Human translation initiation facto
 1074_at M28209 /FEATURE= /DEFINITION=HUMRAB1A Homo sapiens GTP-binding protein (
 853_at S74017 /FEATURE= /DEFINITION=S74017 Nrf2=NF-E2-like basic leucine zipper
25 865_at U08316 /FEATURE= /DEFINITION=HSU08316 Human insulin-stimulated protein ki
 777_at D13988 /FEATURE= /DEFINITION=HUMRABGDI Human rab GDI mRNA, complete
 cds
 757_at D28364 /FEATURE= /DEFINITION=HUMAI23 Human mRNA for annexin II, 5 UTR (se
 584_s_at M30938 /FEATURE=mRNA#1 /DEFINITION=HUMKUP Human Ku (p70/p80)
30 subunit mR
 504_at U39318 /FEATURE= /DEFINITION=HSU39318 Human E2 ubiquitin conjugating enzy
 452_at U66615 /FEATURE= /DEFINITION=HSU66615 Human SWI/SNF complex 155 KDa
 subun
 466_at U77948 /FEATURE= /DEFINITION=HSU77948 Human Bruton s tyrosine kinase-asso
35 442_at X15187 /FEATURE=cds /DEFINITION=HSTRA1 Human tra1 mRNA for human
 homologu
 398_at X98743 /FEATURE=cds /DEFINITION=HSRNAHELC H.sapiens mRNA for RNA
 helicase
 359_at Y10659 /FEATURE=cds /DEFINITION=HSIL13RA H.sapiens IL-13Ra mRNA

- 351_f_atD28423 /FEATURE= /DEFINITION=HUMPSF82 Human mRNA for pre-mRNA splicing
 322_at D88532 /FEATURE= /DEFINITION=D88532 Homo sapiens mRNA for p55pik, complet
 276_at L08069 /FEATURE= /DEFINITION=HUMDNAJHOM Human heat shock protein, E. coli
 289_at L29277 /FEATURE= /DEFINITION=HUMAPRF Homo sapiens DNA-binding protein (AP
5 262_at M21154 /FEATURE=mRNA /DEFINITION=HUMAMD Human S-adenosylmethionine
 decarb

Metagene 408

- 10** 39638_at Cluster Incl. S73885:AP-4=basic helix-loop-helix DNA-binding protein [h
 41071_at Cluster Incl. X57655:H.sapiens RNA for acrosin-trypsin inhibitor (HUSI-
 32642_at Cluster Incl. AF026547:Homo sapiens neurocan (CSPG3) mRNA, complete cds
 35145_at Cluster Incl. X96401:H.sapiens mRNA for ROX protein /cds=(212,1960) /gb
 36012_at Cluster Incl. Y09631:H.sapiens mRNA for PIBF1 protein, complete /cds=(0
15 36514_at Cluster Incl. U66469:Human cell growth regulator CGR19 mRNA, complete c
 36928_at Cluster Incl. X70394:H.sapiens OZF mRNA /cds=(856,1734) /gb=X70394 /gi=
 37229_at Cluster Incl. U49844:Human FRAP-related protein (FRP1) mRNA, complete c
 38322_at Cluster Incl. AI093155:qa97g04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39415_at Cluster Incl. X72727:H.sapiens tulp mRNA for transformation upregulated
20 40092_at Cluster Incl. AB002312:Human mRNA for KIAA0314 gene, partial cds /cds=(
 41187_at Cluster Incl. U26162:Human myosin regulatory light chain mRNA, complete
 41302_at Cluster Incl. R59606:yh02e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 41597_s_at Cluster Incl. AF047442:Homo sapiens vesicle trafficking protein sec22
 1136_at L16991 /FEATURE= /DEFINITION=HUMCDC8X Human thymidylate kinase (CDC8)
25 mR

Metagene 409

- 34985_at Cluster Incl. AF035408:Homo sapiens cartilage intermediate layer protei
30 35898_at Cluster Incl. AF100780:Homo sapiens connective tissue growth factor rel
 36289_f_at Cluster Incl. U27333:Human alpha (1,3) fucosyltransferase (FUT6) mRNA
 39673_i_at Cluster Incl. AB011792:Homo sapiens mRNA for extracellular matrix pro
 39674_r_at Cluster Incl. AB011792:Homo sapiens mRNA for extracellular matrix pro
 40328_at Cluster Incl. X99268:H.sapiens mRNA for B-HLH DNA binding protein /cds=
35 31855_at Cluster Incl. U61374:Human novel protein with short consensus repeats o
 36007_at Cluster Incl. AL050137:Homo sapiens mRNA; cDNA DKFZp586L151 (from
 clone
 36533_at Cluster Incl. D83402:Homo sapiens gene for prostacyclin synthase /cds=(
 39007_at Cluster Incl. M55593:Human collagenase type IV (CLG4) gene /cds=(289,22

- 40856_at Cluster Incl. U29953:Human pigment epithelium-derived factor gene, comp
 41138_at Cluster Incl. M16279:Human MIC2 mRNA, complete cds /cds=(177,734) /gb=M
 32250_at Cluster Incl. X07523:Human mRNA for truncated form of complement factor
 32783_at Cluster Incl. X82494:H.sapiens mRNA for fibulin-2 /cds=(69,3623) /gb=X8
5 37402_at Cluster Incl. D26129:Human mRNA for ribonuclease A (RNase A), complete
 38026_at Cluster Incl. U01244:Human fibulin-1D mRNA, complete cds /cds=(10,2121)
 38052_at Cluster Incl. M14539:Human factor XIII subunit a mRNA, 3 end /cds=(0,2
 38057_at Cluster Incl. AL049798:Human DNA sequence from clone 797M17 on chromoso
 38059_g_at Cluster Incl. Z22865:H.sapiens dermatopontin mRNA, complete CDS /cds=
10 1761_at D37965 /FEATURE= /DEFINITION=HUMPRLTS Human mRNA for PDGF receptor
 beta-
 614_at M22430 /FEATURE= /DEFINITION=HUMRASFA Human RASF-A PLA2 mRNA,
 complete c
15 Metagene 410
 35109_at Cluster Incl. AB018299:Homo sapiens mRNA for KIAA0756 protein, partial
 41866_s_at Cluster Incl. AF022728:Homo sapiens beta-dystrobrevin (BDTN) mRNA, co
 35712_at Cluster Incl. AC004142:Homo sapiens BAC clone RG118D07 from 7q31 /cds=(
20 36460_at Cluster Incl. AF008442:Homo sapiens RNA polymerase I subunit hRPA39 mRN
 37266_at Cluster Incl. U69645:Human zinc finger protein mRNA, complete cds /cds=
 37893_at Cluster Incl. AI828880:wj37b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 38248_at Cluster Incl. AB011124:Homo sapiens mRNA for KIAA0552 protein, complete
 38256_s_at Cluster Incl. W21827:57E11 Homo sapiens cDNA /clone=(not-directional)
25 39417_at Cluster Incl. AB028951:Homo sapiens mRNA for KIAA1028 protein, partial
 32245_at Cluster Incl. AF014837:Homo sapiens m6A methyltransferase (MT-A70) gene
 34315_at Cluster Incl. Y18314:Homo sapiens mRNA for paraplegin-like protein /cds
 34371_at Cluster Incl. U79267:Human clone 23840 mRNA, partial cds /cds=(0,521) /
 34380_at Cluster Incl. AC004472:Homo sapiens chromosome 9, P1 clone 11659 /cds=(
30 782_at U93867 /FEATURE= /DEFINITION=HSU93867 Human RNA polymerase III subunit (R
 Metagene 411
 36492_at Cluster Incl. AI347155:tc04c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35 36561_at Cluster Incl. X73424:Homo sapiens gene for propionyl-CoA carboxylase a
 37911_at Cluster Incl. U07158:Human syntaxin mRNA, complete cds /cds=(66,959) /g
 32828_at Cluster Incl. AF026548:Homo sapiens branched chain alpha-ketoacid dehyd
 36194_at Cluster Incl. M63959:Human alpha-2-macroglobulin receptor-associated pr
 38391_at Cluster Incl. M94345:Homo sapiens macrophage capping protein mRNA, comp

1444_at AB003177 /FEATURE= /DEFINITION=AB003177 Homo sapiens mRNA for proteasome
 239_at M63138 /FEATURE=mRNA /DEFINITION=HUMCATD5 Human cathepsin D (catD)
 gene,

5 Metagene 412

- 37585_at Cluster Incl. X13482:Human mRNA for U2 snRNP-specific A protein /cds=(5
 41199_s_at Cluster Incl. W27050:19f7 Homo sapiens cDNA /gb=W27050 /gi=1306422 /u
 32230_at Cluster Incl. U39067:Homo sapiens translation initiation factor eIF3 p3
 10 36174_at Cluster Incl. X70326:H.sapiens MacMarcks mRNA /cds=(13,600) /gb=X70326
 1644_at U36764 /FEATURE= /DEFINITION=HSU36764 Human TGF-beta receptor interactin
 935_at L12168 /FEATURE= /DEFINITION=HUMADCY Homo sapiens adenylyl cyclase-associ

Metagene 413

15

- 33689_s_at Cluster Incl. AF012434:untitled /cds=(38,394) /gb=AF012434 /gi=235291
 34651_at Cluster Incl. M58525:Homo sapiens catechol-O-methyltransferase (COMT) m
 34443_at Cluster Incl. R61362:yh15c05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 41606_at Cluster Incl. AJ005940:Homo sapiens mRNA for GTP-binding protein /cds=(
 20 35247_at Cluster Incl. AI557062:PT2.1_13_A09.r Homo sapiens cDNA, 3 end /clone_
 32766_at Cluster Incl. Z83840:Human DNA sequence from clone 216E10 on chromosome
 34826_at Cluster Incl. L21936:Human succinate dehydrogenase flavoprotein subunit
 36985_at Cluster Incl. X17025:Human homolog of yeast IPP isomerase /cds=(50,736)
 37666_at Cluster Incl. D29011:Human mRNA for proteasome subunit X, complete cds
 25 38028_at Cluster Incl. AL050152:Homo sapiens mRNA; cDNA DKFZp586K1220 (from
 clon
 40974_at Cluster Incl. U63541:Human mRNA expressed in HC/HCC livers and MolT-4 p
 811_at U64444 /FEATURE= /DEFINITION=HSU64444 Homo sapiens ubiquitin fusion-degra
 372_f_atZ84718 /FEATURE=cds#2 /DEFINITION=HS322B1 Human DNA sequence from clone
 30 374_f_atZ84718 /FEATURE=cds#5 /DEFINITION=HS322B1 Human DNA sequence from clone
 223_at S81003 /FEATURE= /DEFINITION=S81003 L-UBC=ubiquitin conjugating enzyme [h

Metagene 414

- 35 32316_s_at Cluster Incl. X15183:Human mRNA for 90-kDa heat-shock protein /cds=(6
 34680_s_at Cluster Incl. D14663:Human mRNA for KIAA0107 gene, complete cds /cds=
 34773_at Cluster Incl. AF038952:Homo sapiens cofactor A protein mRNA, complete c
 35153_at Cluster Incl. AF058696:Homo sapiens cell cycle regulatory protein p95 (
 38708_at Cluster Incl. AF054183:Homo sapiens GTP binding protein mRNA, complete

- 39079_at Cluster Incl. D85758:Homo sapiens mRNA for human protein homologous to
 39396_at Cluster Incl. AF081281:Homo sapiens lysophospholipase (LPL1) mRNA, comp
 41133_at Cluster Incl. U32519:Human GAP SH3 binding protein mRNA, complete cds /
 32803_at Cluster Incl. AF104398:Homo sapiens cornichon mRNA, complete cds /cds=(
5 34327_at Cluster Incl. Z46606:H.sapiens HLTF gene for helicase-like transcriptio
 34402_at Cluster Incl. AB024327:Homo sapiens pt-wd mRNA for WD-40 repeat protein
 34783_s_at Cluster Incl. AF047473:Homo sapiens testis mitotic checkpoint BUB3 (B
 35272_at Cluster Incl. AI541042:pec1.2-1.D12.r Homo sapiens cDNA, 5 end /clone_
 36112_r_at Cluster Incl. X75755:H.sapiens PR264 gene /cds=(109,774) /gb=X75755 /
10 39860_at Cluster Incl. U05040:Human FUSE binding protein mRNA, complete cds /cds
 41275_at Cluster Incl. U31556:Human transcription factor E2F-5 mRNA, complete cd
 41320_s_at Cluster Incl. U69609:Human transcriptional repressor (GCF2) mRNA, com
 41510_s_at Cluster Incl. L15189:Homo sapiens mitochondrial HSP75 mRNA, complete
 32573_at Cluster Incl. AL021546:Human DNA sequence from BAC 15E1 on chromosome 1
15 1789_at U65928 /FEATURE= /DEFINITION=HSU65928 Human Jun activation domain bindin
 1480_at L12723 /FEATURE= /DEFINITION=HUMHSP70H Human heat shock protein 70 (hsp7
 1213_at U88666 /FEATURE= /DEFINITION=HSU88666 Homo sapiens serine kinase SRPK2 m
 1178_at Dihydrofolate Reductase, Alt. Splice 6
 1073_at M81601 /FEATURE= /DEFINITION=HUMTEFSII Human transcription elongation fa
20 306_s_at J02621 /FEATURE=mRNA /DEFINITION=HUMHMG14 Human non-histone
 chromosomal

Metagene 415

- 25** 34612_at Cluster Incl. L13220:Homo sapiens calbindin D-9k mRNA, complete cds /cd
 32881_at Cluster Incl. U88834:Human clone 295, 5cM region surrounding hepatocyte
 34949_at Cluster Incl. AB028971:Homo sapiens mRNA for KIAA1048 protein, complete
 35005_at Cluster Incl. AF051941:Homo sapiens type 6 nucleoside diphosphate kinas
 35933_f_at Cluster Incl. D38498:Human PMS5 mRNA (yeast mismatch repair gene PMS1
30 36281_at Cluster Incl. M96739:Human NSCL-1 mRNA sequence /cds=UNKNOWN
 /gb=M96739
 37475_at Cluster Incl. AC004144:Homo sapiens chromosome 19, overlapping cosmids
 41074_at Cluster Incl. AF062006:Homo sapiens orphan G protein-coupled receptor H
 41078_at Cluster Incl. D63484:Human mRNA for KIAA0150 gene, partial cds /cds=(0,
35 41374_at Cluster Incl. AB016869:Homo sapiens mRNA for p70 ribosomal S6 kinase be
 41413_at Cluster Incl. AF037339:Homo sapiens cleft lip and palate transmembrane
 34182_at Cluster Incl. U18932:Human heparan sulfate-N-deacetylase/N-sulfotransfe
 35194_at Cluster Incl. X53463:Human mRNA for glutathione peroxidase-like protein
 40840_at Cluster Incl. M80254:H.sapiens cyclophilin isoform (hCyP3) mRNA, comple

- 41227_at Cluster Incl. AL022162:Homo sapiens DNA sequence from PAC 454M7 on chro
 40188_f_at Cluster Incl. W28846:52g2 Homo sapiens cDNA /gb=W28846 /gi=1308812 /u
 726_f_atChorionic Somatomammotropin Hormone Cs-5
 446_at U89896 /FEATURE= /DEFINITION=HSU89896 Homo sapiens casein kinase I gamma
5 440_at X12492 /FEATURE=cds /DEFINITION=HSCTF1 Human mRNA for CAAT-box binding
 tr

Metagene 416

- 10** 34122_at Cluster Incl. AF027807:Homo sapiens beta-casein (CSN2) gene, complete c
 34625_at Cluster Incl. X05153:Human alpha-lactalbumin gene /cds=(26,454) /gb=X05
 36330_at Cluster Incl. Y17448:Homo sapiens CCBL1 gene, last two exons /cds=(0,14
 36043_at Cluster Incl. AF070577:Homo sapiens clone 24461 mRNA sequence /cds=UNKN
 39822_s_at Cluster Incl. AF078077:Homo sapiens growth arrest and DNA-damage-indu
15 40268_at Cluster Incl. X16706:Human fra-2 mRNA /cds=(3,983) /gb=X16706 /gi=31464

Metagene 417

- 37271_at Cluster Incl. L25444:Homo sapiens (TAFII70-alpha) mRNA, complete cds /c
20 39709_at Cluster Incl. U67171:Human selenoprotein W (selW) mRNA, complete cds /c
 33921_at Cluster Incl. Y15409:Homo sapiens mRNA for putative glucose 6-phosphate
 35743_at Cluster Incl. U79569:Human no arches (nar) mRNA, complete cds /cds=(36,
 36183_at Cluster Incl. X86779:H.sapiens mRNA for FAST kinase /cds=(21,1670) /gb=
 37346_at Cluster Incl. M57567:Human ADP-ribosylation factor (hARF5) mRNA, comple
25 38758_at Cluster Incl. R98910:yr31d04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 38831_f_at Cluster Incl. AF053356:Homo sapiens chromosome 7q22 sequence /cds=(25
 41359_at Cluster Incl. Z98265:Homo sapiens mRNA for plakophilin 3 /cds=(74,2467)
 1486_at L37127 /FEATURE= /DEFINITION=HUMRPIA Homo sapiens RNA polymerase II
 mRNA

30

Metagene 418

- 32485_at Cluster Incl. X00371:Human myoglobin gene (exon 1) (and joined CDS) /cd
 35004_at Cluster Incl. U31875:Human Hep27 protein mRNA, complete cds /cds=(433,1
35 33792_at Cluster Incl. AF043498:Homo sapiens prostate stem cell antigen (PSCA) m
 36876_at Cluster Incl. M55150:Human fumarylacetoacetate hydrolase mRNA, complete
 38262_at Cluster Incl. AF052107:Homo sapiens clone 23620 mRNA sequence /cds=UNKN
 32745_at Cluster Incl. AF034091:Homo sapiens nuclear localization signal contain
 34400_at Cluster Incl. AI540957:PEC1.2_15_G03.r Homo sapiens cDNA, 5 end /clone

	36658_at	Cluster Incl. D13643:Human mRNA for KIAA0018 gene, complete cds /cds=(3
	37002_at	Cluster Incl. D32143:Human mRNA for biliverdin-IXbeta reductase I /cds=
	37713_at	Cluster Incl. L07548:Human aminoacylase-1 (ACY1) mRNA, complete cds /cd
	38763_at	Cluster Incl. L29254:Human (clone P1-5) L-iditol-2 dehydrogenase gene /
5	41346_at	Cluster Incl. AJ007583:Homo sapiens mRNA for acetylglucosaminyltransfer
Metagene 419		
	34532_at	Cluster Incl. AF035318:Homo sapiens clone 23705 mRNA sequence /cds=UNKN
10	34928_at	Cluster Incl. AF060865:Homo sapiens chromosome 16 zinc finger protein Z
	37159_at	Cluster Incl. U79259:Human clone 23945 mRNA, complete cds /cds=(636,140
	40705_at	Cluster Incl. AF103905:Homo sapiens Rap1 guanine-nucleotide exchange fa
	41120_at	Cluster Incl. D14686:Human gene for glycine cleavage system T-protein /
	31866_at	Cluster Incl. AC005239:Homo sapiens chromosome 19, cosmid F23149 /cds=(
15	35156_at	Cluster Incl. AL050297:Homo sapiens mRNA; cDNA DKFZp564N123 (from
	clone	
	36480_at	Cluster Incl. X80497:H.sapiens PHKLA mRNA /cds=(126,3833) /gb=X80497 /g
	36538_at	Cluster Incl. AB018314:Homo sapiens mRNA for KIAA0771 protein, partial
	38291_at	Cluster Incl. J00123:Human enkephalin gene /cds=(0,803) /gb=J00123 /gi=
20	38648_at	Cluster Incl. U80760:Homo sapiens CAGH1 alternate open reading frame mR
	38683_s_at	Cluster Incl. AB029008:Homo sapiens mRNA for KIAA1085 protein, partia
	39423_f_at	Cluster Incl. AJ000644:Homo sapiens mRNA for SPOP /cds=(157,1281) /gb
	32198_at	Cluster Incl. W28979:54e8 Homo sapiens cDNA /gb=W28979 /gi=1308927 /ug=
	35355_at	Cluster Incl. AB020697:Homo sapiens mRNA for KIAA0890 protein, complete
25	35840_at	Cluster Incl. AL050060:Homo sapiens mRNA; cDNA DKFZp566H073 (from
	clone	
	36132_at	Cluster Incl. S74728:antiquitin=26g turgor protein homolog [human, kidn
	37339_at	Cluster Incl. U20657:Human ubiquitin protease (Unph) proto-oncogene mRN
	1308_g_at	D14533 /FEATURE= /DEFINITION=HUMXPAC Human mRNA for XPAC
30	protein	
Metagene 420		
	40761_at	Cluster Incl. AA705628:zf40a01.s1 Homo sapiens cDNA, 3 end /clone=3793
35	40846_g_at	Cluster Incl. U10324:Human nuclear factor NF90 mRNA, complete cds /cd
	41780_at	Cluster Incl. U22816:Human LAR-interacting protein 1b mRNA, complete cd
	32185_at	Cluster Incl. U00946:Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containi
	38755_at	Cluster Incl. X84709:H.sapiens mRNA for mediator of receptor-induced to

- 944_s_at D49354 /FEATURE= /DEFINITION=HUMHSP70A Human mRNA for enhancer protein
- Metagene 421
- 5**
- 36745_at Cluster Incl. AF035308:Homo sapiens clone 23798 and 23825 mRNA sequence
- 37444_at Cluster Incl. AF028827:Homo sapiens Tax interaction protein 40 mRNA, pa
- 41624_r_at Cluster Incl. AA932443:oo75b11.s1 Homo sapiens cDNA, 3 end /clone=IM
- 32101_at Cluster Incl. AA112483:zn69a06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 10** 36823_at Cluster Incl. AF055026:Homo sapiens clone 24444 RaP2 interacting protei
- 37184_at Cluster Incl. L37792:Human syntaxin 1A mRNA, complete cds /cds=(1,867)
- 37545_at Cluster Incl. W22110:64F11 Homo sapiens cDNA /clone=(not-directional) /
- 38000_at Cluster Incl. S72370:pyruvate carboxylase [human, kidney, mRNA, 4017 nt
- 15** Metagene 422
- 37107_at Cluster Incl. U78305:Homo sapiens protein phosphatase Wip1 mRNA, comple
- 38169_s_at Cluster Incl. U76368:Human cationic amino acid transporter-2A (ATRC2)
- 40647_at Cluster Incl. Z32684:Homo sapiens mRNA for membrane transport protein (
- 20** 41701_at Cluster Incl. X72177:H.sapiens C6 gene, exon 1 /cds=(20,2824) /gb=X7217
- 35152_at Cluster Incl. AJ001016:Homo sapiens mRNA encoding RAMP3 /cds=(29,475) /
- 38644_at Cluster Incl. U14588:Human paxillin mRNA, complete cds /cds=(74,1747) /
- 32188_at Cluster Incl. M96980:Homo sapiens myelin transcription factor 1 (MTF1)
- 40543_at Cluster Incl. L08424:Homo sapiens achaete scute homologous protein (ASH
- 25** 1332_f_at V00520 /FEATURE=mRNA /DEFINITION=HSGROW2 Human germ line gene for grow
- Metagene 423
- 30** 31492_at Cluster Incl. AB019392:Homo sapiens mRNA of muscle specific gene M9, co
- 34265_at Cluster Incl. Y00757:Human mRNA for polypeptide 7B2 /cds=(28,663) /gb=Y
- 34348_at Cluster Incl. U78095:Homo sapiens placental bikunin mRNA, complete cds
- 34845_at Cluster Incl. AL035398:Human DNA sequence from clone 796I17 on chromoso
- 36204_at Cluster Incl. Y00815:Human mRNA for LCA-homolog. LAR protein (leukocyte
- 35** 38011_at Cluster Incl. AB006572:Homo sapiens RMP mRNA for RPB5 meidating protein
- 32584_at Cluster Incl. D38047:Human mRNA for 26S proteasome subunit p31, complet
- 1312_at D38047 /FEATURE= /DEFINITION=HUMPSP31 Human mRNA for 26S proteasome subu
- Metagene 424

- 39064_at Cluster Incl. L38928:Homo sapiens 5,10-methenyltetrahydrofolate synthet
 39353_at Cluster Incl. AI912041:wd84b06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41212_r_at Cluster Incl. D26068:Human mRNA for KIAA0038 gene, partial cds /cds=(
5 36164_at Cluster Incl. U82328:Homo sapiens pyruvate dehydrogenase complex protei
 37683_at Cluster Incl. D80012:Human mRNA for KIAA0190 gene, partial cds /cds=(0,
 37720_at Cluster Incl. M22382:Human mitochondrial matrix protein P1 (nuclear enc
 41506_at Cluster Incl. AF032437:Homo sapiens mitogen activated protein kinase ac
- 10** Metagene 425
- 31522_f_at Cluster Incl. Z80779:H.sapiens H2B/g gene /cds=(0,380) /gb=Z80779 /gi
 31523_f_at Cluster Incl. Z80780:H.sapiens H2B/h gene /cds=(0,380) /gb=Z80780 /gi
 31524_f_at Cluster Incl. Z80782:H.sapiens H2B/k gene /cds=(0,380) /gb=Z80782 /gi
15 31528_f_at Cluster Incl. Z83738:H.sapiens hH2B/e gene /cds=(0,380) /gb=Z83738 /g
 31693_f_at Cluster Incl. Z80776:H.sapiens H2A/g gene /cds=(0,392) /gb=Z80776 /gi
 34157_f_at Cluster Incl. AI200373:qf98c03.x1 Homo sapiens cDNA, 3 end /clone=IM
 35127_at Cluster Incl. AI039144:ox31b09.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 35576_f_at Cluster Incl. AL009179:dJ97D16.4 (Histone H2B) /cds=(25,405) /gb=AL00
20 36347_f_at Cluster Incl. AA873858:oh79b10.s1 Homo sapiens cDNA, 3 end /clone=IM
 32980_f_at Cluster Incl. AI688098:wc92f08.x1 Homo sapiens cDNA, 3 end /clone=IM
 34964_at Cluster Incl. N35832:yx89b10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 36757_at Cluster Incl. AL009179:dJ97D16.6 (Histone H3.1) /cds=(10,420) /gb=AL009
 38576_at Cluster Incl. AJ223353:Homo sapiens mRNA for histone H2B, clone pJG4-5-
25 32819_at Cluster Incl. AJ223352:Homo sapiens mRNA for for histone H2B, clone pjG
 33352_at Cluster Incl. X57985:H.sapiens genes for histones H2B.1 and H2A /cds=(4
 34308_at Cluster Incl. U90551:Human histone 2A-like protein (H2A/I) mRNA, comple
 37018_at Cluster Incl. AI189287:qd05c04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32609_at Cluster Incl. AI885852:wl62d08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
30 286_at L19779 /FEATURE= /DEFINITION=HUMH2A2A Homo sapiens histone H2A.2 mRNA,
 co
 153_f_atX00088 /FEATURE=cds /DEFINITION=HSHISH2B Human histone H2b gene
- Metagene 426
- 35**
- 34525_at Cluster Incl. AB018563:Homo sapiens TML1 mRNA, complete cds /cds=(30,41
 36683_at Cluster Incl. AI953789:wx69d10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39185_at Cluster Incl. AF091083:Homo sapiens clone 628 unknown mRNA, complete se

Metagene 427

- 35878_at Cluster Incl. AB023141:Homo sapiens mRNA for KIAA0924 protein, complete
 37834_at Cluster Incl. Y17999:Homo sapiens mRNA for protein kinase Dyrk1B /cds=(
5 39258_at Cluster Incl. AI627877:ty20b09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41035_at Cluster Incl. AB018318:Homo sapiens mRNA for KIAA0775 protein, complete
 32025_at Cluster Incl. Y11306:Homo sapiens mRNA for hTCF-4 /cds=(307,2097) /gb=Y
 32105_f_at Cluster Incl. U66063:Homo sapiens calcium/calmodulin-dependent protei
 35188_at Cluster Incl. AB018336:Homo sapiens mRNA for KIAA0793 protein, complete
10 38721_at Cluster Incl. W72733:zd77h11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 39796_at Cluster Incl. U11292:Human Ki nuclear autoantigen mRNA, complete cds /c
 41308_at Cluster Incl. U37408:Homo sapiens phosphoprotein CtBP mRNA, complete cd
 1926_at U48801 /FEATURE= /DEFINITION=HSU48801 Human vascular endothelial growth
 1158_s_at J04046 /FEATURE=mRNA /DEFINITION=HUMCAMA Human calmodulin
15 mRNA, comple
 650_s_at L07044 /FEATURE= /DEFINITION=HUMCCDPKB Homo sapiens
 calcium/calmodulin-
 605_at L78833 /FEATURE=exon#36 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and
 vatI g

20

Metagene 428

- 31715_at Cluster Incl. U93720:Homo sapiens TEX28 mRNA, complete cds /cds=(144,13
 32468_f_at Cluster Incl. D90278:Human CGM1b mRNA for CD66d /cds=(61,594) /gb=D90
25 33011_at Cluster Incl. Y10148:H.sapiens mRNA for NTR2 receptor /cds=(36,1268) /g
 33027_at Cluster Incl. W27906:39d11 Homo sapiens cDNA /gb=W27906 /gi=1307854 /ug
 33622_at Cluster Incl. Z26308:H.sapiens isoform 1 gene for L-type calcium channe
 33640_at Cluster Incl. Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /cds
 34108_g_at Cluster Incl. AJ005577:Homo sapiens pfkfb2 gene, exons 1 to 15 /cds=(
30 34131_at Cluster Incl. AB026891:Homo sapiens mRNA for cystine/glutamate transpor
 36398_at Cluster Incl. W28729:50h2 Homo sapiens cDNA /gb=W28729 /gi=1308677 /ug=
 32866_at Cluster Incl. AB011177:Homo sapiens mRNA for KIAA0605 protein, complete
 32933_r_at Cluster Incl. AL050122:Homo sapiens mRNA; cDNA DKFZp586E121 (from clo
 33558_at Cluster Incl. Y09445:H.sapiens mRNA for transcription factor TBX5 /cds=
35 34502_g_at Cluster Incl. L40992:Homo sapiens (clone PEBP2aA1) core-binding facto
 36298_at Cluster Incl. L14565:Human peripherin (PRPH) gene exons 1-9, complete c
 36754_at Cluster Incl. X60435:H.sapiens gene PACAP for pituitary adenylate cycla
 37140_s_at Cluster Incl. AF061193:Homo sapiens ectodysplasin-A isoform EDA-E (ED.
 37151_at Cluster Incl. AF052120:Homo sapiens clone 23836 mRNA sequence /cds=UNKN

- 37415_at Cluster Incl. AB018258:Homo sapiens mRNA for KIAA0715 protein, partial
 37839_at Cluster Incl. AL109700:Homo sapiens mRNA full length insert cDNA clone
 39609_at Cluster Incl. U80457:Human transcription factor SIM2 short form mRNA, c
 40295_at Cluster Incl. AB009288:Homo sapiens mRNA for N-copine, complete cds /cd
5 40651_s_at Cluster Incl. AF039523:untitled /cds=(0,1334) /gb=AF039523 /gi=282812
 31810_g_at Cluster Incl. Z21488:H.sapiens contactin mRNA /cds=(121,3177) /gb=Z21
 33727_r_at Cluster Incl. AB029011:Homo sapiens mRNA for KIAA1088 protein, partia
 33779_at Cluster Incl. AF060538:Homo sapiens vesicle associated membrane protein
 34294_at Cluster Incl. AL041493:DKFZp434F2117_s1 Homo sapiens cDNA, 3 end /clon
10 35685_at Cluster Incl. Z14000:H.sapiens RING1 gene /cds=(75,1208) /gb=Z14000 /gi
 37905_r_at Cluster Incl. X66436:H.sapiens hsr1 mRNA (partial) /cds=UNKNOWN /gb=X
 37939_at Cluster Incl. AL022318:bK150C2.3 (PUTATIVE novel protein similar to APO
 34846_at Cluster Incl. AF112472:Homo sapiens calcium/calmodulin-dependent protei
 38088_r_at Cluster Incl. M80563:Human CAPL protein mRNA, complete cds /cds=(135,
15 38371_at Cluster Incl. M64992:Human prosomal protein P30-33K (pros-30) mRNA, com
 38822_at Cluster Incl. AB011420:Homo sapiens mRNA for DRAK1, complete cds /cds=(
 39917_at Cluster Incl. AI961040:wq58f01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40959_at Cluster Incl. AB011171:Homo sapiens mRNA for KIAA0599 protein, partial
 41286_at Cluster Incl. X77753:H.sapiens TROP-2 gene /cds=(615,1586) /gb=X77753 /
20 32540_at Cluster Incl. AI762547:wh92e05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 1256_at L38929 /FEATURE=mRNA /DEFINITION=HUMPTPD Homo sapiens protein tyrosine p
 1167_s_at D86331 /FEATURE= /DEFINITION=D86331 Human MT2-MMP gene for matrix
 meta
 970_r_atX98296 /FEATURE=cds /DEFINITION=HSUBIQHYD H.sapiens mRNA for ubiquitin
25 916_at L18983 /FEATURE=mRNA /DEFINITION=HUMTYROPHO Homo sapiens tyrosine
 phospho
 734_at Mucin 4, Tracheobronchial
 396_f_atX97671 /FEATURE=cds /DEFINITION=HSERYTHR H.sapiens mRNA for erythropoie
 188_at U09303 /FEATURE= /DEFINITION=HSU09303 Human T cell leukemia LERK-2 (EPLG2
30 170_at U51096 /FEATURE= /DEFINITION=HSU51096 Human homeobox protein Cdx2 mRNA,
 c
 Metagene 429
35 31557_at Cluster Incl. M17733:Human thymosin beta-4 mRNA, complete cds /cds=(77,
 31719_at Cluster Incl. X02761:Human mRNA for fibronectin (FN precursor) /cds=(0,
 32319_at Cluster Incl. AL022310:dJ395P12.2 (tax-transcriptionally activated glyc
 38181_at Cluster Incl. X57766:Human stromelysin-3 mRNA /cds=(9,1475) /gb=X57766
 39640_at Cluster Incl. AB016789:Homo sapiens mRNA for Glutamine-fructose-6-phosp

	41678_at	Cluster Incl. AF025304:Homo sapiens protein-tyrosine kinase EPHB2v (EPH
	41870_at	Cluster Incl. AF030428:Homo sapiens lung type-I cell membrane-associate
	41871_at	Cluster Incl. AI660929:wf20a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35992_at	Cluster Incl. AF087036:Homo sapiens musculin mRNA, partial cds /cds=(0,
5	36070_at	Cluster Incl. AL049389:Homo sapiens mRNA; cDNA DKFZp586O0118 (from clon
	37892_at	Cluster Incl. J04177:Human alpha-1 type XI collagen (COL11A1) mRNA, com
	37981_at	Cluster Incl. D17530:Homo sapiens mRNA for drebrin E, complete cds /cds
	41779_at	Cluster Incl. U70426:Homo sapiens A28-RGS14p mRNA, complete cds /cds=(9
10	33919_at	Cluster Incl. AF022813:Homo sapiens tetraspan (NAG-2) mRNA, complete cd
	34407_at	Cluster Incl. U77594:Human tazarotene-induced gene 2 (TIG2) mRNA, compl
	37310_at	Cluster Incl. X02419:H.sapiens uPA gene /cds=(119,1414) /gb=X02419 /gi=
	38127_at	Cluster Incl. Z48199:H.sapiens syndecan-1 gene (exons 2-5) /cds=(0,866)
	38428_at	Cluster Incl. M13509:Human skin collagenase mRNA, complete cds /cds=(68
15	39166_s_at	Cluster Incl. D83174:Human mRNA for collagen binding protein 2, compl
	39167_r_at	Cluster Incl. D83174:Human mRNA for collagen binding protein 2, compl
	33143_s_at	Cluster Incl. U81800:Homo sapiens monocarboxylate transporter (MCT3)
	2088_s_at	D31661 /FEATURE= /DEFINITION=HUMERKA Human mRNA for tyrosine
	kinase, c	
20	189_s_at	U09937 /FEATURE=mRNA /DEFINITION=HSUROKR7 Human urokinase-type
	plasmino	
	160023_at	X07876 /FEATURE=cds /DEFINITION=HSIRP Human mRNA for irp protein
	(int-	
25	Metagene 430	
	37109_at	Cluster Incl. M55671:Human protein Z (plus 66 bp insertion) mRNA, compl
	38860_at	Cluster Incl. U66346:Homo sapiens cAMP phosphodiesterase (PDE4C) mRNA,
	37888_at	Cluster Incl. D87449:Human mRNA for KIAA0260 gene, partial cds /cds=(0,
30	32756_at	Cluster Incl. AF030249:Homo sapiens putative dienoyl-CoA isomerase (ECH
	35833_at	Cluster Incl. AL080184:Homo sapiens mRNA; cDNA DKFZp434O071 (from clone
	Metagene 431	
35		
	38522_s_at	Cluster Incl. X52785:H.sapiens CD22 mRNA /cds=(34,1977) /gb=X52785 /g
	39942_at	Cluster Incl. AF016898:Homo sapiens B-ATF gene, complete cds /cds=(241,
	32680_at	Cluster Incl. AB011123:Homo sapiens mRNA for KIAA0551 protein, partial
	33253_at	Cluster Incl. D50919:Human mRNA for KIAA0129 gene, complete cds /cds=(1

	40852_at	Cluster Incl. AB025254:Homo sapiens mRNA for tudor repeat associator wi
	32824_at	Cluster Incl. AF039704:Homo sapiens lysosomal pepstatin insensitive pro
	34311_at	Cluster Incl. X76648:H.sapiens mRNA for glutaredoxin /cds=(63,383) /gb=
	36600_at	Cluster Incl. L07633:Homo sapiens (clone 1950.2) interferon-gamma IEF S
5	Metagene 432	
	35209_at	Cluster Incl. AB018309:Homo sapiens mRNA for KIAA0766 protein, complete
	35614_at	Cluster Incl. AB012124:Homo sapiens TCFL5 mRNA for transcription factor
10	32789_at	Cluster Incl. AA149428:zl26a05.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	33852_at	Cluster Incl. M77142:Human polyadenylate binding protein (TIA-1) mRNA,
	1363_at	M87770 /FEATURE= /DEFINITION=HUMKSAMI Human fibroblast growth factor rec
	1229_at	U78556 /FEATURE= /DEFINITION=HSU78556 Human cisplatin resistance associa
	1143_s_at	Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 3, K-Sam III
15	Metagene 433	
	33787_at	Cluster Incl. AB011109:Homo sapiens mRNA for KIAA0537 protein, complete
	39363_at	Cluster Incl. AF042384:Homo sapiens BC-2 protein mRNA, complete cds /cd
20	33135_at	Cluster Incl. U17566:Human 65 kDa hydrophobic protein mRNA, complete cd
	Metagene 434	
	31439_f_at	Cluster Incl. X63095:H.sapiens mRNA for rhesus polypeptide (RhVI) /cd
25	31502_at	Cluster Incl. W27953:39h7 Homo sapiens cDNA /gb=W27953 /gi=1307901 /ug=
	31590_g_at	Cluster Incl. AL031983:dJ271M21.2 (hs6M1-12 (7 transmembrane receptor
	31759_at	Cluster Incl. W26220:22d9 Homo sapiens cDNA /gb=W26220 /gi=1306631 /ug=
	31775_at	Cluster Incl. X65018:H.sapiens mRNA for lung surfactant protein D /cds=
	33651_at	Cluster Incl. AB013456:Homo sapiens hAQP8 mRNA for aquaporin 8, complet
30	34556_at	Cluster Incl. Z29074:H.sapiens mRNA for cytokeratin 9 /cds=(66,1937) /g
	35091_at	Cluster Incl. AA706226:ah28a07.s1 Homo sapiens cDNA, 3 end /clone=1240
	36411_s_at	Cluster Incl. U29943:Human ELAV-like neuronal protein-2 Hel-N2 mRNA,
	33545_at	Cluster Incl. M81758:Homo sapiens skeletal muscle voltage-dependent sod
	34527_r_at	Cluster Incl. AF052108:Homo sapiens clone 23687 mRNA sequence /cds=UN
35	34981_at	Cluster Incl. M55513:Human potassium channel (HPCN1) mRNA, complete cds
	35395_at	Cluster Incl. X05997:Human mRNA for gastric lipase /cds=UNKNOWN /gb=X05
	35915_at	Cluster Incl. X82540:H.sapiens mRNA for activin beta-C chain /cds=(127,
	35950_at	Cluster Incl. U90841:Homo sapiens SSX4 (SSX4) mRNA, complete cds /cds=(
	38506_at	Cluster Incl. X58840:Human mRNA for variant hepatic nuclear factor 1 (v

- 39242_at Cluster Incl. X96783:H.sapiens Syt V gene (genomic and cDNA sequence) /
 40371_at Cluster Incl. X51362:Human mRNA for dopamine D2 receptor /cds=(165,1496
 41101_at Cluster Incl. D87464:Human mRNA for KIAA0274 gene, complete cds /cds=(1
 41647_at Cluster Incl. W28742:51a7 Homo sapiens cDNA /gb=W28742 /gi=1308690 /ug=
5 38646_s_at Cluster Incl. AI763065:wi64h03.x1 Homo sapiens cDNA, 3 end /clone=IM
 38660_at Cluster Incl. F27891:HSPD16170 Homo sapiens cDNA /clone=s4000025D03 /gb
 40094_r_at Cluster Incl. X80026:H.sapiens B-cam mRNA /cds=(6,1772) /gb=X80026 /g
 40442_f_at Cluster Incl. W26019:18b9 Homo sapiens cDNA /gb=W26019 /gi=1306304 /u
 32810_at Cluster Incl. AF019369:untitled /cds=(89,826) /gb=AF019369 /gi=2623563
10 40941_at Cluster Incl. W27026:19d10 Homo sapiens cDNA /gb=W27026 /gi=1306398 /ug
 41351_at Cluster Incl. AA885106:am31h01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 1552_i_at U22028 /FEATURE=expanded_cds /DEFINITION=HSU22028 Human
 cytochrome P45
 1339_s_at X14675 /FEATURE=cds /DEFINITION=HSBCR3C Human bcr-abl mRNA 5
15 fragment
 1259_at L76568 /FEATURE=exons#13-14 /DEFINITION=HUMERCC4G Homo sapiens excision
 1155_at J03069 /FEATURE=mRNA /DEFINITION=HUMMYCL2A Human MYCL2 gene,
 complete cd
20 Metagene 435
 39310_at Cluster Incl. X86163:H.sapiens mRNA for B2-bradykinin receptor, 3 /cds=
 40716_at Cluster Incl. AL049274:Homo sapiens mRNA; cDNA DKFZp564H203 (from
 clone
25 31902_at Cluster Incl. AF093774:Homo sapiens type 2 iodothyronine deiodinase mRN
 36881_at Cluster Incl. X71129:H.sapiens mRNA for electron transfer flavoprotein
 39332_at Cluster Incl. AF035316:Homo sapiens clone 23678 mRNA, partial cds /cds=
 35792_at Cluster Incl. U67963:Human lysophospholipase homolog (HU-K5) mRNA, comp
 1185_at D49410 /FEATURE=expanded_cds /DEFINITION=HUMIL3RA12 Human gene for inter
30
 Metagene 436
 37193_at Cluster Incl. D78335:Human mRNA for 5-terminal region of UMK, complete
 40954_at Cluster Incl. H94881:yu57f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
35 1594_at J05448 /FEATURE= /DEFINITION=HUMRPOLAA Human RNA polymerase subunit
 hRPB
 Metagene 437

	39932_at	Cluster Incl. AI655015:wb66a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	40308_at	Cluster Incl. AI830496:wh51h03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41379_at	Cluster Incl. AB011166:Homo sapiens mRNA for KIAA0594 protein, partial
	32026_s_at	Cluster Incl. AB002311:Human mRNA for KIAA0313 gene, complete cds /cd
5	35193_at	Cluster Incl. AF060219:Homo sapiens RCC1-like G exchanging factor RLG m
	36849_at	Cluster Incl. U90920:Human PTPL1-associated RhoGAP mRNA, complete cds /
	36926_at	Cluster Incl. X80692:H.sapiens ERK3 mRNA /cds=(478,2643) /gb=X80692 /gi
	37617_at	Cluster Incl. U90912:Human clone 23865 mRNA sequence /cds=UNKNOWN
	/gb=U	
10	39727_at	Cluster Incl. AF023917:Homo sapiens protein tyrosine phosphatase PIR1 m
	40431_at	Cluster Incl. AB007891:Homo sapiens KIAA0431 mRNA, partial cds /cds=(96
	40508_at	Cluster Incl. AF025887:Homo sapiens glutathione S-transferase A4-4 (GST
	41729_at	Cluster Incl. AJ009771:Homo sapiens mRNA for putative RING finger prote
	32835_at	Cluster Incl. AA725102:ai08h05.s1 Homo sapiens cDNA, 3 end /clone=1342
15	34411_at	Cluster Incl. Y10387:H.sapiens mRNA for PAPS synthetase /cds=(36,1910)
	34887_at	Cluster Incl. N92548:zb29g04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	35320_at	Cluster Incl. AB004857:Homo sapiens mRNA for NRAMP2, complete cds /cds=
	36578_at	Cluster Incl. U37547:Human IAP homolog B (MIHB) mRNA, complete cds /cds
	36579_at	Cluster Incl. D50916:Human mRNA for KIAA0126 gene, complete cds /cds=(7
20	36610_at	Cluster Incl. D21852:Human mRNA for KIAA0029 gene, partial cds /cds=(38
	36628_at	Cluster Incl. L42542:Human RLIP76 protein mRNA, complete cds /cds=(223,
	36968_s_at	Cluster Incl. AL050353:Homo sapiens mRNA; cDNA DKFZp547C0410 (from cl
	36980_at	Cluster Incl. U03105:Human B4-2 protein mRNA, complete cds /cds=(113,10
	37036_at	Cluster Incl. AB002299:Human mRNA for KIAA0301 gene, partial cds /cds=(
25	37303_at	Cluster Incl. AF057160:Homo sapiens putative poly(ADP-ribosyl) transfer
	37348_s_at	Cluster Incl. AA845349:ak01g01.s1 Homo sapiens cDNA, 3 end /clone=IM
	37381_g_at	Cluster Incl. X59268:Human mRNA for general transcription factor IIB
	37731_at	Cluster Incl. Z29064:H.sapiens AF-1p mRNA /cds=(92,2782) /gb=Z29064 /gi
	38073_at	Cluster Incl. AB007858:Homo sapiens KIAA0398 mRNA, complete cds /cds=(1
30	38097_at	Cluster Incl. AF010313:Homo sapiens Pig8 (PIG8) mRNA, complete cds /cds
	38104_at	Cluster Incl. U78302:Human 2,4-dienoyl-CoA reductase gene /cds=(73,1080
	38727_at	Cluster Incl. M23161:Human transposon-like element mRNA /cds=UNKNOWN /g
	38782_at	Cluster Incl. M95809:Human basic transcription factor 62kD subunit (BTF
	38829_r_at	Cluster Incl. AA628946:af28f05.s1 Homo sapiens cDNA, 3 end /clone=IM
35	41601_at	Cluster Incl. AA142964:zl43a07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
	2063_at	L20046 /FEATURE= /DEFINITION=HUMERCC5A Human ERCC5 excision repair prote

- 37827_r_at Cluster Incl. AJ237839:Homo sapiens mRNA for hypothetical protein /cd
 38555_at Cluster Incl. AB026436:Homo sapiens mRNA for dual specificity phosphata
 39648_at Cluster Incl. AB015594:Homo sapiens mRNA for Pex11p, complete cds /cds=
 40364_at Cluster Incl. U83460:Human high-affinity copper uptake protein (hCTR1)
 5 41450_at Cluster Incl. AI553878:tn30a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41709_at Cluster Incl. AF034803:Homo sapiens liprin-beta2 mRNA, partial cds /cds
 32083_at Cluster Incl. AF027826:Homo sapiens putative seven pass transmembrane p
 33262_at Cluster Incl. M31659:Human GT mitochondrial solute carrier protein homo
 33807_at Cluster Incl. AB023186:Homo sapiens mRNA for KIAA0969 protein, complete
 10 34214_at Cluster Incl. AB014544:Homo sapiens mRNA for KIAA0644 protein, complete
 37936_at Cluster Incl. AI184802:qd24g04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 38264_at Cluster Incl. U74324:Human guanine nucleotide exchange factor mss4 mRNA
 33369_at Cluster Incl. AI535653:P9-C4.T3.P9.D4 Homo sapiens cDNA, 3 end /clone_
 35313_at Cluster Incl. AB002308:Human mRNA for KIAA0310 gene, complete cds /cds=
 15 36677_at Cluster Incl. X70476:H.sapiens subunit of coatomer complex /cds=(68,278
 864_at U07664 /FEATURE=expanded_cds /DEFINITION=HSHB9HB2 Human HB9 homeobox
 gene

Metagene 439

- 20
 31530_at Cluster Incl. U89344:Human acetyl-CoA carboxylase (ACC2) mRNA, complete
 36326_at Cluster Incl. M96740:Human NSCL-2 gene sequence /cds=UNKNOWN
 /gb=M96740
 35622_at Cluster Incl. AB001451:Homo sapiens mRNA for Sck, partial cds /cds=(0,1
 25 35668_at Cluster Incl. AJ001014:Homo sapiens mRNA encoding RAMP1 /cds=(32,478) /
 35670_at Cluster Incl. M37457:Human Na⁺,K⁺ -ATPase catalytic subunit alpha-III i
 38313_at Cluster Incl. AB028985:Homo sapiens mRNA for KIAA1062 protein, partial
 40825_at Cluster Incl. AB025186:Homo sapiens mRNA for EB3 protein, complete cds
 32796_f_at Cluster Incl. U66061:trypsinogen C /cds=(84,827) /gb=U66061 /gi=15525
 30 33444_at Cluster Incl. D30756:Human mRNA for KIAA0049 gene, complete cds /cds=(1
 34842_at Cluster Incl. U41303:Human small nuclear ribonucleoprotein particle N (S
 35770_at Cluster Incl. D16469:Human mRNA for ORF, Xq terminal portion /cds=(1353
 36148_at Cluster Incl. U48437:Human amyloid precursor-like protein 1 mRNA, compl
 40273_at Cluster Incl. AA485440:zx90g03.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 35 41280_r_at Cluster Incl. AF007134:Homo sapiens clone 23565 unknown mRNA, partial

Metagene 440

- 36253_at Cluster Incl. AI131030:qb82f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG

- 36781_at Cluster Incl. X01683:Human mRNA for alpha 1-antitrypsin /cds=(38,1294)
- 39675_at Cluster Incl. AF009243:Homo sapiens proline-rich Gla protein 2 (PRGP2)
- 40333_at Cluster Incl. U43842:Homo sapiens bone morphogenetic protein-4 (hBMP-4)
- 40683_at Cluster Incl. L76687:Homo sapiens Grb14 mRNA, complete cds /cds=(540,21
- 5** 41475_at Cluster Incl. U91512:Human adhesion molecule ninjurin mRNA, complete cd
- 35619_at Cluster Incl. AB014534:Homo sapiens mRNA for KIAA0634 protein, partial
- 37215_at Cluster Incl. AF046798:untitled /cds=(113,2656) /gb=AF046798 /gi=317040
- 39421_at Cluster Incl. D43969:Human AML1 mRNA for AML1c protein (alternatively s
- 40409_at Cluster Incl. U46689:Human microsomal aldehyde dehydrogenase (ALD10) mR
- 10** 32817_at Cluster Incl. AL096881:Novel human mRNA similar to Rattus norvegicus 45
- 39178_at Cluster Incl. L10333:Homo sapiens neuroendocrine-specific protein A (NS
- 33169_at Cluster Incl. U61262:Human neogenin mRNA, complete cds /cds=(136,4521)
- 943_at D43968 /FEATURE= /DEFINITION=HUMAML1BA Human AML1 mRNA for AML1b protein
- 15** 684_at K02215 /FEATURE=mRNA#1 /DEFINITION=HUMANG Human angiotensinogen mRNA, com
- 251_at L41816 /FEATURE=mRNA /DEFINITION=HUMCKI Homo sapiens cam kinase I mRNA, c
- 20** Metagene 441
- 31697_s_at Cluster Incl. J04755:Human ferritin H processed pseudogene, complete
- 33943_at Cluster Incl. L20941:Human ferritin heavy chain mRNA, complete cds /cds
- 33732_at Cluster Incl. Y08387:H.sapiens mRNA for mu-ARP2 protein /cds=(54,1415)
- 25** 39129_at Cluster Incl. AF052134:Homo sapiens clone 23585 mRNA sequence /cds=UNKN
- Metagene 442
- 35457_at Cluster Incl. U20325:Human cocaine and amphetamine regulated transcript
- 30** 36250_at Cluster Incl. AI889718:wo17c04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 37478_at Cluster Incl. Y16752:Homo sapiens mRNA for secretagogen, complete CDS /
- 38174_at Cluster Incl. X99688:H.sapiens mRNA from TYL gene /cds=(1806,3743) /gb=
- 39619_at Cluster Incl. AF070551:Homo sapiens clone 24515 mRNA sequence /cds=UNKN
- 40649_at Cluster Incl. X64810:H.sapiens encoding PC1/PC3 /cds=(189,2450) /gb=X64
- 35** 36924_r_at Cluster Incl. M25756:Human secretogranin II gene, complete cds /cds=(
- 37183_at Cluster Incl. M81883:Human glutamate decarboxylase (GAD67) mRNA, comple
- 33426_at Cluster Incl. Y00064:Human mRNA for secretogranin I (chromogranin B) /c
- 36160_s_at Cluster Incl. U81561:Human protein tyrosine phosphatase receptor pi (
- 40272_at Cluster Incl. D78012:Homo sapiens mRNA for dihydropyrimidinase related

- 41325_at Cluster Incl. AF006823:Homo sapiens TWIK-related acid-sensitive K⁺ chan
- Metagene 443
- 5** 40735_at Cluster Incl. D16626:Human mRNA for histidase, complete cds /cds=(243,2
32631_at Cluster Incl. J03060:Human glucocerebrosidase (GCB) gene /cds=(229,1774
955_at Calmodulin Type I
- Metagene 444
- 10** 31873_at Cluster Incl. U52112:ARD1 N-acetyl transferase related protein /cds=(97
34670_at Cluster Incl. U60899:Human lysosomal alpha-mannosidase (manB) gene /cds
37940_f_at Cluster Incl. AA806768:ob91d06.s1 Homo sapiens cDNA /clone=IMAGE-1338
37667_at Cluster Incl. AF104421:Homo sapiens isolate normal patient 1 uroporphyr
- 15** Metagene 445
- 35112_at Cluster Incl. AF071476:Homo sapiens regulator of G-protein signaling 9L
36246_at Cluster Incl. Z35309:H.sapiens mRNA for adenylyl cyclase /cds=(2094,584
20 35206_at Cluster Incl. AF049105:Homo sapiens centrosomal Nek2-associated protein
36477_at Cluster Incl. X90780:Homo sapiens TNNT3 gene /cds=(143,775) /gb=X90780
38682_at Cluster Incl. AF045581:Homo sapiens BRCA1 associated protein 1 (BAP1) m
34358_at Cluster Incl. Z49254:H.sapiens L23-related mRNA /cds=(54,515) /gb=Z4925
38397_at Cluster Incl. U09196:Human 1.1 kb mRNA upregulated in retinoic acid tre
- 25** Metagene 446
- 36446_s_at Cluster Incl. L24521:Human transformation-related protein mRNA, 3 en
32878_f_at Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-9542
30 33987_at Cluster Incl. M36340:Human ADP-ribosylation factor 1 (ARF1) mRNA, compl
40032_at Cluster Incl. D50923:Human mRNA for KIAA0133 gene, complete cds /cds=(1
40285_at Cluster Incl. U68140:Homo sapiens nuclear VCP-like protein NVLP.2 (NVLP.
41051_at Cluster Incl. X95073:H.sapiens mRNA for translin associated protein X /
41663_at Cluster Incl. AF038202:Homo sapiens clone 23570 mRNA sequence /cds=UNKN
35 33234_at Cluster Incl. AA887480:oj54a12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
35159_at Cluster Incl. U61232:Human tubulin-folding cofactor E mRNA, complete cd
35677_at Cluster Incl. AL035369:H.sapiens novel gene from PAC 117P20, chromosome
38712_at Cluster Incl. AL035291:H.sapiens gene from PACs 125H23 and 105D12 /cds=
39392_at Cluster Incl. AJ002190:Homo sapiens cDNA for dihydroxyacetone phosphate

- 40832_s_at Cluster Incl. AL050126:Homo sapiens mRNA; cDNA DKFZp586G011 (from clo
41783_at Cluster Incl. M97815:Human retinoic acid-binding protein II (CRABP-II)
32262_at Cluster Incl. AL049669:Human gene from PAC 612B18, chromosome 1 /cds=(2
34385_at Cluster Incl. U57877:Human integral membrane protein CII-3 mRNA, nuclea
5 35294_at Cluster Incl. M25077:Human SS-A/Ro ribonucleoprotein autoantigen 60 kd
35296_at Cluster Incl. AB019036:Homo sapiens mRNA for geranylgeranyl pyrophospha
35318_at Cluster Incl. AB007944:Homo sapiens mRNA for KIAA0475 protein, complete
35779_at Cluster Incl. AJ133421:Homo sapiens mRNA for leucocyte vacuolar protein
36198_at Cluster Incl. D13641:Human mRNA for KIAA0016 gene, complete cds /cds=(1
10 36647_at Cluster Incl. AA526812:ni92a08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
39116_at Cluster Incl. AF070626:Homo sapiens clone 24483 unknown mRNA, parital c
41335_at Cluster Incl. AL050084:Homo sapiens mRNA; cDNA DKFZp566O1646 (from
clon
32504_at Cluster Incl. AW024812:wu69c05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
15 254_at M11353 /FEATURE= /DEFINITION=HUMHISH3C Human H3.3 histone class C mRNA,
c

Metagene 447

20 38259_at Cluster Incl. AB002559:Homo sapiens mRNA for hunc18b2, complete cds /cd
34836_at Cluster Incl. U18420:Human ras-related small GTP binding protein Rab5 (
1788_s_at U48807 /FEATURE= /DEFINITION=HSU48807 Human MAP kinase
phosphatase (MK

25 Metagene 448

34171_at Cluster Incl. AI867349:wi24g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
37471_at Cluster Incl. U94317:Homo sapiens ribonuclease P protein subunit p40 (R
38210_at Cluster Incl. Z35094:H.sapiens mRNA for SURF-2 /cds=(17,787) /gb=Z35094
30 39661_s_at Cluster Incl. AF034102:Homo sapiens NBMPR-insensitive nucleoside tran
41037_at Cluster Incl. U63824:Human transcription factor RTEF-1 (RTEF1) mRNA, co
41407_at Cluster Incl. L03411:Human RD protein (RD) mRNA, complete cds /cds=(86,
35701_at Cluster Incl. AI038821:ox96d03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35715_at Cluster Incl. AL080071:Homo sapiens mRNA; cDNA DKFZp564M082 (from
35 clone
38257_at Cluster Incl. AF038406:Homo sapiens NADH dehydrogenase-ubiquinone Fe-S
38275_at Cluster Incl. AF054996:Homo sapiens clone 23783 mRNA sequence /cds=UNKN
39060_at Cluster Incl. D38048:Human mRNA for proteasome subunit z, complete cds
40408_at Cluster Incl. L06845:Human cysteinyl-tRNA synthetase mRNA, partial cds

	40788_at	Cluster Incl. U84371:Human adenylate kinase 2A (AK2A) mRNA, complete cd
	33906_at	Cluster Incl. AB001740:Homo sapiens mRNA for p27, complete cds /cds=(20
	35326_at	Cluster Incl. AF004876:Homo sapiens 54TmP (54tm) mRNA, complete cds /cd
	36167_at	Cluster Incl. D89052:Homo sapiens mRNA for proton-ATPase-like protein,
5	32518_at	Cluster Incl. AF019767:Homo sapiens zinc finger protein (ZPR1) mRNA, co
Metagene 449		
	33035_at	Cluster Incl. AL021397:dJ69E11.3 (Yeast YPR037W and worm C02C2.6 predic
10	33661_at	Cluster Incl. U66589:Human ribosomal protein L5 pseudogene mRNA, comple
	35579_at	Cluster Incl. AB014524:Homo sapiens mRNA for KIAA0624 protein, partial
	37506_at	Cluster Incl. Z78308:HSZ78308 Homo sapiens cDNA /clone=1.47-(CEPH) /gb=
	38568_at	Cluster Incl. U82939:Homo sapiens p53 binding protein mRNA, complete cd
	39231_at	Cluster Incl. AF006513:Homo sapiens CHD1 mRNA, complete cds /cds=(163,5
15	40343_at	Cluster Incl. AJ005814:Homo sapiens mRNA for hoxA7 protein /cds=(106,79
	40704_at	Cluster Incl. Z29090:H.sapiens mRNA for phosphatidylinositol 3-kinase /
	41466_s_at	Cluster Incl. L04282:Human CACCC box-binding protein mRNA, complete c
	41625_at	Cluster Incl. AB011165:Homo sapiens mRNA for KIAA0593 protein, partial
	41642_at	Cluster Incl. X75940:H.sapiens beta glucuronidase pseudogene /cds=UNKNO
20	31867_at	Cluster Incl. AF052174:Homo sapiens clone 24630 mRNA sequence /cds=UNKN
	32129_at	Cluster Incl. AL079314:Homo sapiens mRNA full length insert cDNA clone
	32628_at	Cluster Incl. D28118:Human mRNA for DB1, complete cds /cds=(41,1591) /g
	33805_at	Cluster Incl. AB007949:Homo sapiens mRNA for KIAA0480 protein, complete
	34278_at	Cluster Incl. L18960:Human protein synthesis factor (eIF-4C) mRNA, comp
25	34676_at	Cluster Incl. AB029022:Homo sapiens mRNA for KIAA1099 protein, complete
	34727_at	Cluster Incl. AI800578:wg12b07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	36002_at	Cluster Incl. AB023229:Homo sapiens mRNA for KIAA1012 protein, complete
	36532_at	Cluster Incl. AF039945:Homo sapiens synaptojanin 2B mRNA, partial cds /
	37535_at	Cluster Incl. M27691:Human transactivator protein (CREB) mRNA, complete
30	37984_s_at	Cluster Incl. M57763:Human ADP-ribosylation factor (hARF6) mRNA, comp
	40105_at	Cluster Incl. M65131:Human methylmalonyl-CoA mutase (MCM) mRNA,
	complet	
	40424_at	Cluster Incl. AI017935:ou43h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	40463_at	Cluster Incl. U70322:Human transportin (TRN) mRNA, complete cds /cds=(9
35	32802_at	Cluster Incl. AB011169:Homo sapiens mRNA for KIAA0597 protein, partial
	33404_at	Cluster Incl. U02390:Human adenylyl cyclase-associated protein homolog
	33845_at	Cluster Incl. W28483:47e11 Homo sapiens cDNA /gb=W28483 /gi=1308431 /ug
	35295_g_at	Cluster Incl. M25077:Human SS-A/Ro ribonucleoprotein autoantigen 60 k
	36209_at	Cluster Incl. S78771:NAT=CpG island-associated gene [human, mRNA, 1741

- 38368_at Cluster Incl. U31930:Human deoxyuridine nucleotidohydrolase mRNA, compl
 38765_at Cluster Incl. AB028449:Homo sapiens mRNA for Helicase-MOI, complete cds
 40217_s_at Cluster Incl. U65887:Human CDP-diacylglycerol synthase mRNA, complete
 40218_at Cluster Incl. U60808:Human CDP-diacylglycerol synthase (CDS) mRNA, comp
 5 40617_at Cluster Incl. AC004381:Homo sapiens Chromosome 16 BAC clone CIT987SK-44
 1801_at U76638 /FEATURE= /DEFINITION=HSU76638 Human BRCA1-associated RING domain
 1603_g_at L33881 /FEATURE= /DEFINITION=HUMPKCI Human protein kinase C iota
 isofo
 1329_s_at U74382 /FEATURE= /DEFINITION=HSU74382 Human telomeric repeat DNA-
 10 bindi
 877_at M27691 /FEATURE= /DEFINITION=HUMCREB Human transactivator protein (CREB)
 693_g_at Adenylyl Cyclase-Associated Protein 2
 663_at L18960 /FEATURE= /DEFINITION=HUMEIF4C Human protein synthesis factor (eIF
 350_at D28118 /FEATURE= /DEFINITION=HUMDB1 Human mRNA for DB1, complete cds
 15 274_at L04282 /FEATURE= /DEFINITION=HUMTB Human CACCC box-binding protein
 mRNA,
 Metagene 450
 20 37449_i_at Cluster Incl. X04409:Human mRNA for coupling protein G(s) alpha-subun
 37450_r_at Cluster Incl. X04409:Human mRNA for coupling protein G(s) alpha-subun
 38918_at Cluster Incl. AF083105:Homo sapiens HMG box factor SOX-13 mRNA, complet
 32063_at Cluster Incl. M86546:H.sapiens PBX1a and PBX1b mRNA, complete cds /cds=
 41226_at Cluster Incl. L05147:Human dual specificity phosphatase tyrosine/serine
 25 38779_r_at Cluster Incl. D16431:Human mRNA for hepatoma-derived growth factor, c
 41836_at Cluster Incl. U94836:Human ERPROT 213-21 mRNA, complete cds /cds=(88,27
 32586_at Cluster Incl. D86971:Human mRNA for KIAA0217 gene, partial cds /cds=(0,
 Metagene 451
 30 40400_at Cluster Incl. L22214:Human adenosine A1 receptor (ADORA1) mRNA exons 1-
 Metagene 452
 35 41097_at Cluster Incl. AF002999:Homo sapiens TTAGGG repeat binding factor 2 (hTR
 33249_at Cluster Incl. M16801:Human mineralocorticoid receptor mRNA (hMR), compl
 34340_at Cluster Incl. AA173896:zp03b02.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 35335_at Cluster Incl. AB014519:Homo sapiens mRNA for KIAA0619 protein, complete
 38032_at Cluster Incl. AB018279:Homo sapiens mRNA for KIAA0736 protein, complete

39550_at Cluster Incl. AB011156:Homo sapiens mRNA for KIAA0584 protein, partial

Metagene 453

- 5** 39400_at Cluster Incl. AB028978:Homo sapiens mRNA for KIAA1055 protein, partial
 40841_at Cluster Incl. AF049910:Homo sapiens TACC1 (TACC1) mRNA, complete cds /c
 40877_s_at Cluster Incl. AF041080:Homo sapiens D15F37 pseudogene, S3 allele, mRN
 37716_at Cluster Incl. X05323:Human MRC OX-2 gene signal sequence /cds=(0,824) /
 38747_at Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=
10 32562_at Cluster Incl. X72012:H.sapiens end mRNA for endoglin /cds=(281,2158) /g
 1954_at AF035121 /FEATURE= /DEFINITION=AF035121 Homo sapiens KDR/flk-1 protein m
 1001_at X60957 /FEATURE=cds /DEFINITION=HSTIEMR Human tie mRNA for putative rece
 538_at S53911 /FEATURE= /DEFINITION=S53911 CD34=glycoprotein expressed in lympho

15 Metagene 454

- 32246_g_at Cluster Incl. AF014837:Homo sapiens m6A methyltransferase (MT-A70) ge
 38479_at Cluster Incl. Y07969:H.sapiens mRNA for APRIL protein /cds=(230,979) /g
 33120_at Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10
20 33121_g_at Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling

Metagene 455

- 41634_at Cluster Incl. D87445:Human mRNA for KIAA0256 gene, complete cds /cds=(1
25 31854_at Cluster Incl. AF035582:Homo sapiens CASK mRNA, complete cds /cds=(15,27
 39914_r_at Cluster Incl. W28976:54c5 Homo sapiens cDNA /gb=W28976 /gi=1308924 /u

Metagene 456

- 30** 37237_at Cluster Incl. D38293:Homo sapiens mRNA for clathrin-like protein, compl
 36102_at Cluster Incl. AF038962:Homo sapiens voltage dependent anion channel pro
 37297_at Cluster Incl. AL049422:Homo sapiens mRNA; cDNA DKFZp586A191 (from
 clone
 38377_at Cluster Incl. U47742:Human monocytic leukaemia zinc finger protein (MOZ
35 1696_at D29013 /FEATURE= /DEFINITION=HUMLNCA Human mRNA for DNA polymerase
 beta
 1052_s_at M83667 /FEATURE=mRNA /DEFINITION=HUMNFIL6BA Human NF-IL6-beta
 protein
 840_at U47742 /FEATURE= /DEFINITION=HSU47742 Human monocytic leukaemia zinc fing

Metagene 457

- 36703_at Cluster Incl. U86358:Human chemokine (TECK) mRNA, complete cds /cds=(0,
5 39260_at Cluster Incl. U59185:Human putative monocarboxylate transporter (MCT) m
41381_at Cluster Incl. AB002306:Human mRNA for KIAA0308 gene, partial cds /cds=(
36864_at Cluster Incl. AJ001625:Homo sapiens mRNA for Pex3 protein /cds=(63,1184
37563_at Cluster Incl. AB007871:Homo sapiens KIAA0411 mRNA, complete cds /cds=(0
41744_at Cluster Incl. AF070533:Homo sapiens clone 24619 mRNA sequence /cds=UNKN
10 34884_at Cluster Incl. D90282:Human carbamyl phosphate synthetase I (EC 6.3.4.16
1527_s_at U50527 /FEATURE= /DEFINITION=HSU50527 Human BRCA2 region, mRNA
sequenc

Metagene 458

- 15**
38610_s_at Cluster Incl. X14487:Human gene for acidic (type I) cytokeratin 10 /c
39751_at Cluster Incl. AF052182:Homo sapiens clone 24590 mRNA sequence /cds=UNKN
41198_at Cluster Incl. AF055008:Homo sapiens clone 24720 epithelin 1 and 2 mRNA,
1191_s_at AB003102 /FEATURE= /DEFINITION=AB003102 Homo sapiens mRNA for 26S
20 prot

Metagene 459

- 35868_at Cluster Incl. M91211:Human receptor for advanced glycosylation end prod
25 37462_i_at Cluster Incl. L21990:Human spliceosomal protein (SAP 62) gene, comple
41004_at Cluster Incl. U43431:Human DNA topoisomerase III mRNA, complete cds /cd
41114_at Cluster Incl. AB018350:Homo sapiens mRNA for KIAA0807 protein, partial
41869_at Cluster Incl. U78310:Homo sapiens pescadillo mRNA, complete cds /cds=(5
31837_at Cluster Incl. U62317:Chromosome 22q13 BAC Clone CIT987SK-384D8 complete
30 32032_at Cluster Incl. L77566:Homo sapiens DGS-I mRNA, 3 end /cds=UNKNOWN
/gb=L
32095_at Cluster Incl. AB018267:Homo sapiens mRNA for KIAA0724 protein, complete
34185_at Cluster Incl. W22541:69B4 Homo sapiens cDNA /clone=(not-directional) /g
34705_at Cluster Incl. AJ224335:Homo sapien mRNA for putative secretory protein,
35 35191_at Cluster Incl. AB002373:Human mRNA for KIAA0375 gene, complete cds /cds=
35983_at Cluster Incl. AC004528:Homo sapiens chromosome 19, cosmid R32184 /cds=(
37269_at Cluster Incl. D38496:Human mRNA for LZTR-1, complete cds /cds=(862,2520
38340_at Cluster Incl. AB014555:Homo sapiens mRNA for KIAA0655 protein, partial
40842_at Cluster Incl. M60784:Human U1 snRNP-specific protein A gene /cds=(137,9

- 41160_at Cluster Incl. AC005943:Homo sapiens chromosome 19, cosmid R30538 /cds=(
 41753_at Cluster Incl. U48734:Human non-muscle alpha-actinin mRNA, complete cds
 32151_at Cluster Incl. X82260:H.sapiens mRNA for RanGTPase activating protein 1
 32852_at Cluster Incl. U78678:Human thioredoxin mRNA, nuclear gene encoding mito
5 35826_at Cluster Incl. AF040253:Homo sapiens transcription factor Tat-CT1 mRNA,
 38464_at Cluster Incl. X87237:H.sapiens mRNA for processing a-glucosidase I /cds
 39141_at Cluster Incl. AF027302:Homo sapiens TNF-alpha stimulated ABC protein (A
 39824_at Cluster Incl. AI391564:tg16b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41804_at Cluster Incl. W80358:zh49a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
10 1091_at M65066 /FEATURE= /DEFINITION=HUMRIB Human cAMP-dependent protein kinase
 505_at U43077 /FEATURE= /DEFINITION=HSU43077 Human CDC37 homolog mRNA,
 complete
 320_at D83703 /FEATURE= /DEFINITION=D83703 Homo sapiens mRNA for peroxisome asse

15 Metagene 460

 31342_at Cluster Incl. X85019:H.sapiens mRNA for UDP-GalNAc-polypeptide N-acetyl
 31451_at Cluster Incl. U62794:Human CDC42 GAP-related protein mRNA, partial cds
 32996_g_at Cluster Incl. AC003079:Human BAC clone GS303P24 from 7q21-22 /cds=(0,
20 35520_at Cluster Incl. AI701514:we35h02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 36337_at Cluster Incl. AI760801:wi67f11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32919_at Cluster Incl. AC004010:Human BAC clone GS099H08 /cds=(0,1568) /gb=AC004
 34505_at Cluster Incl. AL109725:Homo sapiens mRNA full length insert cDNA clone
 35884_at Cluster Incl. Y07829:Homo sapiens RFB30 gene for RING finger protein /c
25 40681_at Cluster Incl. AB008375:Homo sapiens mRNA for osteoblast specific cystei
 41076_at Cluster Incl. AF099730:Homo sapiens connexin 31 (GJB3) gene, complete c
 33843_g_at Cluster Incl. AC004472:Homo sapiens chromosome 9, P1 clone 11659 /cds
 32505_at Cluster Incl. W28652:50f5 Homo sapiens cDNA /gb=W28652 /gi=1308663 /ug=
 33142_at Cluster Incl. AF034633:Homo sapiens orphan G protein-coupled receptor (
30 2060_at M13995 /FEATURE=mRNA /DEFINITION=HUMBCL2B Human B-cell
 leukemia/lymphoma
 2041_i_at M14752 /FEATURE= /DEFINITION=HUMABLA Human c-abl gene, complete
 cds

35 Metagene 461

 33503_at Cluster Incl. W29105:56d8 Homo sapiens cDNA /gb=W29105 /gi=1309071 /ug=
 41108_at Cluster Incl. Y14391:Homo sapiens mRNA for putative GTP-binding protein
 38719_at Cluster Incl. U03985:Human N-ethylmaleimide-sensitive factor mRNA, part

38053_s_at Cluster Incl. AF015767:Homo sapiens brain and reproductive organ-expr
109_at Z97074 /FEATURE= /DEFINITION=HSRAB9P40 Homo sapiens mRNA for Rab9 effecto

Metagene 462

5

35414_s_at Cluster Incl. U77914:Human soluble protein Jagged mRNA, partial cds /
36790_at Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,114
36791_g_at Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1
36792_at Cluster Incl. Z24727:H.sapiens tropomyosin isoform mRNA, complete CDS /
10 37422_at Cluster Incl. S71018:cyclophilin C [human, kidney, mRNA, 883 nt] /cds=(
36550_at Cluster Incl. AL049538:Human DNA sequence from clone 117516 on chromoso
37283_at Cluster Incl. X82209:H.sapiens MN1 mRNA /cds=(887,4915) /gb=X82209 /gi=
38643_at Cluster Incl. W87466:zh67c05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
38653_at Cluster Incl. D11428:Homo sapiens mRNA for PMP-22(PAS-II/SR13/Gas-3), c
15 39071_at Cluster Incl. M14648:Human cell adhesion protein (vitronectin) receptor
39754_at Cluster Incl. X53002:Human mRNA for integrin beta-5 subunit /cds=(336,2
32818_at Cluster Incl. X78565:H.sapiens mRNA for tenascin-C, 7560bp /cds=(313,69
32838_at Cluster Incl. S67247:smooth muscle myosin heavy chain isoform SMemb [hu
33431_at Cluster Incl. U05291:Human fibromodulin mRNA, partial cds /cds=(0,177)
20 36142_at Cluster Incl. X79204:H.sapiens SCA1 mRNA for ataxin /cds=(935,3385) /gb
37762_at Cluster Incl. Y07909:H.sapiens mRNA for Progression Associated Protein
38422_s_at Cluster Incl. U29332:Homo sapiens heart protein (FHL-2) mRNA, complet
38465_at Cluster Incl. M37721:Human peptidylglycine alpha-amidating monooxygenas
38761_s_at Cluster Incl. AA487755:ab13f01.r1 Homo sapiens cDNA, 5 end /clone=IM
25 41273_at Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clon
2058_s_at M35011 /FEATURE= /DEFINITION=HUMIBSUB Human integrin beta-5 subunit
mR
1507_s_at D11151 /FEATURE=_expandCDS /DEFINITION=HUMETAR8 Human DNA for
endothel
30 273_g_at K02054 /FEATURE=mRNA /DEFINITION=HUMGRP5E Human gastrin-
releasing pepti

Metagene 463

35 31431_at Cluster Incl. U12255:Human IgG Fc receptor hFcRn mRNA, complete cds /cd
31731_at Cluster Incl. AF013956:Homo sapiens Polycomb 2 homolog (hPc2) mRNA, com
39235_at Cluster Incl. AC003038:Human DNA from chromosome 19-specific cosmid R30
36531_r_at Cluster Incl. AC005757:Homo sapiens chromosome 19, cosmid R32611 /cds
36554_at Cluster Incl. Y15521:Homo sapiens ASMTL gene /cds=(0,1889) /gb=Y15521 /

- 39075_at Cluster Incl. AF040958:Homo sapiens lysosomal neuraminidase precursor,
 33414_at Cluster Incl. X57398:Human mRNA for pM5 protein /cds=(0,3572) /gb=X5739
 33888_at Cluster Incl. X82207:H.sapiens mRNA for beta-actin (PC3) /cds=(56,
 38372_at Cluster Incl. U66042:Human clone 191B7 placenta expressed mRNA from chr
5 38373_g_at Cluster Incl. U66042:Human clone 191B7 placenta expressed mRNA from c
 39863_at Cluster Incl. AB002294:Human mRNA for KIAA0296 gene, complete cds /cds=
 40280_at Cluster Incl. U72508:Human B7 mRNA, complete cds /cds=(112,1050) /gb=U7
 40626_at Cluster Incl. AI693193:wd68f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41310_f_at Cluster Incl. X12794:Human v-erbA related ear-2 gene /cds=(0,1211) /g
10 1749_at AD000092 /FEATURE=cds#4 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro
 1315_at D78361 /FEATURE= /DEFINITION=HUMODAZ Human mRNA for ornithine decarboxyl
 1218_at X12794 /FEATURE=cds /DEFINITION=HSEAR2 Human v-erbA related ear-2 gene
 634_at L41351 /FEATURE=mRNA /DEFINITION=HUMPROS Homo sapiens prostatic mRNA,
 com
15 497_at U32680 /FEATURE= /DEFINITION=HSU32680 Human CLN3 mRNA, complete cds
 362_at Z15108 /FEATURE=cds /DEFINITION=HSPKCZ H.sapiens mRNA for protein kinase
 318_at D64142 /FEATURE=mRNA /DEFINITION=D64142 Human mRNA for histone H1x,
 compl
 180_at S82470 /FEATURE= /DEFINITION=S82470 BB1=malignant cell expression-enhance
20
 Metagene 464
 41107_at Cluster Incl. AB002372:Human mRNA for KIAA0374 gene, complete cds /cds=
 35653_at Cluster Incl. U28963:Human Gps2 (GPS2) mRNA, complete cds /cds=(90,1073
25 36008_at Cluster Incl. AF041434:Homo sapiens potentially prenylated protein tyro
 39176_f_at Cluster Incl. M54994:Human bile salt-activated lipase (BAL) mRNA, com
 41497_at Cluster Incl. AI401296:tg92c03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 Metagene 465
30
 36392_at Cluster Incl. U09413:Human zinc finger protein ZNF135 mRNA, complete cd
 39967_at Cluster Incl. AB019527:Homo sapiens mRNA for LDOC1 protein, complete cd
 40701_at Cluster Incl. U75362:Homo sapiens isopeptidase T-3 (ISOT-3) mRNA, compl
 33319_at Cluster Incl. AF009674:Homo sapiens axin (AXIN) mRNA, partial cds /cds=
35 1562_g_at U27193 /FEATURE= /DEFINITION=HSU27193 Human protein-tyrosine
 phosphata
 1171_s_at Transcription Factor Oct-1a/1b, Alt. Splice 2, Oct-1b
 Metagene 466

	39994_at	Cluster Incl. D10925:Human mRNA for HM145 /cds=(22,1089) /gb=D10925 /gi
	40401_at	Cluster Incl. AL050069:Homo sapiens mRNA; cDNA DKFZp566A0946 (from clon
5	32066_g_at	Cluster Incl. S68134:CREM=cyclic AMP-responsive element modulator bet
	36472_at	Cluster Incl. U32849:Homo sapiens Nmi mRNA, complete cds /cds=(280,1203
	40771_at	Cluster Incl. Z98946:Human DNA sequence from clone 376D21 on chromosome
	35353_at	Cluster Incl. D11094:Human mRNA for MSS1, complete cds /cds=(66,1367) /
	41549_s_at	Cluster Incl. AF091077:Homo sapiens clone 558 unknown mRNA, complete
10	32616_at	Cluster Incl. M16038:Human lyn mRNA encoding a tyrosine kinase /cds=(29
	2024_s_at	M79321 /FEATURE= /DEFINITION=HUMLYNTK Human Lyn B protein mRNA, comple
	1848_at	M22995 /FEATURE= /DEFINITION=HUMKREV1A Human ras-related protein (Krev-1
	1456_s_at	M63838 /FEATURE= /DEFINITION=HUMIFI16A Human interferon-gamma
15	induced	
	1402_at	M16038 /FEATURE= /DEFINITION=HUMLYN Human lyn mRNA encoding a tyrosine k
	Metagene 467	
20	31636_s_at	Cluster Incl. U09210:Human vesicular acetylcholine transporter mRNA,
	34089_at	Cluster Incl. AB028953:Homo sapiens mRNA for KIAA1030 protein, partial
	34146_at	Cluster Incl. AB019529:Homo sapiens mRNA for OGG1 protein type 2c, part
	34161_at	Cluster Incl. U39573:Human salivary peroxidase mRNA, complete cds /cds=
	33985_s_at	Cluster Incl. W28616:49b9 Homo sapiens cDNA /gb=W28616 /gi=1308564 /u
25	33986_r_at	Cluster Incl. W28616:49b9 Homo sapiens cDNA /gb=W28616 /gi=1308564 /u
	34902_at	Cluster Incl. AB007961:Homo sapiens mRNA, chromosome 1 specific transcr
	36307_at	Cluster Incl. D87468:Human mRNA for KIAA0278 gene, partial cds /cds=(0,
	39225_at	Cluster Incl. Y09443:H.sapiens mRNA for alkyl-dihydroxyacetonephosphate
	34832_s_at	Cluster Incl. AB018306:Homo sapiens mRNA for KIAA0763 protein, comple
30	35737_at	Cluster Incl. U90549:Human non-histone chromosomal protein (NHC) mRNA,
	38447_at	Cluster Incl. U08438:Human beta-adrenergic receptor kinase (ADRBK1) gen
	33151_s_at	Cluster Incl. W25932:15b1 Homo sapiens cDNA /gb=W25932 /gi=1306055 /u
	1796_s_at	U05681 /FEATURE=expanded_cds /DEFINITION=HSBCL3S2 Human proto-
	oncogene	
35	Metagene 468	
	36761_at	Cluster Incl. AL079276:Homo sapiens mRNA full length insert cDNA clone
	41655_at	Cluster Incl. AL034399:dA191P20.2 (novel Fibronectin type III domain co

- 33296_at Cluster Incl. AB020643:Homo sapiens mRNA for KIAA0836 protein, partial
 33766_at Cluster Incl. X77777:H.sapiens intestinal VIP receptor related protein
 35669_at Cluster Incl. AB014533:Homo sapiens mRNA for KIAA0633 protein, partial
 36074_at Cluster Incl. U12897:Homo sapiens IPW mRNA sequence /cds=UNKNOWN
5 /gb=U1
 37891_at Cluster Incl. U79272:Human clone 23720 mRNA sequence /cds=UNKNOWN
 /gb=U
 37909_at Cluster Incl. L34155:Homo sapiens laminin-related protein (LamA3) mRNA,
 38274_at Cluster Incl. U09584:Human PL6 protein (PL6) mRNA, complete cds /cds=(2
10 38292_at Cluster Incl. AF093264:Homo sapiens homer-2b mRNA, complete cds /cds=(0
 39356_at Cluster Incl. AB007899:Homo sapiens KIAA0439 mRNA, partial cds /cds=(0,
 40445_at Cluster Incl. AF017307:Homo sapiens Ets-related transcription factor (E
 41728_at Cluster Incl. D63486:Human mRNA for KIAA0152 gene, complete cds /cds=(1
 32809_at Cluster Incl. AL118582:DKFZp761B0810_r1 Homo sapiens cDNA, 5 end /clon
15 34798_at Cluster Incl. Z35491:H.sapiens mRNA for novel glucocorticoid receptor-a
 34873_at Cluster Incl. Y16241:Homo sapiens mRNA for nebullette /cds=(397,3441) /g
 39087_at Cluster Incl. U28249:Human 11kd protein mRNA, complete cds /cds=(259,59
 39103_s_at Cluster Incl. H98552:yv97h03.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 40220_at Cluster Incl. AB021179:Homo sapiens mRNA for HEXIM1 protein, complete c
20 41816_at Cluster Incl. AL049851:Human DNA sequence from clone 889J22B on chromos
 33136_at Cluster Incl. AL031714:Human DNA sequence from clone 356B7 on chromosom

Metagene 469

- 25** 37058_at Cluster Incl. Y00317:Human mRNA for liver microsomal UDP-glucuronosyltr
 33880_at Cluster Incl. D89053:Homo sapiens mRNA for Acyl-CoA synthetase 3, compl
 33881_at Cluster Incl. AA977580:on61b02.s1 Homo sapiens cDNA, 3 end /clone=IMAG

Metagene 470

- 30**
 32323_at Cluster Incl. M63582:Human preprothyrotropin-releasing hormone gene /cd
 36267_at Cluster Incl. X77909:H.sapiens IKBL mRNA /cds=(68,1213) /gb=X77909 /gi=
 39587_at Cluster Incl. AJ005890:Homo sapiens mRNA for JM1 protein, complete CDS
 33741_at Cluster Incl. AI741756:wg22e12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35 33752_at Cluster Incl. AB020657:Homo sapiens mRNA for KIAA0850 protein, complete
 36916_at Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2

Metagene 471

- 31637_s_at Cluster Incl. X72631:H.sapiens mRNA encoding Rev-ErbAalpha /cds=UNKNO
 33586_at Cluster Incl. AF070620:Homo sapiens clone 24694 mRNA sequence /cds=UNKN
 34289_f_at Cluster Incl. D50920:Human mRNA for KIAA0130 gene, complete cds /cds=
 34290_f_at Cluster Incl. W29091:56c5 Homo sapiens cDNA /gb=W29091 /gi=1309057 /u
5 40787_at Cluster Incl. U90911:Human clone 23652 mRNA sequence /cds=UNKNOWN
 /gb=U
 32195_at Cluster Incl. AL049450:Homo sapiens mRNA; cDNA DKFZp586B1922 (from
 clon
 35846_at Cluster Incl. M24899:Human triiodothyronine (ear7) mRNA, complete cds /
10 38437_at Cluster Incl. X80199:H.sapiens MLN51 mRNA /cds=(233,1837) /gb=X80199 /g
 39155_at Cluster Incl. D67025:Homo sapiens mRNA for proteasome subunit p58, comp
 616_s_at M24748 /FEATURE=cds#2 /DEFINITION=HUMTHRA1A Human thyroid
 hormone recep
15 Metagene 472
 31320_at Cluster Incl. U18548:Human GPR12 G protein coupled-receptor gene, compl
 35104_r_at Cluster Incl. M26682:Human T-cell translocation gene 1 (Ttg-1) mRNA,
 35503_at Cluster Incl. M81590:Homo sapiens serotonin 1D receptor (5-HT1D~) mRNA,
20 32898_at Cluster Incl. U20582:Human actin-like peptide mRNA, partial cds /cds=(2
 33510_s_at Cluster Incl. U31216:Human metabotropic glutamate receptor 1 beta (mG
 34495_r_at Cluster Incl. AJ011733:Homo sapiens mRNA for synaptogyrin 4 protein /
 34926_at Cluster Incl. M28825:Human thymocyte antigen CD1a mRNA, complete cds /c
 35923_at Cluster Incl. D13305:Human mRNA for brain cholecystokinin receptor /cds
25 38229_at Cluster Incl. X90579:H.sapiens DNA for cyp related pseudogene /cds=UNKN
 33935_at Cluster Incl. AL035305:H.sapiens gene from PAC 102G20 /cds=(117,803) /g
 41347_at Cluster Incl. AI814659:wj75g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 255_s_at M13981 /FEATURE= /DEFINITION=HUMINHA Human inhibin A-subunit
 mRNA, comp
30 259_s_at M16441 /FEATURE=cds#2 /DEFINITION=HUMTNFAB Human tumor necrosis
 factor
 Metagene 473
35 41420_at Cluster Incl. AF055033:Homo sapiens clone 24645 insulin-like growth fac
 38650_at Cluster Incl. L27560:Human insulin-like growth factor binding protein 5
 1677_at M65062 /FEATURE= /DEFINITION=HUMIGFBP6 Human insulin-like growth factor
 1678_g_at M65062 /FEATURE= /DEFINITION=HUMIGFBP6 Human insulin-like growth
 facto

1601_s_at L27559 /FEATURE=mRNA /DEFINITION=HUMIGFBP04 Human insulin-like growth
 1396_at L27560 /FEATURE=mRNA /DEFINITION=HUMIGFBP5X Human insulin-like growth fa

5 Metagene 474

33499_s_at Cluster Incl. AF067420:Homo sapiens SNC73 protein (SNC73) mRNA, compl
 33500_i_at Cluster Incl. S71043:Ig alpha 2=immunoglobulin A heavy chain allotype
 33501_r_at Cluster Incl. S71043:Ig alpha 2=immunoglobulin A heavy chain allotype
 10 36021_at Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from
 clon
 37006_at Cluster Incl. AI660656:wf23c07.x1 Homo sapiens cDNA, 3 end /clone=IMAG

Metagene 475

15

37130_g_at Cluster Incl. AI936758:wp69b11.x1 Homo sapiens cDNA, 3 end /clone=IM
 37136_at Cluster Incl. AB000520:Homo sapiens mRNA for APS, complete cds /cds=(12
 41443_at Cluster Incl. U63127:Human SEC7 homolog Tic (TIC) mRNA, complete cds /c
 33223_at Cluster Incl. AB011133:Homo sapiens mRNA for KIAA0561 protein, partial
 20 33307_at Cluster Incl. AL022316:Human DNA sequence from clone 126B4 on chromosom
 34206_at Cluster Incl. AB018325:Homo sapiens mRNA for KIAA0782 protein, partial
 35179_at Cluster Incl. AB009598:Homo sapiens mRNA for glucuronyltransferase I, c
 36004_at Cluster Incl. AF074382:Homo sapiens Ikb kinase gamma subunit (IKK-gamma
 36058_at Cluster Incl. AL096741:Homo sapiens mRNA; cDNA DKFZp586O0223 (from

25

clon
 38290_at Cluster Incl. AF037195:Homo sapiens regulator of G protein signaling RG
 38297_at Cluster Incl. X98654:H.sapiens mRNA for DRES9 protein /cds=(189,3923) /
 40098_at Cluster Incl. AF001434:Human Hpast (HPAST) mRNA, complete cds /cds=(255
 40416_at Cluster Incl. U04847:Human Ini1 mRNA, complete cds /cds=(69,1226) /gb=U
 30 41734_at Cluster Incl. AB020677:Homo sapiens mRNA for KIAA0870 protein, complete
 32166_at Cluster Incl. AB028950:Homo sapiens mRNA for KIAA1027 protein, partial
 33349_at Cluster Incl. AL049378:Homo sapiens mRNA; cDNA DKFZp586I1518 (from clon
 37410_at Cluster Incl. AJ224358:Homo sapiens surf5a mRNA, clone 1de /cds=(218,64
 40206_at Cluster Incl. AI767675:wh38d11.x1 Homo sapiens cDNA, 3 end /clone=IMAG

35

1706_at U01337 /FEATURE=expanded_cds /DEFINITION=HSU01337 Human Ser/Thr protein
 1547_at U09607 /FEATURE= /DEFINITION=HSU09607 Human JAK family protein tyrosine
 1127_at L07597 /FEATURE= /DEFINITION=HUMS6KINA Homo sapiens ribosomal protein S6
 496_s_at U32324 /FEATURE= /DEFINITION=HSU32324 Human interleukin-11 receptor
 alp

371_at Z56281 /FEATURE=cds /DEFINITION=HSIRF3MR H.sapiens mRNA for interferon re

Metagene 476

- 5 36363_at Cluster Incl. U30930:Human UDP-Galactose ceramide galactosyl transferas
32331_at Cluster Incl. X60673:Human AK3 mRNA for adenylate kinase 3
/cds=UNKNOWN
35413_s_at Cluster Incl. AA258092:zs30g01.r1 Homo sapiens cDNA, 5 end /clone=IM
37156_at Cluster Incl. AF070641:Homo sapiens clone 24421 mRNA sequence /cds=UNKN
10 37162_at Cluster Incl. S72869:H4(D10S170)=putative cytoskeletal protein [human,
35211_at Cluster Incl. L07590:Human protein phosphatase 2A 130 kDa regulatory su
35638_at Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(4
37929_at Cluster Incl. AB017563:Homo sapiens IGSF4 gene /cds=(0,1328) /gb=AB0175
39692_at Cluster Incl. AL080209:Homo sapiens mRNA; cDNA DKFZp586F2423 (from
15 clon
40478_at Cluster Incl. AL021396:Human DNA sequence from clone 971N18 on chromoso
40990_at Cluster Incl. AF065389:Homo sapiens tetraspan NET-4 mRNA, complete cds
1269_at M61906 /FEATURE= /DEFINITION=HUMP13KIN Human P13-kinase associated p85 m
462_at U70862 /FEATURE= /DEFINITION=HSU70862 Human nuclear factor I B3 mRNA, com

20

Metagene 477

- 37498_at Cluster Incl. AL050404:Human DNA sequence from clone 955M13 on chromoso
31850_at Cluster Incl. M90656:Human gamma-glutamylcysteine synthetase (GCS) mRNA
25 34277_at Cluster Incl. AB018195:Homo sapiens ca xi mRNA for carbonic anhydrase-r
34724_at Cluster Incl. AI670100:wc11g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
40455_at Cluster Incl. AB020637:Homo sapiens mRNA for KIAA0830 protein, partial
37656_at Cluster Incl. D83782:Human mRNA for KIAA0199 gene, partial cds /cds=(0,
1649_at U61836 /FEATURE=mRNA /DEFINITION=HSU61836 Human putative cyclin G1 inter

30

Metagene 478

- 32394_s_at Cluster Incl. X55954:Human mRNA for HL23 ribosomal protein homologue
32395_r_at Cluster Incl. X55954:Human mRNA for HL23 ribosomal protein homologue
35 32435_at Cluster Incl. X63527:H.sapiens mRNA for ribosomal protein L19 /cds=(28,
36555_at Cluster Incl. AF044311:Homo sapiens gamma-synuclein gene, complete cds
38272_at Cluster Incl. AF038844:Homo sapiens MKP-1 like protein tyrosine phospho
38358_at Cluster Incl. AJ010840:Homo sapiens mRNA for ATP-dependent RNA helicase
38623_at Cluster Incl. AI014538:ou40e01.x1 Homo sapiens cDNA, 3 end /clone=IMAG

- 32191_at Cluster Incl. D13969:Human mRNA for Mel-18 protein, complete cds /cds=(
 32192_g_at Cluster Incl. D13969:Human mRNA for Mel-18 protein, complete cds /cds
 35741_at Cluster Incl. U85245:Human phosphatidylinositol-4-phosphate 5-kinase ty
 36181_at Cluster Incl. X82456:H.sapiens MLN50 mRNA /cds=(75,860) /gb=X82456 /gi=
5 40187_at Cluster Incl. AW016815:UI-H-BI0-aam-c-09-0-UI.s1 Homo sapiens cDNA, 3
 1309_at D26598 /FEATURE= /DEFINITION=HUMPSH1 Human mRNA for proteasome subunit H

Metagene 479

- 10** 38584_at Cluster Incl. AF026939:Homo sapiens CIG49 (cig49) mRNA, complete cds /c
 35718_at Cluster Incl. L22342:Human nuclear phosphoprotein mRNA, complete cds /c
 37641_at Cluster Incl. D28915:Human gene for hepatitis C-associated microtubular
 37353_g_at Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA, complet
 37360_at Cluster Incl. U66711:Human Ly-6-related protein (9804) gene, complete c
15 908_at M14660 /FEATURE=cds /DEFINITION=HUMISG2 Human ISG-54K gene (interferon st
 909_g_at M14660 /FEATURE=cds /DEFINITION=HUMISG2 Human ISG-54K gene
 (interferon

Metagene 480

- 20**
 41063_g_at Cluster Incl. AA037278:zc52c04.r1 Homo sapiens cDNA, 5 end /clone=IM
 41375_at Cluster Incl. AJ245416:Homo sapiens mRNA for G7b protein (G7b gene, loc
 33750_at Cluster Incl. X97198:H.sapiens mRNA for receptor phosphate PCP-2 /cds=(
 37216_at Cluster Incl. AB023180:Homo sapiens mRNA for KIAA0963 protein, complete
25 39067_at Cluster Incl. M27937:Human male-enhanced antigen mRNA (Mea), complete c
 39722_at Cluster Incl. AF044209:Homo sapiens nuclear receptor co-repressor N-CoR
 40489_at Cluster Incl. D31840:Human DRPLA mRNA for ORF, complete cds /cds=(238,3
 32842_at Cluster Incl. X89984:H.sapiens mRNA for BCL7A protein /cds=(953,1648) /
 37753_at Cluster Incl. U66617:Human SWI/SNF complex 60 KDa subunit (BAF60a) mRNA
30 39530_at Cluster Incl. L35240:Human enigma gene, complete cds /cds=(0,1367) /gb=
 39833_at Cluster Incl. R54564:yg81b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 33206_at Cluster Incl. C18655:C18655 Homo sapiens cDNA, 5 end /clone=GEN-565G08
 868_at U13991 /FEATURE= /DEFINITION=HSU13991 Human TATA-binding protein associat
 410_s_at X57152 /FEATURE=mRNA#1 /DEFINITION=HSCKIIBE Human gene for casein
35 kinas

Metagene 481

- 31472_s_at Cluster Incl. AF098641:Homo sapiens CD44 isoform RC (CD44) mRNA, comp

- 36759_at Cluster Incl. U29589:Human m3 muscarinic acetylcholine receptor (CHRM3)
- 39779_at Cluster Incl. U38847:Human TAR RNA loop binding protein (TRP-185) mRNA,
- 40423_at Cluster Incl. AB020710:Homo sapiens mRNA for KIAA0903 protein, partial
- 33410_at Cluster Incl. S66213:integrin alpha 6B [human, mRNA Partial, 528 nt] /c
- 5** 39556_at Cluster Incl. M96803:Human general beta-spectrin (SPTBN1) mRNA, complet
- 41266_at Cluster Incl. X53586:Human mRNA for integrin alpha 6 /cds=UNKNOWN /gb=X
- 2036_s_at M59040 /FEATURE= /DEFINITION=HUMCD44B Human cell adhesion molecule (CD
- 1125_s_at L05424 /FEATURE=cds#1 /DEFINITION=HUMSCG19 Human cell surface
- 10** glycopro
- 1126_s_at L05424 /FEATURE=cds#5 /DEFINITION=HUMSCG19 Human cell surface glycopro
- Metagene 482
- 15**
- 39605_at Cluster Incl. X74142:H.sapiens HBF-1 mRNA for transcription factor /cds
- 41637_at Cluster Incl. AF108145:Homo sapiens MYLE mRNA, complete cds /cds=(52,25
- 33836_at Cluster Incl. AC002045:Human Chromosome 16 BAC clone CIT987SK-A-589H1 /
- 20** 1563_s_at M58286 /FEATURE= /DEFINITION=HUMTNFRB Homo sapiens tumor necrosis fact
- 897_at L33243 /FEATURE=mRNA /DEFINITION=HUMPKD1A Homo sapiens polycystic kidney
- Metagene 483
- 25**
- 31638_at Cluster Incl. AC005329:Homo sapiens chromosome 19, cosmid R34382 /cds=(
- 36519_at Cluster Incl. M13194:Human excision repair protein (ERCC1) mRNA, comple
- 37992_s_at Cluster Incl. AI436567:ti03b09.x1 Homo sapiens cDNA, 3 end /clone=IM
- 39443_s_at Cluster Incl. M19961:Human cytochrome c oxidase subunit Vb (coxVb) mR
- 30** 33409_at Cluster Incl. AA158243:zo76c01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 34893_at Cluster Incl. AI557064:PT2.1_13_A12.r Homo sapiens cDNA, 3 end /clone_
- 35774_r_at Cluster Incl. AA527880:nh86h10.s1 Homo sapiens cDNA, 3 end /clone=IM
- 38451_at Cluster Incl. T58471:yb61c11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
- 32522_f_at Cluster Incl. M20469:Human brain-type clathrin light-chain b mRNA, co
- 35** 1902_at M13194 /FEATURE=mRNA /DEFINITION=HUMERCC1 Human excision repair protein
- 1878_g_at M13194 /FEATURE=mRNA /DEFINITION=HUMERCC1 Human excision repair protei
- Metagene 484

- 32670_at Cluster Incl. L38969:Homo sapiens thrombospondin 3 (THBS3) gene, comple
 32689_s_at Cluster Incl. D86096:Human DNA for prostaglandin E receptor EP3 subty
 33291_at Cluster Incl. AF081195:Homo sapiens calcium and DAG-regulated guanine n
5 1790_s_at Cell Division Cycle Protein 2-Related Protein Kinase (Pisslre)

Metagene 485

- 39364_s_at Cluster Incl. Y18207:Homo sapiens mRNA for protein phosphatase 1 (PPP
10 33370_r_at Cluster Incl. U60205:Human methyl sterol oxidase (ERG25) mRNA, comple
 36982_at Cluster Incl. U30888:Human tRNA-guanine transglycosylase mRNA, complete
 40553_at Cluster Incl. AI742087:wg38g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40592_at Cluster Incl. L13329:Homo sapiens iduronate-2-sulfatase (IDS) gene /cds
 41287_s_at Cluster Incl. W28510:48f3 Homo sapiens cDNA /gb=W28510 /gi=1308521 /u
15 1719_at U61981 /FEATURE= /DEFINITION=HSU61981 Human putative mismatch repair/bin

Metagene 486

- 34506_at Cluster Incl. M13928:Human delta-aminolevulinate dehydratase mRNA, comp
20 37886_at Cluster Incl. AB015332:Homo sapiens HRIHFB2018 mRNA, partial cds /cds=(
 33417_at Cluster Incl. D31886:Human mRNA for KIAA0066 gene, partial cds /cds=(0,
 36632_at Cluster Incl. U00957:Human clone KDB1.2 (CAC)n/(GTG)n repeat-containing
 37048_at Cluster Incl. U58970:Human putative outer mitochondrial membrane 34 kDa
 40935_at Cluster Incl. W28516:47h7 Homo sapiens cDNA /gb=W28516 /gi=1308464 /ug=
25 33124_at Cluster Incl. AB000450:Homo sapiens mRNA for VRK2, complete cds /cds=(1
 1917_at X03484 /FEATURE=cds /DEFINITION=HSRAFR Human mRNA for raf oncogene
 1615_at Z23115 /FEATURE=cds /DEFINITION=HSBCLXL H.sapiens bcl-xL mRNA
 1454_at U68019 /FEATURE= /DEFINITION=HSU68019 Homo sapiens mad protein homolog (
 673_at J04031 /FEATURE= /DEFINITION=HUMMDMCSF Human methylenetetrahydrofolate de
30

Metagene 487

- 34533_at Cluster Incl. AF038192:Homo sapiens clone 23808 mRNA sequence /cds=UNKN
 37817_at Cluster Incl. AF052087:Homo sapiens clone 23604 mRNA sequence /cds=UNKN
35 1683_at X69950 /FEATURE=exon#2 /DEFINITION=HSWT1WIT H.sapiens DNA sequence for W

Metagene 488

- 35411_at Cluster Incl. AB018551:Homo sapiens ATPBL mRNA for coiled-coil protein,

- 41106_at Cluster Incl. AF022797:Homo sapiens intermediate conductance calcium-ac
 41414_at Cluster Incl. AL050346:Novel human gene mapping to chromosome 22 /cds=(3
 33816_at Cluster Incl. AF020267:Homo sapiens myosin-IXb splice variant (Myo9b) m
 34259_at Cluster Incl. AB014564:Homo sapiens mRNA for KIAA0664 protein, partial
5 35629_at Cluster Incl. AL022238:dJ1042K10.3 (novel protein) /cds=(0,731) /gb=AL0
 38007_at Cluster Incl. L11353:Human moesin-ezrin-radixin-like protein mRNA, comp
 38278_at Cluster Incl. M62324:Human modulator recognition factor I (MRF-1) mRNA,
 38617_at Cluster Incl. D45906:Homo sapiens mRNA for LIMK-2, complete cds /cds=(1
 32806_at Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mR
10 32856_at Cluster Incl. AB020626:Homo sapiens mRNA for KIAA0819 protein, partial
 35796_at Cluster Incl. Y17169:Homo sapiens mRNA for A6 related protein /cds=(104
 38750_at Cluster Incl. U97669:Homo sapiens Notch3 (NOTCH3) mRNA, complete cds /c
 38788_at Cluster Incl. M82827:Human fusion protein mRNA, complete cds /cds=(324,
 1729_at L41690 /FEATURE= /DEFINITION=HUMTRADD Homo sapiens TNF receptor-1 associ
15 1622_at D87116 /FEATURE= /DEFINITION=D87116 Human mRNA for MAP kinase kinase 3b
 844_at U48707 /FEATURE= /DEFINITION=HSU48707 Human protein phosphatase-1 inhibit
 241_g_at M64231 /FEATURE=mRNA /DEFINITION=HUMSPERSYN Human spermidine
 synthase g

20 Metagene 489

 34069_s_at Cluster Incl. S79325:SYT...SSX1 {translocation breakpoint} [human, sy
 38171_at Cluster Incl. U94747:Human WD repeat protein HAN11 mRNA, complete cds /
 39251_at Cluster Incl. M74091:Human cyclin mRNA /cds=UNKNOWN /gb=M74091
25 /gi=1806
 32725_at Cluster Incl. AF042083:Homo sapiens BH3 interacting domain death agonis

 Metagene 490

30 31663_at Cluster Incl. AB016902:Homo sapiens HGC6.3 mRNA, complete cds /cds=(287
 35544_at Cluster Incl. Y16280:Homo sapiens mRNA for G protein-coupled receptor E
 34496_at Cluster Incl. AB017165:Homo sapiens PIG-L mRNA, complete cds /cds=(5,76
 39322_at Cluster Incl. AL109693:Homo sapiens mRNA full length insert cDNA clone
 41003_at Cluster Incl. U41816:Human C-1 mRNA, complete cds /cds=(11,403) /gb=U41
35 33237_at Cluster Incl. AB018344:Homo sapiens mRNA for KIAA0801 protein, complete
 36865_at Cluster Incl. AB018302:Homo sapiens mRNA for KIAA0759 protein, partial
 40076_at Cluster Incl. AF004430:Homo sapiens hD54+ins2 isoform (hD54) mRNA, comp
 40110_at Cluster Incl. U49283:Human NAD+-specific isocitrate dehydrogenase beta
 40152_r_at Cluster Incl. Z48054:H.sapiens mRNA for peroxisomal targeting signal

	35850_at	Cluster Incl. AI950382:wp10g06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	36173_r_at	Cluster Incl. AF002163:Homo sapiens delta-adaptin mRNA, complete cds
	38741_at	Cluster Incl. U70728:Human cytohesin-2 mRNA, complete cds /cds=(158,136
	1805_g_at	X07730 /FEATURE= /DEFINITION=HSPSA Human mRNA for prostate specific
5	an	
	Metagene 491	
	31497_at	Cluster Incl. U19142:Human GAGE-1 protein mRNA, complete cds /cds=(48,4
10	32426_f_at	Cluster Incl. M77481:Human antigen (MAGE-1) gene, complete cds /cds=(
	33058_at	Cluster Incl. Y17282:Homo sapiens mRNA for cytokeratin type II /cds=(18
	34164_at	Cluster Incl. R42599:yg02e11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	34539_at	Cluster Incl. AF065854:Homo sapiens OR7E12P pseudogene, complete sequen
	35534_at	Cluster Incl. AB011086:Homo sapiens mRNA for KIAA0514 protein, complete
15	36302_f_at	Cluster Incl. U10688:Human MAGE-4b antigen (MAGE4b) gene, complete cd
	36702_at	Cluster Incl. AJ010277:Homo sapiens mRNA for TBX19 protein /cds=(51,139
	38154_at	Cluster Incl. AF038199:Homo sapiens clone 23728 mRNA sequence /cds=UNKN
	38162_at	Cluster Incl. AF007156:Homo sapiens clone 23617 unknown mRNA, partial c
	38193_at	Cluster Incl. X96754:H.sapiens gene encoding kappa light chain constant
20	38854_at	Cluster Incl. AB014535:Homo sapiens mRNA for KIAA0635 protein, complete
	38925_at	Cluster Incl. X95239:H.sapiens mRNA for cysteine-rich secretory protein
	39306_at	Cluster Incl. AF052514:Homo sapiens thymus specific serine peptidase mR
	40402_at	Cluster Incl. X91117:H.sapiens HG NET gene exon 1 /cds=(49,1902) /gb=X9
	40740_at	Cluster Incl. M93650:Human paired box gene (PAX6) homologue, complete c
25	33808_at	Cluster Incl. AL022721:dJ109F14.1.1 (Transcriptional Enhancer Factor TE
	36557_at	Cluster Incl. M92303:Human voltage-dependent calcium channel beta-1 sub
	38991_at	Cluster Incl. U55980:HSU55980 Homo sapiens cDNA, 3 end /clone=25453 /c
	39399_at	Cluster Incl. AJ006417:Homo sapiens mRNA for beta-tubulin folding cofac
	40507_at	Cluster Incl. K03195:Human (HepG2) glucose transporter gene mRNA, compl
30	32220_at	Cluster Incl. D63874:Human mRNA for HMG-1, complete cds /cds=(76,723) /
	1967_f_at	U18334 /FEATURE=cds /DEFINITION=HSUNOSIIC1 Human nitric oxide
	synthase	
	222_at	S79639 /FEATURE= /DEFINITION=S79639 EXT1=putative tumour suppressor/hered
35	Metagene 492	
	35021_at	Cluster Incl. U89326:Homo sapiens bone morphogenetic protein receptor t
	41428_at	Cluster Incl. AF104942:Homo sapiens ABC transporter MOAT-C (MOAT-C)
	mRN	

- 32598_at Cluster Incl. D83018:Homo sapiens mRNA for nel-related protein 2, compl
1932_at U83661 /FEATURE= /DEFINITION=HSU83661 Homo sapiens multidrug resistance
1933_g_at U83661 /FEATURE= /DEFINITION=HSU83661 Homo sapiens multidrug
resistanc
- 5** 1433_g_at U68019 /FEATURE= /DEFINITION=HSU68019 Homo sapiens mad protein
homolog
- Metagene 493
- 10** 31526_f_at Cluster Incl. X63547:H.sapiens mRNA for tre oncogene (clone 213) /cds
34647_at Cluster Incl. X52104:Human mRNA for p68 protein /cds=(175,2019) /gb=X52
34231_at Cluster Incl. AF074606:Homo sapiens histone acetyltransferase (HBO1) mR
34677_f_at Cluster Incl. AJ012755:Homo sapiens mRNA for TL132 /cds=(1241,2305) /
35618_at Cluster Incl. D29677:Human mRNA for KIAA0054 gene, complete cds /cds=(1
15 39073_at Cluster Incl. AL038662:DKFZp566I0346_r1 Homo sapiens cDNA, 5 end /clon
39707_at Cluster Incl. AB014547:Homo sapiens mRNA for KIAA0647 protein, partial
41159_at Cluster Incl. D21260:Human mRNA for KIAA0034 gene, complete cds /cds=(1
33354_at Cluster Incl. AA630312:ac08f05.s1 Homo sapiens cDNA, 3 end /clone=IMAG
33415_at Cluster Incl. X58965:H.sapiens RNA for nm23-H2 gene /cds=(72,530) /gb=X
20 34397_at Cluster Incl. AF069250:Homo sapiens okadaic acid-inducible phosphoprote
35321_at Cluster Incl. AB004884:Homo sapiens mRNA for PKU-alpha, partial cds /cd
35760_at Cluster Incl. AF087135:Homo sapiens F1FO-type ATPase subunit d mRNA, nu
38470_i_at Cluster Incl. D86981:Human mRNA for KIAA0228 gene, partial cds /cds=(
38762_at Cluster Incl. AF083255:Homo sapiens RNA helicase-related protein mRNA,
25 39152_f_at Cluster Incl. U06632:Homo sapiens p80-coilin mRNA, complete cds /cds=
40533_at Cluster Incl. AI417038:tg78b04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
41824_at Cluster Incl. AI140114:qa95c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
33107_at Cluster Incl. AB020705:Homo sapiens mRNA for KIAA0898 protein, partial
2037_s_at M60725 /FEATURE= /DEFINITION=HUMP70S6KB Human p70 ribosomal S6
30 kinase
1980_s_at X58965 /FEATURE= /DEFINITION=HSNM23H2G H.sapiens RNA for nm23-H2
gene
1985_s_at X73066 /FEATURE=cds /DEFINITION=HSNM23H1A H.sapiens NM23-H1
mRNA
35 1521_at X17620 /FEATURE=mRNA /DEFINITION=HSNM23 Human mRNA for Nm23 protein,
inv
1192_at AB003103 /FEATURE= /DEFINITION=AB003103 Homo sapiens mRNA for 26S protea

Metagene 494

- 31544_at Cluster Incl. L13203:Human HNF-3/fork-head homolog-3 HFH-3 mRNA, comple
 34430_at Cluster Incl. U70732:Human glutamate pyruvate transaminase (GPT) gene,
 40291_r_at Cluster Incl. L13972:Homo sapiens beta-galactoside alpha-2,3-sialyltr
 5 36035_at Cluster Incl. AB002135:Homo sapiens mRNA for glycosylphosphatidylinosit

Metagene 495

- 10 31785_f_at Cluster Incl. U92817:Homo sapiens unnamed HERV-H protein mRNA, comple
 32971_at Cluster Incl. L27479:Human X123 mRNA, 3 end /cds=(2,739) /gb=L27479 /g
 35858_at Cluster Incl. AA996066:os33d01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 35955_at Cluster Incl. S80864:cytochrome c-like polypeptide [human, lung adenoca
 37129_at Cluster Incl. AI936758:wp69b11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39995_s_at Cluster Incl. U13395:Human oxidoreductase (HHCMA56) mRNA, complete cd
 15 41387_r_at Cluster Incl. AB002344:Human mRNA for KIAA0346 gene, partial cds /cds
 41406_at Cluster Incl. AL080172:Homo sapiens mRNA; cDNA DKFZp434G231 (from
 clone
 31904_at Cluster Incl. U67733:Human cGMP-stimulated 3,5 -cyclic nucleotide phosp
 35137_at Cluster Incl. X69090:H.sapiens mRNA for skeletal muscle 190kD protein /
 20 36815_at Cluster Incl. AF038185:Homo sapiens clone 23700 mRNA sequence /cds=UNKN
 38320_s_at Cluster Incl. L11706:Human hormone-sensitive lipase (LIPE) gene, comp
 39044_s_at Cluster Incl. D73409:Homo sapiens mRNA for diacylglycerol kinase delt
 40446_at Cluster Incl. AL021366:cICK0721Q.4.1 (PHD finger protein 2) (isoform 2)
 40466_at Cluster Incl. Z74792:H.sapiens mRNA for CCAAT transcription binding fac
 25 41130_at Cluster Incl. Y08698:H.sapiens mRNA for RanBP3 (59 kDa) /cds=(20,1708)
 32163_f_at Cluster Incl. AA216639:zq95f07.s1 Homo sapiens cDNA, 3 end /clone=IM
 33398_at Cluster Incl. AB014570:Homo sapiens mRNA for KIAA0670 protein, partial
 38810_at Cluster Incl. AF039241:AF039241 Homo sapiens cDNA /clone=11-67js /gb=AF
 41264_at Cluster Incl. AL050172:Homo sapiens mRNA; cDNA DKFZp586F1322 (from
 30 clon
 41483_s_at Cluster Incl. X56681:Human junD mRNA /cds=(174,1217) /gb=X56681 /gi=3
 1612_s_at X56681 /FEATURE=mRNA /DEFINITION=HSJUNDR Human junD mRNA

Metagene 496

- 35 34262_at Cluster Incl. Y15909:Homo sapiens mRNA for dia-156 protein /cds=(350,36
 36536_at Cluster Incl. AF070614:Homo sapiens clone 24732 unknown mRNA, partial c
 36890_at Cluster Incl. AF001691:Homo sapiens 195 kDa cornified envelope precurs
 39388_at Cluster Incl. AA902713:ok71f11.s1 Homo sapiens cDNA, 3 end /clone=IMAG

- 39416_at Cluster Incl. U90913:Human clone 23665 mRNA sequence /cds=UNKNOWN
/gb=U
- 39690_at Cluster Incl. AF002282:Homo sapiens alpha-actinin-2 associated LIM prot
- 32206_at Cluster Incl. AB007920:Homo sapiens mRNA for KIAA0451 protein, complete
- 5** 33357_at Cluster Incl. AB011159:Homo sapiens mRNA for KIAA0587 protein, complete
- 36577_at Cluster Incl. Z24725:H.sapiens mitogen inducible gene mig-2, complete C
- 36588_at Cluster Incl. AB018353:Homo sapiens mRNA for KIAA0810 protein, partial
- 36601_at Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /
- 37308_at Cluster Incl. AI888084;wm29g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 10** 40612_at Cluster Incl. AB029040:Homo sapiens mRNA for KIAA1117 protein, partial
- 1495_at M34057 /FEATURE= /DEFINITION=HUMTGFB1B Human transforming growth factor-
- 1058_at S69790 /FEATURE= /DEFINITION=S69790 Brush-1=tumor suppressor {3 region}

TABLE 6 Characteristics of Patient Samples for Example 3B

TABLE 7 Metagene Characteristics for Breast Cancer Recurrence Study in Example 3B

Table 8: List of Genes Within the 498 Metagenes Generated by the Analysis of Breast Cancer Recurrence

METAGENE 1 :

5	36488_at	Cluster Incl. AB011542:Homo sapiens mRNA for MEGF9, partial cds /cds=(0
	32776_at	Cluster Incl. M35416:Human GTP-binding protein (RALB) mRNA, complete cd
	36123_at	Cluster Incl. D87292:Homo sapiens mRNA for rhodanese, complete cds /cds
	40898_at	Cluster Incl. U46751:Human phosphotyrosine independent ligand p62 for t
10	1825_at L33075	/FEATURE= /DEFINITION=HUMIQGA Homo sapiens ras GTPase-activating-

METAGENE 2 :

	36711_at	Cluster Incl. AL021977:bK447C4.1 (novel MAFF (v-maf musculoaponeurotic
15	37863_at	Cluster Incl. J04076:Human early growth response 2 protein (EGR2) mRNA,
	40448_at	Cluster Incl. M92843:H.sapiens zinc finger transcriptional regulator mR
	41755_at	Cluster Incl. AB023194:Homo sapiens mRNA for KIAA0977 protein, complete
	32786_at	Cluster Incl. X51345:Human jun-B mRNA for JUN-B protein /cds=(253,1296)
	33439_at	Cluster Incl. D15050:Human mRNA for transcription factor AREB6, complet
20	36097_at	Cluster Incl. M62831:Human transcription factor ETR101 mRNA, complete c
	36669_at	Cluster Incl. L49169:Human G0S3 mRNA, complete cds /cds=(593,1609) /gb=
	36979_at	Cluster Incl. M20681:Human glucose transporter-like protein-III (GLUT3)
	38772_at	Cluster Incl. Y11307:H.sapiens CYR61 mRNA /cds=(223,1368) /gb=Y11307 /g
	39822_s_at	Cluster Incl. AF078077:Homo sapiens growth arrest and DNA-damage-indu
25	32583_at	Cluster Incl. J04111:Human c-jun proto oncogene (JUN), complete cds, cl
	33146_at	Cluster Incl. L08246:Human myeloid cell differentiation protein (MCL1)
	1915_s_at	V01512 /FEATURE=mRNA#1 /DEFINITION=HSCFOS Human cellular
	oncogene c-fo	
	1916_s_at	V01512 /FEATURE=mRNA#2 /DEFINITION=HSCFOS Human cellular
30	oncogene c-fo	
	1895_at J04111	/FEATURE=exon#1 /DEFINITION=HUMJUNA Human c-jun proto oncogene (J
	1776_at L24564	/FEATURE= /DEFINITION=HUMRAD Human Rad mRNA, complete cds
	789_at X52541	/FEATURE=cds /DEFINITION=HSEGR1 Human mRNA for early growth respon
	277_at L08246	/FEATURE= /DEFINITION=HUMMCL1X Human myeloid cell differentiation
35	279_at L13740	/FEATURE= /DEFINITION=HUMTR3A Human TR3 orphan receptor mRNA,
	comp	
	280_g_at	L13740 /FEATURE= /DEFINITION=HUMTR3A Human TR3 orphan receptor
	mRNA, co	

287_at L19871 /FEATURE= /DEFINITION=HUMATF3X Human activating transcription fact
 190_at U12767 /FEATURE= /DEFINITION=HSU12767 Human mitogen induced nuclear orpha

METAGENE 3 :

5

- 31598_s_at Cluster Incl. L41668:Homo sapiens UDP-galactose-4-epimerase (GALE) mR
 32893_s_at Cluster Incl. M30474:Human kidney gamma-glutamyl transpeptidase type
 41868_at Cluster Incl. J04131:Human gamma-glutamyl transpeptidase (GGT) protein
 31844_at Cluster Incl. AF000573:Homo sapiens homogentisate 1,2-dioxygenase gene,
 10 34213_at Cluster Incl. AB020676:Homo sapiens mRNA for KIAA0869 protein, partial
 34214_at Cluster Incl. AB014544:Homo sapiens mRNA for KIAA0644 protein, complete
 37956_at Cluster Incl. U37519:Human aldehyde dehydrogenase (ALDH8) mRNA, complet
 39328_at Cluster Incl. M11058:Human 3-hydroxy-3-methylglutaryl coenzyme A reduct
 41776_at Cluster Incl. U70660:Human copper transport protein HAH1 (HAH1) mRNA, c
 15 35345_at Cluster Incl. X83618:H.sapiens mRNA for 3-hydroxy-3-methylglutaryl coen
 36658_at Cluster Incl. D13643:Human mRNA for KIAA0018 gene, complete cds /cds=(3
 38780_at Cluster Incl. J04794:Human aldehyde reductase mRNA, complete cds /cds=(
 715_s_at D87002 /FEATURE=cds#4 /DEFINITION=D87002 Homo sapiens
 immunoglobulin la
 20 501_g_at U37143 /FEATURE= /DEFINITION=HSU37143 Human cytochrome P450
 monooxygena

METAGENE 4 :

- 25 33069_f_at Cluster Incl. U06641:Human UDP glucuronosyltransferase mRNA, partial
 32878_f_at Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-9542
 35896_at Cluster Incl. D87002:Human (lambda) DNA for immunoglobulin light chain /c
 39586_at Cluster Incl. AF097935:Homo sapiens desmoglein 1 (DSG1) mRNA, complete
 36001_at Cluster Incl. Y18643:Homo sapiens mRNA for methyltransferase-like prote
 30 36567_at Cluster Incl. W26700:11h4 Homo sapiens cDNA /gb=W26700 /gi=1305802 /ug=
 36611_at Cluster Incl. U25849:Human red cell-type low molecular weight acid phos
 40253_at Cluster Incl. AJ011123:Homo sapiens mRNA for phosphatidylinositol 4-kin
 948_s_at D63861 /FEATURE=expanded_cds /DEFINITION=D63861 Homo sapiens DNA
 for cy
 35 725_i_atChorionic Somatomammotropin Hormone Cs-5

METAGENE 5 :

- 36224_g_at Cluster Incl. AI827895:wf12b02.x1 Homo sapiens cDNA, 3 end /clone=IM

	39989_at	Cluster Incl. X90530:H.sapiens mRNA for ragB protein /cds=(442,1566) /g
	41077_at	Cluster Incl. AB011115:Homo sapiens mRNA for KIAA0543 protein, partial
	41120_at	Cluster Incl. D14686:Human gene for glycine cleavage system T-protein /
	41366_at	Cluster Incl. AB023219:Homo sapiens mRNA for KIAA1002 protein, complete
5	41421_at	Cluster Incl. AB020716:Homo sapiens mRNA for KIAA0909 protein, partial
	41649_at	Cluster Incl. AF038177:Homo sapiens clone 23899 mRNA sequence /cds=UNKN
	31896_at	Cluster Incl. AL050281:Homo sapiens mRNA; cDNA DKFZp586G1219 (from clon
	33788_at	Cluster Incl. AB002390:Human mRNA for KIAA0392 gene, partial cds /cds=(
10	35138_at	Cluster Incl. Y11997:H.sapiens mRNA for A-kinase anchoring protein AKAP
	36480_at	Cluster Incl. X80497:H.sapiens PHKLA mRNA /cds=(126,3833) /gb=X80497 /g
	36529_at	Cluster Incl. AI885381:wl93b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	37964_at	Cluster Incl. W25793:13c7 Homo sapiens cDNA /gb=W25793 /gi=1305934 /ug=
	38332_at	Cluster Incl. U83993:Human P2X4 purinoreceptor mRNA, complete cds /cds=
15	38682_at	Cluster Incl. AF045581:Homo sapiens BRCA1 associated protein 1 (BAP1) m
	39348_at	Cluster Incl. X99209:H.sapiens mRNA for arginine methyltransferase /cds
	40154_at	Cluster Incl. AL096725:Homo sapiens mRNA; cDNA DKFZp434B103 (from clone
	40498_g_at	Cluster Incl. AF040707:Homo sapiens candidate tumor suppressor gene 2
20	40869_at	Cluster Incl. AF069517:Homo sapiens RNA binding protein DEF-3 mRNA, com
	40870_g_at	Cluster Incl. AF069517:Homo sapiens RNA binding protein DEF-3 mRNA, c
	33350_s_at	Cluster Incl. Z78315:HSZ78315 Homo sapiens cDNA /clone=2.120-(CEPH) /
	33915_at	Cluster Incl. W22655:71B9 Homo sapiens cDNA /clone=(not-directional) /g
	34376_at	Cluster Incl. AB019517:Homo sapiens PKIG mRNA for protein kinase inhibi
25	34396_at	Cluster Incl. AB023195:Homo sapiens mRNA for KIAA0978 protein, partial
	35355_at	Cluster Incl. AB020697:Homo sapiens mRNA for KIAA0890 protein, complete
	35815_at	Cluster Incl. AL049470:Homo sapiens mRNA; cDNA DKFZp586L012 (from clone
	36154_at	Cluster Incl. D87452:Human mRNA for KIAA0263 gene, complete cds /cds=(3
30	38115_at	Cluster Incl. AF055479:Homo sapiens lung cancer candidate FUS1 (FUS1) m
	38794_at	Cluster Incl. X53390:Human mRNA for upstream binding factor (hUBF) /cds
	38812_at	Cluster Incl. X79683:H.sapiens LAMB2 mRNA for beta2 laminin /cds=(165,5
	40593_at	Cluster Incl. X66975:H.sapiens mRNA for heterogeneous nuclear ribonucle
	40629_at	Cluster Incl. L19783:Human GPI-H mRNA, complete cds /cds=(60,626) /gb=L
35	41590_at	Cluster Incl. AI652660:wb30c10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41600_at	Cluster Incl. U59435:Human cell cycle protein p38-2G4 homolog (hG4-1) m
	1357_at	U20657 /FEATURE= /DEFINITION=HSU20657 Human ubiquitin protease (Unph) pr

METAGENE 6 :

- 31955_at Cluster Incl. X65923:H.sapiens fau mRNA /cds=(56,457) /gb=X65923 /gi=31
- 34705_at Cluster Incl. AJ224335:Homo sapien mRNA for putative secretory protein,
- 36891_at Cluster Incl. AL022237:bK1191B2.3.1 (PUTATIVE novel Acyl Transferase si
- 5 37189_at Cluster Incl. AL023553:dJ347H13.3 (phosphomannomutase 1 (PMMH-22, yeast
- 38613_at Cluster Incl. U61837:Homo sapiens putative cyclin G1 interacting protei
- 39341_at Cluster Incl. AJ001902:Homo sapiens mRNA for TRIP6 (thyroid receptor in
- 39711_at Cluster Incl. J03075:Human 80K-H protein (kinase C substrate) mRNA, com
- 40807_at Cluster Incl. X86018:H.sapiens mRNA for MUF1 protein /cds=(0,1853) /gb=
- 10 35323_at Cluster Incl. U78525:Homo sapiens eukaryotic translation initiation fac
- 35773_i_at Cluster Incl. AA527880:nh86h10.s1 Homo sapiens cDNA, 3 end /clone=IM
- 35774_r_at Cluster Incl. AA527880:nh86h10.s1 Homo sapiens cDNA, 3 end /clone=IM
- 37667_at Cluster Incl. AF104421:Homo sapiens isolate normal patient 1 uroporphyr
- 1902_at M13194 /FEATURE=mRNA /DEFINITION=HUMERCC1 Human excision repair protein
- 15 1749_at AD000092 /FEATURE=cds#4 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro
- 1351_at U07695 /FEATURE= /DEFINITION=HSU07695 Human tyrosine kinase (HTK) mRNA,
- 499_at U33822 /FEATURE= /DEFINITION=HSU33822 Human tax1-binding protein TXBP181
- METAGENE 7 :
- 20 40300_g_at Cluster Incl. AF091890:Homo sapiens G-protein coupled receptor RE2 mR
- METAGENE 8 :
- 25 34147_g_at Cluster Incl. AB019529:Homo sapiens mRNA for OGG1 protein type 2c, pa
- 38132_at Cluster Incl. M88338:Human serum constituent protein (MSE55) mRNA, comp
- 38191_at Cluster Incl. AI040181:ox42d12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 39972_at Cluster Incl. Z94155:H.sapiens mRNA for P2Y-like G-protein coupled rece
- 31830_s_at Cluster Incl. Y13492:Homo sapiens mRNA for smoothelin-B /cds=(219,297
- 30 31831_at Cluster Incl. AI888563:wn33a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 35986_at Cluster Incl. AL050395:Homo sapiens mRNA; cDNA DKFZp586D1020 (from
- clon
- 40836_s_at Cluster Incl. W26677:11f7 Homo sapiens cDNA /gb=W26677 /gi=1305788 /u
- 32811_at Cluster Incl. X98507:H.sapiens mRNA for myosin-I beta /cds=(65,3151) /g
- 35 34779_at Cluster Incl. R90942:yp92b03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
- 37387_r_at Cluster Incl. X55885:Human mRNA for a presumptive KDEL receptor /cds=
- 37744_r_at Cluster Incl. U60062:Human FEZ1-T mRNA, alternatively spliced form, c
- 38019_at Cluster Incl. L37043:Homo sapiens casein kinase I epsilon mRNA, complet
- 39854_r_at Cluster Incl. AF055000:Homo sapiens clone 24519 unknown mRNA, partial

- 39855_at Cluster Incl. AC005787:Homo sapiens chromosome 19, cosmid R33374 /cds=(
 39908_at Cluster Incl. AF069735:Homo sapiens PCAF associated factor 65 alpha mRNA
 40169_at Cluster Incl. AF057140:Homo sapiens cargo selection protein TIP47 (TIP4
 41305_at Cluster Incl. M95549:Homo sapiens sodium/glucose cotransporter-like pro
5 2076_s_at L37361 /FEATURE= /DEFINITION=HUMEFL3 Homo sapiens (clone hELK-L)
 ELK r
 806_at U56998 /FEATURE= /DEFINITION=HSU56998 Human putative serine/threonine pro
 793_at X54936 /FEATURE=cds /DEFINITION=HSPLGF H.sapiens mRNA for placenta growth
 552_at U02570 /FEATURE= /DEFINITION=HSU02570 Human CDC42 GTPase-activating prote
10 344_s_at D13146 /FEATURE=mRNA#1 /DEFINITION=HUM3CNP3 Homo sapiens gene
 for 2,3

METAGENE 9 :

- 15** 41169_at Cluster Incl. X74039:H.sapiens mRNA for urokinase plasminogen activator
 32164_at Cluster Incl. S79639:EXT1=putative tumour suppressor/hereditary multipl
 33423_g_at Cluster Incl. AF052155:Homo sapiens clone 24761 mRNA sequence /cds=UN
 37386_i_at Cluster Incl. X55885:Human mRNA for a presumptive KDEL receptor /cds=
 136_at U65402 /FEATURE=cds /DEFINITION=HSU65402 Human seven transmembrane G-coup

20

METAGENE 10 :

- 37181_at Cluster Incl. X76538:H.sapiens Mpv17 mRNA /cds=(29,559) /gb=X76538 /gi=

25 METAGENE 11 :

- 36731_g_at Cluster Incl. U66684:HSU66684 Homo sapiens cDNA /gb=U66684 /gi=190656
 39330_s_at Cluster Incl. M95178:Human non-muscle alpha-actinin mRNA, complete cd
 32749_s_at Cluster Incl. AL050396:Homo sapiens mRNA; cDNA DKFZp586K1720 (from cl
30 35813_at Cluster Incl. AA192359:zp91c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 36958_at Cluster Incl. X95735:Homo sapiens mRNA for zyxin /cds=(71,1789) /gb=X95
 37026_at Cluster Incl. AF001461:Homo sapiens Kruppel-like zinc finger protein Zf
 40562_at Cluster Incl. M69013:Human guanine nucleotide-binding regulatory protei
 41000_at Cluster Incl. U68723:Human checkpoint suppressor 1 mRNA, complete cds /
35 33131_at Cluster Incl. X70683:H.sapiens mRNA for SOX-4 protein /cds=(350,1774) /
 564_at M69013 /FEATURE= /DEFINITION=HUMGTPBRPA Human guanine nucleotide-binding
 489_at U63329 /FEATURE=cds /DEFINITION=HSU63329 Human mutY homolog (hMYH) gene,

METAGENE 12 :

- 37842_at Cluster Incl. AF054589:Homo sapiens HIC protein mRNA, complete cds /cds
 38488_s_at Cluster Incl. AF031167:Homo sapiens interleukin 15 precursor (IL-15)
 32747_at Cluster Incl. X05409:Human RNA for mitochondrial aldehyde dehydrogenase
5 37398_at Cluster Incl. AA100961:zn40b06.s1 Homo sapiens cDNA, 3' end /clone=IMAG
 1693_s_at D11139 /FEATURE=exons#1-4 /DEFINITION=HUMTIMP Human gene for
 tissue in
 1173_g_at Spermidine/Spermine N1-Acetyltransferase, Alt. Splice 2
 994_at X58288 /FEATURE=mRNA /DEFINITION=HSHRPPTU H.sapiens hR-PTPu gene for prot
10 268_at L34657 /FEATURE=mRNA /DEFINITION=HUMPECAM27 Homo sapiens
 platelet/endothe

METAGENE 13 :

- 15** 40663_at Cluster Incl. AF010233:Homo sapiens RalBP1-interacting protein (POB1) m
 40063_at Cluster Incl. U22897:Homo sapiens nuclear domain 10 protein (ndp52) mRN
 40469_at Cluster Incl. AB011144:Homo sapiens mRNA for KIAA0572 protein, partial
 1932_at U83661 /FEATURE= /DEFINITION=HSU83661 Homo sapiens multidrug resistance
 1890_at AB000584 /FEATURE= /DEFINITION=AB000584 Homo sapiens mRNA for TGF-beta s

20

METAGENE 14 :

- 38285_at Cluster Incl. AF039397:untitled /cds=(30,974) /gb=AF039397 /gi=2746761
 39326_at Cluster Incl. Z71460:H.sapiens mRNA for vacuolar-type H(+)-ATPase 115 k
25 36950_at Cluster Incl. X90872:H.sapiens mRNA for gp25L2 protein /cds=(91,735) /g
 1291_s_at L03840 /FEATURE= /DEFINITION=HUMFGFR4X Human fibroblast growth
 factor

METAGENE 15 :

30

- 34669_at Cluster Incl. X96717:H.sapiens mRNA for transcription factor TFE3 /cds=
 35194_at Cluster Incl. X53463:Human mRNA for glutathione peroxidase-like protein
 39183_at Cluster Incl. X66363:H.sapiens mRNA PCTAIRE-1 for serine/threonine prot
 32518_at Cluster Incl. AF019767:Homo sapiens zinc finger protein (ZPR1) mRNA, co
35 1534_at U64198 /FEATURE= /DEFINITION=HSU64198 Human IL-12 receptor beta2 mRNA, c

METAGENE 16 :

- 31557_at Cluster Incl. M17733:Human thymosin beta-4 mRNA, complete cds /cds=(77,

- 36227_at Cluster Incl. AF043129:untitled /cds=(0,1379) /gb=AF043129 /gi=3978161
- 37509_at Cluster Incl. AF046059:Homo sapiens cytokine receptor related protein 4
- 39994_at Cluster Incl. D10925:Human mRNA for HM145 /cds=(22,1089) /gb=D10925 /gi
- 32066_g_at Cluster Incl. S68134:CREM=cyclic AMP-responsive element modulator bet
- 5 35985_at Cluster Incl. AB023137:Homo sapiens mRNA for KIAA0920 protein, complete
- 39777_at Cluster Incl. AF075587:Homo sapiens protein associated with Myc mRNA, c
- 40480_s_at Cluster Incl. M14333:Homo sapiens c-syn protooncogene mRNA, complete
- 40771_at Cluster Incl. Z98946:Human DNA sequence from clone 376D21 on chromosome
- 35341_at Cluster Incl. U90547:Human Ro/SSA ribonucleoprotein homolog (RoRet) mRNA
- 10 38051_at Cluster Incl. X76220:H.sapiens MAL gene exon 1 (and joined CDS) /cds=(5
- 41549_s_at Cluster Incl. AF091077:Homo sapiens clone 558 unknown mRNA, complete
- 32616_at Cluster Incl. M16038:Human lyn mRNA encoding a tyrosine kinase /cds=(29
- 2039_s_at M14333 /FEATURE= /DEFINITION=HUMCSYNA Homo sapiens c-syn
protooncogene
- 15 1779_s_at M16750 /FEATURE= /DEFINITION=HUMPIM1 Human pim-1 oncogene
mRNA, comple
- 1461_at M69043 /FEATURE= /DEFINITION=HUMMAD3A Homo sapiens MAD-3 mRNA
encoding I
- 1402_at M16038 /FEATURE= /DEFINITION=HUMLYN Human lyn mRNA encoding a tyrosine k
- 20 1370_at M29696 /FEATURE= /DEFINITION=HUMIL7AA Human interleukin-7 receptor (IL-7
- 883_s_at M54915 /FEATURE= /DEFINITION=HUMPIM1LE Human h-pim-1 protein (h-
pim-1)
- 595_at M59465 /FEATURE= /DEFINITION=HUMA20 Human tumor necrosis factor alpha ind
- 25 METAGENE 17 :
- 40877_s_at Cluster Incl. AF041080:Homo sapiens D15F37 pseudogene, S3 allele, mRN
- 40878_f_at Cluster Incl. AF041081:Homo sapiens D15F37 pseudogene, S4 allele, mRN
- 32833_at Cluster Incl. M59287:Human protein kinase mRNA /cds=UNKNOWN
- 30 /gb=M59287
- 35843_at Cluster Incl. L40402:Homo sapiens (clone Zap2) mRNA fragment /cds=UNKNO
- 36991_at Cluster Incl. L14076:Human pre-mRNA splicing factor SRp75 mRNA, complet
- 38011_at Cluster Incl. AB006572:Homo sapiens RMP mRNA for RPB5 meidating protein
- 38030_at Cluster Incl. AB002330:Human mRNA for KIAA0332 gene, partial cds /cds=(
- 35 38072_at Cluster Incl. AL031432:Human DNA sequence from clone 465N24 on chromoso
- 40885_s_at Cluster Incl. N30151:yx81f01.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 292_s_at Protein Kinase

METAGENE 18 :

- 31505_at Cluster Incl. Z28407:H.sapiens mRNA for ribosomal protein L8 /cds=(43,8
 34969_s_at Cluster Incl. AL096750:Homo sapiens mRNA; cDNA DKFZp434H244 (from clo
 41078_at Cluster Incl. D63484:Human mRNA for KIAA0150 gene, partial cds /cds=(0,
5 33224_at Cluster Incl. AB007965:Homo sapiens mRNA, chromosome 1 specific transcr
 33225_at Cluster Incl. AI928387:wo96f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 34255_at Cluster Incl. AF059202:Homo sapiens ACAT related gene product 1 mRNA, c
 34743_at Cluster Incl. D63481:Human mRNA for KIAA0147 gene, partial cds /cds=(0,
 35615_at Cluster Incl. D50914:Human mRNA for KIAA0124 gene, partial cds /cds=(0,
10 36035_at Cluster Incl. AB002135:Homo sapiens mRNA for glycosylphosphatidylinosit
 35819_at Cluster Incl. X06994:Human mRNA for cytochrome c1 /cds=(8,985) /gb=X069
 36145_at Cluster Incl. U51586:Human siah binding protein 1 (SiahBP1) mRNA, parti
 36936_at Cluster Incl. U58766:Human FX protein mRNA, complete cds /cds=(74,1039)
 40200_at Cluster Incl. M64673:Human heat shock factor 1 (TCF5) mRNA, complete cd
15 41256_at Cluster Incl. Z21507:H.sapiens EF-1delta gene encoding human elongation
 33132_at Cluster Incl. U37012:Human cleavage and polyadenylation specificity fac
 1160_at J04444 /FEATURE=cds /DEFINITION=HUMCYC1A Human cytochrome c-1 gene, comp
 244_at M64673 /FEATURE= /DEFINITION=HUMHSF1 Human heat shock factor 1 (TCF5) mRN
- 20** METAGENE 19 :
- 35933_f_at Cluster Incl. D38498:Human PMS5 mRNA (yeast mismatch repair gene PMS1
 36275_at Cluster Incl. AB002438:Homo sapiens mRNA from chromosome 5q21-22, clone
 31860_at Cluster Incl. X51804:Human PMI gene for a putative receptor protein /cd
25 37926_at Cluster Incl. D14520:Human mRNA for GC-Box binding protein BTEB2, compl
 40484_g_at Cluster Incl. U49857:Human transcriptional activator mRNA, complete c
 2075_s_at L36719 /FEATURE=mRNA /DEFINITION=HUMMKK3A Homo sapiens MAP
 kinase kina
- 30** METAGENE 20 :
- 32352_at Cluster Incl. X52730:Human gene for phenylethanolamine N-methylase (PNM
 37772_at Cluster Incl. AB020711:Homo sapiens mRNA for KIAA0904 protein, partial
 32064_at Cluster Incl. Y13467:Homo sapiens mRNA for RB18A protein /cds=(235,4935
35 32679_at Cluster Incl. D13634:Human mRNA for KIAA0009 gene, complete cds /cds=(1
 33218_at Cluster Incl. M11730:Human tyrosine kinase-type receptor (HER2) mRNA, c
 38672_at Cluster Incl. Y13247:Homo sapiens fb19 mRNA /cds=(539,3361) /gb=Y13247
 36139_at Cluster Incl. AL050289:Homo sapiens mRNA; cDNA DKFZp586G0522 (from
 clon

37355_at Cluster Incl. D38255:Homo sapiens mRNA for CAB1, complete cds /cds=(121
 1802_s_at X03363 /FEATURE=cds /DEFINITION=HSERB2R Human c-erb-B-2 mRNA
 1680_at D43772 /FEATURE= /DEFINITION=HUMGRB7 Human squamous cell carcinoma of es

5 METAGENE 21 :

31732_at Cluster Incl. X00948:Human mRNA for prepro-relaxin H2 /cds=(0,557) /gb=
 33803_at Cluster Incl. J02973:Human thrombomodulin gene, complete cds /cds=(541,
 32743_at Cluster Incl. AB007922:Homo sapiens mRNA for KIAA0453 protein, partial
 10 38383_at Cluster Incl. U73338:Human methionine synthase mRNA, complete cds /cds=
 38422_s_at Cluster Incl. U29332:Homo sapiens heart protein (FHL-2) mRNA, complet
 40916_at Cluster Incl. AL035494:Human DNA sequence from clone 635G19 on chromoso

METAGENE 22 :

15

31944_at Cluster Incl. AI028290:ov84f11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 33004_g_at Cluster Incl. AI275502:ql74d06.x1 Homo sapiens cDNA, 3 end /clone=IM
 33690_at Cluster Incl. AL080190:Homo sapiens mRNA; cDNA DKFZp434A202 (from
 clone

20

32872_at Cluster Incl. AL049279:Homo sapiens mRNA; cDNA DKFZp564I083 (from clone
 34936_at Cluster Incl. AB012130:Homo sapiens SBC2 mRNA for sodium bicarbonate co
 35958_at Cluster Incl. AL050379:Homo sapiens mRNA; cDNA DKFZp586F1922 (from
 clon

25

36225_s_at Cluster Incl. W27611:35b9 Homo sapiens cDNA /gb=W27611 /gi=1307559 /u
 36234_at Cluster Incl. U79273:Human clone 23933 mRNA sequence /cds=UNKNOWN
 /gb=U

30

37487_at Cluster Incl. AB029016:Homo sapiens mRNA for KIAA1093 protein, partial
 39286_at Cluster Incl. D64109:Homo sapiens mRNA for tob family, complete cds /cd
 39615_at Cluster Incl. AB028949:Homo sapiens mRNA for KIAA1026 protein, partial
 39634_at Cluster Incl. AB017168:Homo sapiens mRNA for Slit-2 protein, complete c
 40725_at Cluster Incl. AF047438:Homo sapiens GOS28/P28 protein mRNA, complete cd
 41386_i_at Cluster Incl. AB002344:Human mRNA for KIAA0346 gene, partial cds /cds
 41642_at Cluster Incl. X75940:H.sapiens beta glucuronidase pseudogene /cds=UNKNO
 41644_at Cluster Incl. AB018333:Homo sapiens mRNA for KIAA0790 protein, partial

35

33229_at Cluster Incl. U08316:Human insulin-stimulated protein kinase 1 (ISPK-1)
 35204_at Cluster Incl. U52840:Homo sapiens semaphorin F homolog mRNA, complete c
 36532_at Cluster Incl. AF039945:Homo sapiens synaptojanin 2B mRNA, partial cds /
 36905_at Cluster Incl. AB009356:Homo sapiens mRNA for TGF-beta activated kinase
 37280_at Cluster Incl. U59912:Human chromosome 4 Mad homolog Smad1 mRNA, complet

- 37947_at Cluster Incl. D26362:Human mRNA for KIAA0043 gene, complete cds /cds=(1
38639_at Cluster Incl. AF040963:Homo sapiens Mad4 homolog (Mad4) mRNA, complete
32847_at Cluster Incl. U48959:Homo sapiens myosin light chain kinase (MLCK) mRNA
33829_at Cluster Incl. Y12670:Homo sapiens mRNA for leptin receptor gene-related
5 33862_at Cluster Incl. AF017786:Homo sapiens phosphatidic acid phosphohydrolase
37710_at Cluster Incl. L08895:Homo sapiens MADS/MEF2-family transcription factor
39450_s_at Cluster Incl. AF050145:Homo sapiens iduronate-2-sulfatase (IDS) mRNA,
40191_s_at Cluster Incl. AI761647:wg66h09.x1 Homo sapiens cDNA, 3 end /clone=IM
40589_at Cluster Incl. U40572:Human beta2-syntrophin (SNT B2) mRNA, complete cds
10 40617_at Cluster Incl. AC004381:Homo sapiens Chromosome 16 BAC clone CIT987SK-44
40928_at Cluster Incl. W26496:30d2 Homo sapiens cDNA /gb=W26496 /gi=1307195 /ug=
32588_s_at Cluster Incl. X78992:H.sapiens ERF-2 mRNA /cds=(66,1544) /gb=X78992 /
33207_at Cluster Incl. AI095508:qb29a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
1636_g_at U07563 /FEATURE=Poly_A_Site#1 /DEFINITION=HSABLGR3 Human proto-
15 oncogen
1591_s_at J03242 /FEATURE= /DEFINITION=HUMGFIL2 Human insulin-like growth
factor
1325_at U59423 /FEATURE= /DEFINITION=HSU59423 Human Smad1 mRNA, complete cds
479_at U53446 /FEATURE= /DEFINITION=HSU53446 Human mitogen-responsive phosphopro
20
METAGENE 23 :

40659_at Cluster Incl. U12767:Human mitogen induced nuclear orphan receptor (MIN
40761_at Cluster Incl. AA705628:zf40a01.s1 Homo sapiens cDNA, 3 end /clone=3793
25 40762_g_at Cluster Incl. AA705628:zf40a01.s1 Homo sapiens cDNA, 3 end /clone=37
1138_at L20859 /FEATURE= /DEFINITION=HUMGLVR1X Human leukemia virus receptor 1 (

METAGENE 24 :

30 33062_at Cluster Incl. AL096729:Homo sapiens mRNA; cDNA DKFZp434D044 (from
clone
33636_at Cluster Incl. U87459:Human autoimmunogenic cancer/testis antigen NY-ESO
32918_at Cluster Incl. AL080182:Homo sapiens mRNA; cDNA DKFZp434O151 (from
clone
35 38550_at Cluster Incl. AB021638:Homo sapiens X11L2 mRNA for X11-like protein 2,
38915_at Cluster Incl. AB011135:Homo sapiens mRNA for KIAA0563 protein, complete
39234_at Cluster Incl. AL050131:Homo sapiens mRNA; cDNA DKFZp586I111 (from clone
39588_at Cluster Incl. AF055872:Homo sapiens Apo3/DR3 ligand (APO3L) mRNA, compl
31814_i_at Cluster Incl. AB009462:Homo sapiens hLRp105 mRNA for LDL receptor rel

- 35165_at Cluster Incl. AF070582:Homo sapiens clone 24766 mRNA sequence /cds=UNKN
 35190_at Cluster Incl. AL031447:dJ126A5.2.1 (novel protein) (isoform 1) /cds=(0,
 36847_r_at Cluster Incl. AA121509:zk88c10.s1 Homo sapiens cDNA, 3 end /clone=IM
- 5 37538_at Cluster Incl. AL049354:Homo sapiens mRNA; cDNA DKFZp566E183 (from
 clone
 37597_s_at Cluster Incl. AF055006:Homo sapiens clone 24666 sec6 homolog mRNA, pa
 40152_r_at Cluster Incl. Z48054:H.sapiens mRNA for peroxisomal targeting signal
 32176_at Cluster Incl. AB011110:Homo sapiens mRNA for KIAA0538 protein, partial
- 10 33850_at Cluster Incl. W28892:53c11 Homo sapiens cDNA /gb=W28892 /gi=1308840 /ug
 36095_at Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /
 37041_at Cluster Incl. AB023160:Homo sapiens mRNA for KIAA0943 protein, partial
 38396_at Cluster Incl. Y09836:H.sapiens mRNA for 3UTR of unknown protein /cds=UN
 39838_at Cluster Incl. AB014522:Homo sapiens mRNA for KIAA0622 protein, partial
- 15 39842_at Cluster Incl. AF059293:Homo sapiens cytokine-like factor-1 precursor (C
 40224_s_at Cluster Incl. AB014585:Homo sapiens mRNA for KIAA0685 protein, comple
 1805_g_at X07730 /FEATURE= /DEFINITION=HSPSA Human mRNA for prostate specific
 an
 1063_s_at U02566 /FEATURE= /DEFINITION=HSU02566 Human receptor tyrosine kinase t
- 20 METAGENE 25 :
- 38516_at Cluster Incl. L10338:Human sodium channel beta-1 subunit (SCN1B) mRNA,
 39646_at Cluster Incl. S60415:myasthenic syndrome antigen B [human, fetal brain,
 25 39665_at Cluster Incl. U33267:Human glycine receptor beta subunit (GLRB) mRNA, c
 36059_at Cluster Incl. AB011540:Homo sapiens mRNA for MEGF7, partial cds /cds=(0
 36900_at Cluster Incl. U52426:Homo sapiens GOK (STIM1) mRNA, complete cds /cds=(
 39846_at Cluster Incl. AF071748:Homo sapiens cathepsin F (CATSF) mRNA, complete
- 30 METAGENE 26 :
- 34496_at Cluster Incl. AB017165:Homo sapiens PIG-L mRNA, complete cds /cds=(5,76
 35944_at Cluster Incl. AL031228:dJ1033B10.3 (GalT3 (beta3-Galactosyltransferase)
 37834_at Cluster Incl. Y17999:Homo sapiens mRNA for protein kinase Dyrk1B /cds=(
 35 38544_at Cluster Incl. M13981:Human inhibin A-subunit mRNA, complete cds /cds=(1
 39587_at Cluster Incl. AJ005890:Homo sapiens mRNA for JM1 protein, complete CDS
 35225_at Cluster Incl. M91592:Human zinc-finger protein (ZNF76) gene, partial cd
 36522_at Cluster Incl. AB014516:Homo sapiens mRNA for KIAA0616 protein, partial
 38795_s_at Cluster Incl. X56687:H.sapiens mRNA for autoantigen NOR-90 /cds=(179,

1003_s_at X68149 /FEATURE=cds /DEFINITION=HSBLR1A Homo sapiens BLR1 gene for
Bur

METAGENE 27 :

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32393_s_at Cluster Incl. W27466:31c9 Homo sapiens cDNA /gb=W27466 /gi=1307270 /u
34530_at Cluster Incl. W73822:zd52f10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
37445_at Cluster Incl. AB015633:Homo sapiens mRNA for type II membrane protein,
38139_at Cluster Incl. AF017445:Homo sapiens GDP-L-fucose pyrophosphorylase (GFP
10 38850_at Cluster Incl. M11119:Human endogenous retrovirus envelope region mRNA (
40312_at Cluster Incl. AJ005670:Homo sapiens mRNA for dachshund protein /cds=(24
40349_at Cluster Incl. AL049442:Homo sapiens mRNA; cDNA DKFZp586N1720 (from
clon

15

41457_at Cluster Incl. AB007883:Homo sapiens KIAA0423 mRNA, partial cds /cds=(0,
41476_at Cluster Incl. N36926:yy38e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
32624_at Cluster Incl. AL050050:Homo sapiens mRNA; cDNA DKFZp566D133 (from
clone

20

32654_g_at Cluster Incl. AW020536:df11b12.y1 Homo sapiens cDNA, 5 end /clone=IM
34676_at Cluster Incl. AB029022:Homo sapiens mRNA for KIAA1099 protein, complete
35142_at Cluster Incl. AF070617:Homo sapiens clone 24812 mRNA sequence /cds=UNKN
35180_at Cluster Incl. AL050205:Homo sapiens mRNA; cDNA DKFZp586F1323 (from
clon

25

35232_f_at Cluster Incl. AI056696:oz26h05.x1 Homo sapiens cDNA, 3 end /clone=IM
35648_at Cluster Incl. AB007902:Homo sapiens KIAA0442 mRNA, partial cds /cds=(0,
36033_at Cluster Incl. AL049309:Homo sapiens mRNA; cDNA DKFZp564B176 (from
clone

30

36083_at Cluster Incl. U01160:Human transmembrane 4 superfamily protein (SAS) mR
36092_at Cluster Incl. AL080213:Homo sapiens mRNA; cDNA DKFZp586I1823 (from clon
36511_at Cluster Incl. AB020658:Homo sapiens mRNA for KIAA0851 protein, complete
36818_at Cluster Incl. AF052100:Homo sapiens clone 23645 mRNA sequence /cds=UNKN
36910_at Cluster Incl. L36870:Homo sapiens MAP kinase kinase 4 (MKK4) mRNA, comp
37616_at Cluster Incl. X79888:H.sapiens AUH mRNA /cds=(4,1023) /gb=X79888 /gi=78
38659_at Cluster Incl. AB020669:Homo sapiens mRNA for KIAA0862 protein, complete
38674_at Cluster Incl. AA115140:zl10d12.r1 Homo sapiens cDNA, 5 end /clone=IMAG

35

38687_at Cluster Incl. AL050051:Homo sapiens mRNA; cDNA DKFZp566D193 (from
clone
38711_at Cluster Incl. AB014527:Homo sapiens mRNA for KIAA0627 protein, partial
39046_at Cluster Incl. AL049324:Homo sapiens mRNA; cDNA DKFZp564D246 (from
clone

	39734_at	Cluster Incl. U10117:Human endothelial-monocyte activating polypeptide
	40108_at	Cluster Incl. D13630:Human mRNA for KIAA0005 gene, complete cds /cds=(8
	40517_at	Cluster Incl. AB002370:Human mRNA for KIAA0372 gene, complete cds /cds=
	40832_s_at	Cluster Incl. AL050126:Homo sapiens mRNA; cDNA DKFZp586G011 (from clo
5	40839_at	Cluster Incl. AL080177:Homo sapiens mRNA; cDNA DKFZp434K151 (from clone
	40859_at	Cluster Incl. AI561196:tg27a01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	40868_at	Cluster Incl. AA442799:zv69b10.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	41153_f_at	Cluster Incl. AF102803:untitled /cds=(2,2722) /gb=AF102803 /gi=409276
10	41156_g_at	Cluster Incl. U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=
	41759_at	Cluster Incl. Z47087:H.sapiens mRNA for RNA polymerase II elongation fa
	32165_at	Cluster Incl. L41887:Homo sapiens splicing factor, arginine/serine-rich
	32217_at	Cluster Incl. AF052105:Homo sapiens clone 23965 mRNA sequence /cds=UNKN
	32777_at	Cluster Incl. Y12478:H.sapiens mRNA for CHD5 protein /cds=(42,566) /gb=
15	32788_at	Cluster Incl. D42063:Human mRNA for RanBP2 (Ran-binding protein 2), com
	33355_at	Cluster Incl. AL049381:Homo sapiens mRNA; cDNA DKFZp586J2118 (from clon
	33386_at	Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosome
	33861_at	Cluster Incl. AI123426:qa49c09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	33880_at	Cluster Incl. D89053:Homo sapiens mRNA for Acyl-CoA synthetase 3, compl
20	34873_at	Cluster Incl. Y16241:Homo sapiens mRNA for nebulin /cds=(397,3441) /g
	35787_at	Cluster Incl. AI986201:wr81a01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35845_at	Cluster Incl. AJ131245:Homo sapiens mRNA for Sec24 protein (Sec24B isof
	35848_at	Cluster Incl. AL049432:Homo sapiens mRNA; cDNA DKFZp586J231 (from clone
	36998_s_at	Cluster Incl. Y08262:H.sapiens mRNA for SCA2 protein /cds=(0,2746) /g
25	37031_at	Cluster Incl. D80005:Human mRNA for KIAA0183 gene, partial cds /cds=(0,
	37306_at	Cluster Incl. D38549:Human mRNA for KIAA0068 gene, partial cds /cds=(0,
	37655_at	Cluster Incl. X75304:H.sapiens giantin mRNA /cds=(126,9905) /gb=X75304
	37732_at	Cluster Incl. AL049940:Homo sapiens mRNA; cDNA DKFZp564E1922 (from clon
30	37735_at	Cluster Incl. U31383:Human G protein gamma-10 subunit mRNA, complete cd
	38070_at	Cluster Incl. AL080234:Homo sapiens mRNA; cDNA DKFZp586L081 (from clone
	38106_at	Cluster Incl. AJ012409:Homo sapiens mRNA for hypothetical protein, clon
	38385_at	Cluster Incl. S65738:actin depolymerizing factor [human, fetal brain, m
35	38814_at	Cluster Incl. AF038954:Homo sapiens vacuolar H(+)-ATPase subunit mRNA,
	39510_r_at	Cluster Incl. AL049932:Homo sapiens mRNA; cDNA DKFZp564H2416 (from cl
	39557_at	Cluster Incl. AI625844:ty65d07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39823_at	Cluster Incl. U06631:Human (H326) mRNA, complete cds /cds=(176,1969) /g
	39841_at	Cluster Incl. U79745:Homo sapiens monocarboxylate transporter homologue

- 39923_at Cluster Incl. AI935420:wo84c08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 40184_at Cluster Incl. L37042:Homo sapiens casein kinase I alpha isoform (CSNK1A
- 40238_at Cluster Incl. AI674208:wc07f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 40239_g_at Cluster Incl. AI674208:wc07f02.x1 Homo sapiens cDNA, 3 end /clone=IM
- 5 40615_at Cluster Incl. AA780049:zj24f06.s1 Homo sapiens cDNA, 3 end /clone=4512
- 40623_at Cluster Incl. AI749193:at40e04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 41277_at Cluster Incl. AW021542:df25a06.y1 Homo sapiens cDNA, 5 end /clone=IMAG
- 41488_at Cluster Incl. AC002394:Human Chromosome 16 BAC clone CIT987SK-A-211C6
- /
- 10 33170_at Cluster Incl. AB023179:Homo sapiens mRNA for KIAA0962 protein, partial
- 1846_at L78132 /FEATURE= /DEFINITION=HUMPCTA1A Human prostate carcinoma tumor an
- 1725_s_at Oncogene E6-Ap, Papillomavirus
- 1252_at M73547 /FEATURE= /DEFINITION=HUMPOLLA Human polyposis locus (DP1 gene) m
- 507_s_at U43189 /FEATURE= /DEFINITION=HSU43189 Human Ets transcription factors
- 15 N
- 237_s_at M60483 /FEATURE=mRNA /DEFINITION=HUMPP2AA Human protein
- phosphatase 2A
- METAGENE 28 :
- 20
- 31315_at Cluster Incl. D84143:Human immunoglobulin (mAb59) light chain V region
- 31319_at Cluster Incl. M20707:Human kappa-immunoglobulin germline pseudogene (Ch
- 31344_at Cluster Incl. AF063725:Homo sapiens clone BCSynL38 immunoglobulin lambd
- 31347_at Cluster Incl. AF058075:Homo sapiens clone ASPBLL54 immunoglobulin lambd
- 25 31460_f_at Cluster Incl. AF043586:Homo sapiens clone CPRF1-T2 immunoglobulin lam
- 31512_at Cluster Incl. Z00010:H.sapiens germ line pseudogene for immunoglobulin
- 31586_f_at Cluster Incl. X72475:H.sapiens mRNA for rearranged Ig kappa light cha
- 31596_f_at Cluster Incl. L02326:Homo sapiens (clone Hu lambda-17) lambda-like ge
- 34094_i_at Cluster Incl. U80114:Human immunoglobulin heavy chain variable region
- 30 34095_f_at Cluster Incl. U80114:Human immunoglobulin heavy chain variable region
- 34098_f_at Cluster Incl. AI799757:wc37g12.x1 Homo sapiens cDNA, 3 end /clone=IM
- 34105_f_at Cluster Incl. AI147237:qb36f02.x1 Homo sapiens cDNA, 3 end /clone=IM
- 35530_f_at Cluster Incl. X92997:H.sapiens mRNA for IgG lambda light chain V-J-C
- 35566_f_at Cluster Incl. AF015128:Homo sapiens IgG heavy chain variable region (
- 35 35607_at Cluster Incl. AA934573:oo67b04.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 41064_at Cluster Incl. AL049296:Homo sapiens mRNA; cDNA DKFZp564P013 (from
- clone
- 38635_at Cluster Incl. Z69043:H.sapiens mRNA translocon-associated protein delta
- 32533_s_at Cluster Incl. AF054825:Homo sapiens VAMP5 mRNA, complete cds /cds=(57

1652_at U77735 /FEATURE= /DEFINITION=HSU77735 Human pim-2 protooncogene homolog
 1633_g_at U77735 /FEATURE= /DEFINITION=HSU77735 Human pim-2 protooncogene
 homolo

5 METAGENE 29 :

41430_at Cluster Incl. AB011113:Homo sapiens mRNA for KIAA0541 protein, partial
 37239_r_at Cluster Incl. AF014118:Homo sapiens membrane-associated kinase (Myt1)
 41140_at Cluster Incl. U05875:Human clone pSK1 interferon gamma receptor accesso

10

METAGENE 30 :

39957_at Cluster Incl. AF150247:AF150247 Homo sapiens cDNA /clone=CBFBCC09
 /gb=A

15 35692_at Cluster Incl. AL080235:Homo sapiens mRNA; cDNA DKFZp586E1621 (from clon

39696_at Cluster Incl. AB028974:Homo sapiens mRNA for KIAA1051 protein, partial
 34342_s_at Cluster Incl. AF052124:Homo sapiens clone 23810 osteopontin mRNA, com
 33128_s_at Cluster Incl. W68521:zd36f07.r1 Homo sapiens cDNA, 5 end /clone=IMAG

20 2092_s_at J04765 /FEATURE= /DEFINITION=HUMOSTRO Human osteopontin mRNA, complete

METAGENE 31 :

25 37835_at Cluster Incl. M28827:Human thymocyte antigen CD1c mRNA, complete cds /c 39971_at Cluster Incl. M22637:Human LYL-1 protein mRNA, complete cds /cds=UNKNOWN

40366_at Cluster Incl. M25322:Human granule membrane protein-140 mRNA, complete
 32140_at Cluster Incl. Y08110:H.sapiens mRNA for mosaic protein LR11 /cds=(80,67

30 32625_at Cluster Incl. X15357:Human mRNA for natriuretic peptide receptor (ANP-A 33295_at Cluster Incl. X85785:H.sapiens DARC gene /cds=(494,1510) /gb=X85785 /gi

33790_at Cluster Incl. AI720438:as81g04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 34708_at Cluster Incl. D88587:Homo sapiens mRNA for Hakata antigen, complete cds

36503_at Cluster Incl. AB002409:Homo sapiens mRNA for SLC, complete cds /cds=(58
 37543_at Cluster Incl. D25304:Human mRNA for KIAA0006 gene, partial cds /cds=(0,

35 38995_at Cluster Incl. AF000959:Homo sapiens transmembrane protein mRNA, complet 40841_at Cluster Incl. AF049910:Homo sapiens TACC1 (TACC1) mRNA, complete cds /c

32184_at Cluster Incl. X61118:Human TTG-2 mRNA for a cysteine rich protein with
 32851_at Cluster Incl. AF036956:Homo sapiens neuroblastoma apoptosis-related RNA

- 37394_at Cluster Incl. J03507:Human complement protein component C7 mRNA, comple
 37716_at Cluster Incl. X05323:Human MRC OX-2 gene signal sequence /cds=(0,824) /
 38119_at Cluster Incl. X12496:Human mRNA for erythrocyte membrane sialoglycoprot
 38406_f_at Cluster Incl. AI207842:ao89h09.x1 Homo sapiens cDNA, 3 end /clone=IM
5 38407_r_at Cluster Incl. AI207842:ao89h09.x1 Homo sapiens cDNA, 3 end /clone=IM
 38453_at Cluster Incl. X15606:Human mRNA for ICAM-2, cell adhesion ligand for LF
 38454_g_at Cluster Incl. X15606:Human mRNA for ICAM-2, cell adhesion ligand for
 39114_at Cluster Incl. AB022718:Homo sapiens mRNA for DEPP (decidual protein ind
 40994_at Cluster Incl. L15388:Human G protein-coupled receptor kinase (GRK5) mRN
10 41522_at Cluster Incl. Z93096:Human DNA sequence from BAC 390B3 on chromosome 22
 32562_at Cluster Incl. X72012:H.sapiens end mRNA for endoglin /cds=(281,2158) /g
 1135_at L15388 /FEATURE= /DEFINITION=HUMGRK5A Human G protein-coupled receptor k
 1001_at X60957 /FEATURE=cds /DEFINITION=HSTIEMR Human tie mRNA for putative rece
 590_at M32334 /FEATURE=cds /DEFINITION=HUMICAM4 Homo sapiens intercellular adhe
15 459_s_at U68485 /FEATURE= /DEFINITION=HSU68485 Homo sapiens bridging
 integrator
 265_s_at M24736 /FEATURE= /DEFINITION=HUMELAM1A Human endothelial
 leukocyte adhe
 216_at M98539 /FEATURE=exon /DEFINITION=HUMPDS03 Human prostaglandin D2 synthase
20
 METAGENE 32 :

 38505_at Cluster Incl. AL050151:Homo sapiens mRNA; cDNA DKFZp586J0720 (from clon
 38932_at Cluster Incl. M29580:Human zinc-finger protein 7 (ZFP7) mRNA, complete
25 32706_at Cluster Incl. X89887:Homo sapiens mRNA for WD repeat protein (HIRA) /cd
 32723_at Cluster Incl. L02547:Homo sapiens (clone pZ50-19) cleavage stimulation
 38296_at Cluster Incl. AL050196:Homo sapiens mRNA; cDNA DKFZp586D2223 (from
 clon
 38720_at Cluster Incl. AF026292:Homo sapiens chaperonin containing t-complex pol
30 35831_at Cluster Incl. AB014511:Homo sapiens mRNA for KIAA0611 protein, partial
 38755_at Cluster Incl. X84709:H.sapiens mRNA for mediator of receptor-induced to
 41259_at Cluster Incl. AI553745:tn28c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 1561_at U27193 /FEATURE= /DEFINITION=HSU27193 Human protein-tyrosine phosphatase
 1376_at M36067 /FEATURE=mRNA /DEFINITION=HUMLIGAA Human DNA ligase I mRNA,
35 compl
 142_at U75308 /FEATURE= /DEFINITION=HSU75308 Human TBP-associated factor (hTAFII

 METAGENE 33 :

	33942_s_at	Cluster Incl. AF004563:Homo sapiens hUNC18b alternatively-spliced mRNA
	35008_at	Cluster Incl. AB002345:Human mRNA for KIAA0347 gene, complete cds /cds=
	36260_at	Cluster Incl. AB002448:Homo sapiens mRNA from chromosome 5q21-22, clone
	37161_at	Cluster Incl. W28948:54b12 Homo sapiens cDNA /gb=W28948 /gi=1308896 /ug
5	38957_at	Cluster Incl. AB002367:Human mRNA for KIAA0369 gene, complete cds /cds=
	40646_at	Cluster Incl. U20350:Human G protein-coupled receptor V28 mRNA, complet
	41679_at	Cluster Incl. AF035282:Homo sapiens clone 23703 mRNA sequence /cds=UNKN
	32668_at	Cluster Incl. AL080076:Homo sapiens mRNA; cDNA DKFZp564C0362 (from clon
10	33296_at	Cluster Incl. AB020643:Homo sapiens mRNA for KIAA0836 protein, partial
	34767_at	Cluster Incl. AI670788:tz10c02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	35213_at	Cluster Incl. AF071185:Homo sapiens formin binding protein 21 mRNA, com
	35221_at	Cluster Incl. X91648:H.sapiens mRNA for pur alpha extended 3untranslate
	36042_at	Cluster Incl. X75958:H.sapiens trkB mRNA for protein-tyrosine kinase /c
15	36814_at	Cluster Incl. AB029032:Homo sapiens mRNA for KIAA1109 protein, partial
	37199_at	Cluster Incl. AI760932:wi70d01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	37623_at	Cluster Incl. X75918:H.sapiens mRNA for NOT /cds=(317,2113) /gb=X75918
	37934_at	Cluster Incl. AL080078:Homo sapiens mRNA; cDNA DKFZp564D1462 (from clon
20	38704_at	Cluster Incl. AB007934:Homo sapiens mRNA for KIAA0465 protein, partial
	38990_at	Cluster Incl. AL031178:Human DNA sequence from clone 341E18 on chromoso
	32804_at	Cluster Incl. AF091263:Homo sapiens RNA binding motif protein 5 (RBM5)
	34800_at	Cluster Incl. AL039458:DKFZp434N0910_s1 Homo sapiens cDNA, 3 end /clon
	34809_at	Cluster Incl. H53921:yq87g03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
25	35363_at	Cluster Incl. AL080113:Homo sapiens mRNA; cDNA DKFZp586K2322 (from clon
	35736_at	Cluster Incl. AL050091:Homo sapiens mRNA; cDNA DKFZp586F1918 (from clon
	35789_at	Cluster Incl. AB028965:Homo sapiens mRNA for KIAA1042 protein, complete
30	35808_at	Cluster Incl. AL031681:dJ862K6.2.2 (splicing factor, arginine/serine-ri
	39864_at	Cluster Incl. D78134:Homo sapiens mRNA for CIRP, complete cds /cds=(80,
	40196_at	Cluster Incl. D88153:Homo sapiens mRNA for HYA22, complete cds /cds=(14
	40576_f_at	Cluster Incl. D89678:Homo sapiens mRNA for A+U-rich element RNA bindi
	1924_at	U11791 /FEATURE= /DEFINITION=HSU11791 Human cyclin H mRNA, complete cds
35	1556_at	U23946 /FEATURE= /DEFINITION=HSU23946 Human putative tumor suppressor (L
	1529_at	U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence
	185_at	U04840 /FEATURE= /DEFINITION=HSU04840 Human onconeural ventral antigen-1

METAGENE 34 :

- 32310_f_at Cluster Incl. AI341574:qq94h09.x1 Homo sapiens cDNA, 3 end /clone=IM
 36248_at Cluster Incl. AF070572:Homo sapiens clone 24778 unknown mRNA /cds=(0,17
 36039_s_at Cluster Incl. X93498:H.sapiens mRNA for 21-Glutamic Acid-Rich Protein
5 36040_at Cluster Incl. AI337192:qx88h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40114_at Cluster Incl. J00077:Human alpha-fetoprotein (AFP) mRNA, complete cds /

METAGENE 35 :

- 10** 36759_at Cluster Incl. U29589:Human m3 muscarinic acetylcholine receptor (CHRM3)
 38491_at Cluster Incl. U11732:Human ets-like gene (tel) mRNA, complete cds /cds=
 35697_at Cluster Incl. L76259:Homo sapiens PTS gene, complete cds /cds=(68,505)

METAGENE 36 :

15

- 31610_at Cluster Incl. U21049:Human DD96 mRNA, complete cds /cds=(0,344) /gb=U21
 32275_at Cluster Incl. X04470:Human mRNA for antileukoprotease (ALP) from cervix
 33505_at Cluster Incl. AI887421:wm05c01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40686_at Cluster Incl. AI985272:ws06b05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
20 34280_at Cluster Incl. Y09765:Homo sapiens mRNA for putative GABA receptor epsil
 35977_at Cluster Incl. AB020315:Homo sapiens Dickkopf-1 (hdck-1) gene /cds=(0,80
 37218_at Cluster Incl. D64110:Homo sapiens mRNA for ANA, complete cds /cds=(94,8
 37244_at Cluster Incl. AA746355:oa56f02.r1 Homo sapiens cDNA /clone=IMAGE-130898
 38354_at Cluster Incl. X52560:Human gene for nuclear factor NF-IL6 /cds=(0,1037)
25 38615_at Cluster Incl. AF097021:Homo sapiens GW112 protein (GW112) mRNA, complet
 32210_at Cluster Incl. M83088:Human phosphoglucomutase 1 (PGM1) mRNA, complete c
 37730_at Cluster Incl. U22055:Human 100 kDa coactivator mRNA, complete cds /cds=
 1042_at U27185 /FEATURE= /DEFINITION=HSU27185 Human RAR-responsive (TIG1) mRNA,
 821_s_at U78793 /FEATURE= /DEFINITION=HSU78793 Human folate receptor alpha
30 (hFR)

METAGENE 37 :

- 31637_s_at Cluster Incl. X72631:H.sapiens mRNA encoding Rev-ErbAalpha /cds=UNKNO
35 34939_r_at Cluster Incl. AF070536:Homo sapiens clone 24566 mRNA sequence /cds=UN
 37821_at Cluster Incl. AF041260:Homo sapiens AIBC1 (AIBC1) mRNA, complete cds /c
 41867_at Cluster Incl. AF055009:Homo sapiens clone 24747 mRNA sequence /cds=UNKN
 36105_at Cluster Incl. M18728:Human nonspecific crossreacting antigen mRNA, comp
 41288_at Cluster Incl. AL036744:DKFZp564I1663_r1 Homo sapiens cDNA, 5 end /clon

METAGENE 38 :

- 32905_s_at Cluster Incl. M30038:Human tryptase mRNA, complete cds /cds=(17,844)
- 5** 40332_at Cluster Incl. AF109134:Homo sapiens 7-60 mRNA, complete cds /cds=(205,2
- 32046_at Cluster Incl. D10495:Homo sapiens mRNA for protein kinase C delta-type,
- 33321_r_at Cluster Incl. M33494:Homo sapiens tryptase-I gene, complete cds /cds=
- 34690_at Cluster Incl. U66616:Human SWI/SNF complex 170 KDa subunit (BAF170) mRN
- 37013_at Cluster Incl. X16295:Human mRNA for angiotensin I converting enzyme (AC
- 10** 37307_at Cluster Incl. X04828:Human mRNA for G(i) protein alpha-subunit (adenyla
- 1810_s_at D10495 /FEATURE= /DEFINITION=HUMPKSCD Homo sapiens mRNA for
- protein ki
- 411_i_atX57351 /FEATURE=cds /DEFINITION=HS18D Human 1-8D gene from interferon-i

15 METAGENE 39 :

- 32003_at Cluster Incl. D49357:Human mRNA for S-adenosylmethionine synthetase, co
- 34154_at Cluster Incl. U62437:Human nicotinic acetylcholine receptor beta2 subun
- 34589_f_at Cluster Incl. AC002366:Human Xp22 BAC CT-285I15 (from CalTech/Researc
- 20** 32907_at Cluster Incl. L41147:Homo sapiens 5-HT6 serotonin receptor mRNA, comple
- 35448_at Cluster Incl. U37219:Human cyclophilin-like protein CyP-60 mRNA, comple
- 35897_r_at Cluster Incl. AB005297:Homo sapiens BAI 1 mRNA, complete cds /cds=(18
- 37530_s_at Cluster Incl. U79716:Human reelin (RELN) mRNA, complete cds /cds=(175
- 38190_r_at Cluster Incl. AB014545:Homo sapiens mRNA for KIAA0645 protein, comple
- 25** 40324_r_at Cluster Incl. AF070585:Homo sapiens clone 24675 mRNA sequence /cds=UN
- 40650_r_at Cluster Incl. X72304:H.sapiens mRNA for corticotrophin releasing fact
- 41720_r_at Cluster Incl. AF009767:AF009767 Homo sapiens cDNA /clone=C97A-12 /gb=
- 31807_at Cluster Incl. U69190:U69190 Homo sapiens cDNA /clone=27655 /gb=U69190 /
- 32631_at Cluster Incl. J03060:Human glucocerebrosidase (GCB) gene /cds=(229,1774
- 30** 35634_at Cluster Incl. U49928:Homo sapiens TAK1 binding protein (TAB1) mRNA, com
- 36547_r_at Cluster Incl. AA521233:aa79a12.s1 Homo sapiens cDNA, 3 end /clone=IM
- 38258_at Cluster Incl. U79290:Human clone 23908 mRNA sequence /cds=UNKNOWN
- /gb=U
- 40481_r_at Cluster Incl. M14333:Homo sapiens c-syn protooncogene mRNA, complete
- 35** 40499_r_at Cluster Incl. AF040708:Homo sapiens candidate tumor suppressor gene 2
- 40769_r_at Cluster Incl. D14689:Human mRNA for KIAA0023 gene, complete cds /cds=
- 40776_at Cluster Incl. M63391:Human desmin gene, complete cds /cds=(80,1489) /gb
- 32166_at Cluster Incl. AB028950:Homo sapiens mRNA for KIAA1027 protein, partial
- 32197_at Cluster Incl. AF070548:Homo sapiens clone 24408 2-oxoglutarate carrier

- 33432_at Cluster Incl. AI547308:PN001_AH_B03.r Homo sapiens cDNA, 5 end /clone_
 33826_at Cluster Incl. AL120500:DKFZp761M078_s1 Homo sapiens cDNA, 3 end /clone_
 37410_at Cluster Incl. AJ224358:Homo sapiens surf5a mRNA, clone 1de /cds=(218,64
 38478_at Cluster Incl. U08377:Human homolog of Drosophila splicing regulator sup
5 40264_g_at Cluster Incl. AF001891:Homo sapiens clone lambda MEN1 region unknown
 40265_s_at Cluster Incl. AI401287:tg92b04.x1 Homo sapiens cDNA, 3 end /clone=IM
 41312_r_at Cluster Incl. AI189624:qd32h08.x1 Homo sapiens cDNA, 3 end /clone=IM
 1998_i_at U19599 /FEATURE= /DEFINITION=HSU19599 Human (BAX delta) mRNA,
 complete
10 1569_r_at L42243 /FEATURE=exon#3 /DEFINITION=HUMIFNAM08 Homo sapiens
 (clone 51H8
 1553_r_at U22028 /FEATURE=expanded_cds /DEFINITION=HSU22028 Human
 cytochrome P45
 568_at M80335 /FEATURE= /DEFINITION=HUMPKACATO Homo sapiens protein kinase A cat
15 533_g_at U17418 /FEATURE= /DEFINITION=HSU17418 Human parathyroid
 hormone/parathy
 293_at Homeotic Protein Hpx-42
 METAGENE 40 :
20
 32874_at Cluster Incl. M65214:Human (HeLa) helix-loop-helix protein HE47 (E2A) m
 36288_at Cluster Incl. X81420:H.sapiens mRNA for hHKb1 protein /cds=(0,1279) /gb
 37136_at Cluster Incl. AB000520:Homo sapiens mRNA for APS, complete cds /cds=(12
 39929_at Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial
25 40362_at Cluster Incl. X61498:H.sapiens mRNA for NF-kB subunit /cds=(163,2964) /
 40385_at Cluster Incl. U64197:Homo sapiens chemokine exodus-1 mRNA, complete cds
 40756_at Cluster Incl. AF081280:Homo sapiens nucleoplasmin-3 (NPM3) mRNA, comple
 41375_at Cluster Incl. AJ245416:Homo sapiens mRNA for G7b protein (G7b gene, loc
 32116_at Cluster Incl. AB002405:Homo sapiens mRNA for LAK-4p, complete cds /cds=
30 38661_at Cluster Incl. X75315:H.sapiens seb4B mRNA /cds=(0,693) /gb=X75315 /gi=4
 39412_at Cluster Incl. U09825:Human acid finger protein mRNA, complete cds /cds=
 32856_at Cluster Incl. AB020626:Homo sapiens mRNA for KIAA0819 protein, partial
 35256_at Cluster Incl. AL096737:Homo sapiens mRNA; cDNA DKFZp434F152 (from
 clone
35 36175_s_at Cluster Incl. AL023584:Human DNA sequence from clone 67K17 on chromos
 38788_at Cluster Incl. M82827:Human fusion protein mRNA, complete cds /cds=(324,
 40249_at Cluster Incl. M55040:Human acetylcholinesterase (ACHE) mRNA, complete c
 41294_at Cluster Incl. AJ238246:Homo sapiens mRNA for sarcolectin /cds=(61,1470)

- 545_g_at S76638 /FEATURE= /DEFINITION=S76638 p50-NF-kappa B homolog [human, peri
 404_at X52425 /FEATURE=mRNA /DEFINITION=HSIL4R Human IL-4-R mRNA for the interle
 241_g_at M64231 /FEATURE=mRNA /DEFINITION=HUMSPERSYN Human spermidine
 5 synthase g
 187_at U07349 /FEATURE= /DEFINITION=HSU07349 Human B lymphocyte serine/threonine

METAGENE 41 :

- 10 31935_s_at Cluster Incl. U75968:Human clone C3 CHL1 protein (CHLR1) mRNA, altern
 32452_at Cluster Incl. X66357:H.sapiens mRNA cdk3 for serine/threonine protein k
 37877_at Cluster Incl. AL050269:Homo sapiens mRNA; cDNA DKFZp564C103 (from
 clone
 39965_at Cluster Incl. AI570572:tm78c02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 15 32133_at Cluster Incl. AB011161:Homo sapiens mRNA for KIAA0589 protein, partial
 35239_at Cluster Incl. X86810:Homo sapiens EDMD gene /cds=(110,874) /gb=X86810 /
 35630_at Cluster Incl. X87342:H.sapiens mRNA for human giant larvae homolog /cds
 38284_at Cluster Incl. AJ007041:Homo sapiens mRNA for trithorax homologue 2 /cds
 38699_at Cluster Incl. X00734:Human beta-tubulin gene (5-beta) with ten Alu fami
 20 39398_s_at Cluster Incl. AB023205:Homo sapiens mRNA for KIAA0988 protein, comple
 40164_at Cluster Incl. X69550:H.sapiens mRNA for rho GDP-dissociation Inhibitor
 40414_at Cluster Incl. X59303:Human G7a mRNA for valyl-tRNA synthetase /cds=(219
 41220_at Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete
 33454_at Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /
 25 33887_at Cluster Incl. D84064:Homo sapiens mRNA for Hrs, complete cds /cds=(60,2
 39833_at Cluster Incl. R54564:yg81b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 41565_at Cluster Incl. AF034373:Homo sapiens ataxin-2-like protein A2LP (A2LG) m
 32553_at Cluster Incl. M94046:Human zinc finger protein (MAZ) mRNA /cds=UNKNOWN
 493_at U29171 /FEATURE= /DEFINITION=HSU29171 Human casein kinase I delta mRNA, c
 30 454_at U66617 /FEATURE= /DEFINITION=HSU66617 Human SWI/SNF complex 60 KDa
 subuni

METAGENE 42 :

- 35 34003_at Cluster Incl. U47924:Human chromosome 12p13 sequence /cds=(373,1122) /g
 37458_at Cluster Incl. AJ223728:Homo sapiens Porc-P1 gene similar to yeast CDC45
 38943_at Cluster Incl. U36787:Human putative holocytochrome c-type synthetase mR
 41060_at Cluster Incl. M74093:Human cyclin mRNA /cds=UNKNOWN /gb=M74093
 /gi=8066

- 31845_at Cluster Incl. U32645:Human myeloid elf-1 like factor (MEF) mRNA, comple
36457_at Cluster Incl. U10860:Human guanosine 5-monophosphate synthase mRNA, com
36837_at Cluster Incl. U63743:Homo sapiens mitotic centromere-associated kinesin
38331_at Cluster Incl. Y07566:H.sapiens mRNA for RIT protein /cds=(145,804) /gb=
5 39801_at Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3)
32263_at Cluster Incl. AL080146:Homo sapiens mRNA; cDNA DKFZp434B174 (from
clone
32801_at Cluster Incl. AB002315:Human mRNA for KIAA0317 gene, complete cds /cds=
33380_at Cluster Incl. AB005754:Homo sapiens mRNA for LAK-1, complete cds /cds=(
10 34852_g_at Cluster Incl. AF011468:Homo sapiens serine/threonine kinase (BTAK) mR
36581_at Cluster Incl. U09510:Human glycyl-tRNA synthetase mRNA, complete cds /c
36582_g_at Cluster Incl. U09510:Human glycyl-tRNA synthetase mRNA, complete cds
37295_at Cluster Incl. X63469:H.sapiens mRNA for transcription factor TFIIE beta
37351_at Cluster Incl. X90858:H.sapiens mRNA for uridine phosphorylase /cds=(352
15 38416_at Cluster Incl. L27706:Human chaperonin protein (Tcp20) gene complete cds
39175_at Cluster Incl. D25328:Human mRNA for platelet-type phosphofructokinase,
39826_f_at Cluster Incl. W29115:56e8 Homo sapiens cDNA /gb=W29115 /gi=1309081 /u
39827_at Cluster Incl. AA522530:ni38d12.s1 Homo sapiens cDNA, 3 end /clone=IMAG
41516_at Cluster Incl. U95735:Human SNARE protein Ykt6 (YKT6) mRNA, complete cds
20 1347_at S78187 /FEATURE= /DEFINITION=S78187 CDC25Hu2=cdc25+ homolog [human,
mRNA
1310_at D26599 /FEATURE= /DEFINITION=HUMPSH2 Human mRNA for proteasome subunit H
811_at U64444 /FEATURE= /DEFINITION=HSU64444 Homo sapiens ubiquitin fusion-degra
688_at L02426 /FEATURE= /DEFINITION=HUM26SPSIV Human 26S protease (S4) regulator
25 157_at U65011 /FEATURE= /DEFINITION=HSU65011 Human preferentially expressed anti
METAGENE 43 :
38148_at Cluster Incl. D83702:Homo sapiens mRNA for photolyase, complete cds /cd
30 38152_at Cluster Incl. AI632589:wb10h03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
41381_at Cluster Incl. AB002306:Human mRNA for KIAA0308 gene, partial cds /cds=(
41634_at Cluster Incl. D87445:Human mRNA for KIAA0256 gene, complete cds /cds=(1
32119_at Cluster Incl. AL049423:Homo sapiens mRNA; cDNA DKFZp586B211 (from
clone
35 32643_at Cluster Incl. L07956:Homo sapiens 1,4-alpha-glucan branching enzyme (HG
32696_at Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841
/gi=35314
35209_at Cluster Incl. AB018309:Homo sapiens mRNA for KIAA0766 protein, complete
36032_at Cluster Incl. AL031427:dJ167A19.3 (novel protein) /cds=(123,557) /gb=AL

- 37242_at Cluster Incl. U79260:Human clone 23745 mRNA, complete cds /cds=(609,102
 37615_at Cluster Incl. D86962:Human mRNA for KIAA0207 gene, complete cds /cds=(7
 38685_at Cluster Incl. AL035306:H.sapiens gene from PAC 426I6, similar to syntax
 39344_at Cluster Incl. U53209:Human transformer-2 alpha (htra-2 alpha) mRNA, com
 5 40091_at Cluster Incl. U00115:Human zinc-finger protein (bcl-6) mRNA, complete c
 41225_at Cluster Incl. AL049417:Homo sapiens mRNA; cDNA DKFZp586O1919 (from
 clon
 41729_at Cluster Incl. AJ009771:Homo sapiens mRNA for putative RING finger prote
 32792_at Cluster Incl. AL031432:Human DNA sequence from clone 465N24 on chromoso
 10 32854_at Cluster Incl. AB014596:Homo sapiens mRNA for KIAA0696 protein, partial
 34369_at Cluster Incl. D86987:Homo sapiens mRNA for KIAA0214 protein, complete c
 36948_at Cluster Incl. AL109701:Homo sapiens mRNA full length insert cDNA clone
 36974_at Cluster Incl. D88378:Homo sapiens mRNA for proteasome inhibitor hPI31 s
 37308_at Cluster Incl. AI888084:wm29g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 15 38727_at Cluster Incl. M23161:Human transposon-like element mRNA /cds=UNKNOWN /g
 38821_at Cluster Incl. AJ002030:Homo sapiens mRNA for putative progesterone bind
 38836_at Cluster Incl. AL008583:dJ327J16.2 (human ortholog of rat Neuronal Pentr
 41498_at Cluster Incl. AB020718:Homo sapiens mRNA for KIAA0911 protein, complete
 498_at U33821 /FEATURE= /DEFINITION=HSU33821 Homo sapiens tax1-binding protein T
 20
 METAGENE 44 :
 32959_at Cluster Incl. M25809:Human endomembrane proton pump subunit mRNA, compl
 37865_at Cluster Incl. J05081:Human endothelin 3 (EDN3) mRNA, complete cds /cds=
 25 38202_at Cluster Incl. AB011535:Homo sapiens mRNA for MEGF1, partial cds /cds=(0
 31791_at Cluster Incl. Y16961:Homo sapiens mRNA for KET protein /cds=(27,2069) /
 35178_at Cluster Incl. W27944:39g8 Homo sapiens cDNA /gb=W27944 /gi=1307892 /ug=
 35976_at Cluster Incl. U65092:Human melanocyte-specific gene 1 (msg1) mRNA, comp
 37909_at Cluster Incl. L34155:Homo sapiens laminin-related protein (LamA3) mRNA,
 30 38298_at Cluster Incl. U25138:Human MaxiK potassium channel beta subunit mRNA, c
 38673_s_at Cluster Incl. D64137:Human KIP2 gene for Cdk-inhibitor p57KIP2, compl
 38700_at Cluster Incl. M33146:Human cysteine-rich peptide mRNA, complete cds /cd
 38721_at Cluster Incl. W72733:zd77h11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 32610_at Cluster Incl. X93510:H.sapiens mRNA for 37 kDa LIM domain protein /cds=
 35 1673_at M14764 /FEATURE=mRNA /DEFINITION=HUMNGFR Human nerve growth factor
 recep
 996_at X59065 /FEATURE=exon /DEFINITION=HSFGFEX3 H.sapiens FGF gene, exon 3
 469_at U66406 /FEATURE= /DEFINITION=HSU66406 Human putative EPH-related PTK rece

234_s_at M57399 /FEATURE= /DEFINITION=HUMHBNF1 Human nerve growth factor
(HBNF-1
160040_at X52001 /FEATURE=cds /DEFINITION=HSET3AA H.sapiens endothelin 3
mRNA /N

5

METAGENE 45 :

34216_at Cluster Incl. AA478904:zv20c05.r1 Homo sapiens cDNA, 5' end /clone=IMAG
36918_at Cluster Incl. Y15723:Homo sapiens mRNA for soluble guanylyl cyclase /cd
10 40949_at Cluster Incl. AF035812:Homo sapiens dynein light intermediate chain 2 (

METAGENE 46 :

31386_at Cluster Incl. M20812:Human kappa-immunoglobulin germline pseudogene (co
15 31669_s_at Cluster Incl. AF039307:Homo sapiens homeobox A11 (HOXA11) gene, compl
33601_at Cluster Incl. AF052145:Homo sapiens clone 24400 mRNA sequence /cds=UNKN
35096_at Cluster Incl. U18244:Human excitatory amino acid transporter 4 mRNA, co
32913_i_at Cluster Incl. AC005175:Homo sapiens chromosome 19, cosmid R31449 /cds
34454_r_at Cluster Incl. U32576:Human apolipoprotein apoC-IV (APOC4) gene, compl
20 34894_r_at Cluster Incl. AC003965:Homo sapiens chromosome 16, cosmid clone 325D7
36252_at Cluster Incl. U43030:Human cardiotrophin-1 (CTF1) mRNA, complete cds /c
38166_r_at Cluster Incl. AF010403:Homo sapiens ALR mRNA, complete cds /cds=(0,15
38597_f_at Cluster Incl. D50402:Human mRNA for NRAMP1, complete cds /cds=(175,18
40336_at Cluster Incl. J03826:Human adrenodoxin reductase mRNA, complete cds /cd
25 41117_s_at Cluster Incl. AB016243:Homo sapiens gene for regulatory factor 2 of s
41426_at Cluster Incl. U38864:Human zinc-finger protein C2H2-150 mRNA, complete
31815_r_at Cluster Incl. AB009462:Homo sapiens hLRp105 mRNA for LDL receptor rel
33268_at Cluster Incl. L25270:Human XE169 mRNA, complete cds /cds=(531,5213) /gb
33275_at Cluster Incl. AB016194:Homo sapiens elk1 oncogene, complete cds /cds=(3
30 36038_r_at Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /c
37267_at Cluster Incl. Z50115:H.sapiens mRNA for thimet oligopeptidase (metallo
38265_at Cluster Incl. AI538172:ti75f08.x1 Homo sapiens cDNA, 3' end /clone=IMAG
38282_at Cluster Incl. U41767:Human metargidin precursor mRNA, complete cds /cds
40138_at Cluster Incl. U70735:Homo sapiens 34 kDa Mov34 homolog mRNA, complete c
35 40494_at Cluster Incl. AF043733:Homo sapiens death effector domain-containing te
40840_at Cluster Incl. M80254:H.sapiens cyclophilin isoform (hCyP3) mRNA, comple
41227_at Cluster Incl. AL022162:Homo sapiens DNA sequence from PAC 454M7 on chro
32848_at Cluster Incl. AF020736:Homo sapiens ATPase homolog mRNA, complete cds /
33361_at Cluster Incl. AF052149:Homo sapiens clone 24733 mRNA sequence /cds=UNKN

- 35262_at Cluster Incl. AF022229:Homo sapiens translation initiation factor 6 (el
 36094_at Cluster Incl. M21984:Human (clone PWHtT16) skeletal muscle Troponin T
 38055_at Cluster Incl. AI683748:tw53e07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 39113_at Cluster Incl. AI262789:qk35e02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 5 39543_at Cluster Incl. AI077476:oz49b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40183_at Cluster Incl. AI660225:we68f05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40186_at Cluster Incl. Y08302:H.sapiens mRNA for MAP kinase phosphatase 4 /cds=(
 40594_r_at Cluster Incl. Z22533:H.sapiens ALK-1 mRNA /cds=(282,1793) /gb=Z22533
 40598_at Cluster Incl. W20138:zb40d12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 10 40888_f_at Cluster Incl. W28170:43a12 Homo sapiens cDNA /gb=W28170 /gi=1308118 /
 2078_s_at M13228 /FEATURE=cds /DEFINITION=HUMNMCY1A Human N-myc
 oncogene protein
 1547_at U09607 /FEATURE= /DEFINITION=HSU09607 Human JAK family protein tyrosine
 1127_at L07597 /FEATURE= /DEFINITION=HUMS6KINA Homo sapiens ribosomal protein S6
 15 648_at L37112 /FEATURE=mRNA /DEFINITION=HUMVVR Homo sapiens vasopressin V3
 recep
 632_at L40027 /FEATURE=mRNA /DEFINITION=HUMGLYSYN Homo sapiens glycogen
 synthase
 567_s_at M79463 /FEATURE= /DEFINITION=HUMPML2 Human PML-2 mRNA,
 20 complete CDS
 440_at X12492 /FEATURE=cds /DEFINITION=HSCTF1 Human mRNA for CAAT-box binding
 tr
 301_at Mucin 6, Gastric
 272_at K02054 /FEATURE=mRNA /DEFINITION=HUMGRP5E Human gastrin-releasing peptide
 25
 METAGENE 47 :
 36392_at Cluster Incl. U09413:Human zinc finger protein ZNF135 mRNA, complete cd
 38935_at Cluster Incl. X72790:Human endogenous retrovirus mRNA for ORF /cds=(524
 30 32065_at Cluster Incl. S68134:CREM=cyclic AMP-responsive element modulator beta
 32142_at Cluster Incl. U26424:Human Ste20-like kinase (MST2) mRNA, complete cds
 41241_at Cluster Incl. D84273:Homo sapiens mRNA for Asparaginyl tRNA Synthetase,
 41744_at Cluster Incl. AF070533:Homo sapiens clone 24619 mRNA sequence /cds=UNKN
 32835_at Cluster Incl. AA725102:ai08h05.s1 Homo sapiens cDNA, 3 end /clone=1342
 35 34839_at Cluster Incl. AB029027:Homo sapiens mRNA for KIAA1104 protein, complete
 35847_at Cluster Incl. AB028980:Homo sapiens mRNA for KIAA1057 protein, partial
 36953_at Cluster Incl. U44378:Human homozygous deletion target in pancreatic car
 37755_at Cluster Incl. AB023169:Homo sapiens mRNA for KIAA0952 protein, complete

38748_at Cluster Incl. U76421:Human dsRNA adenosine deaminase DRADA2b
(DRADA2b)
32602_at Cluster Incl. X63465:H.sapiens hGDS mRNA for smg GDS /cds=(0,1676) /gb=

5 METAGENE 48 :

35906_at Cluster Incl. L29339:Homo sapiens Na⁺/glucose co-transporter (SGLT1) ge
39230_at Cluster Incl. AL022318:bK150C2.2 (Phorbolin 3) /cds=(29,1177) /gb=AL022
33337_at Cluster Incl. AF002668:Homo sapiens putative fatty acid desaturase MLD
10 36014_at Cluster Incl. AL033377:Human DNA sequence from clone 287G14 on chromoso
40803_at Cluster Incl. AL050161:Homo sapiens mRNA; cDNA DKFZp586B0222 (from
clon
41535_at Cluster Incl. AF006484:Homo sapiens putative oral tumor suppressor prot
1739_at M99487 /FEATURE= /DEFINITION=HUMPSM Human prostate-specific membrane ant
15 988_at X16354 /FEATURE= /DEFINITION=HSTM1CEA Human mRNA for transmembrane
carcin
935_at L12168 /FEATURE= /DEFINITION=HUMADCY Homo sapiens adenylyl cyclase-associ

METAGENE 49 :

20

32991_f_at Cluster Incl. M86933:Human amelogenin (AMELY) mRNA, complete cds /cds
36709_at Cluster Incl. Y00093:H.sapiens mRNA for leukocyte adhesion glycoprotein
41678_at Cluster Incl. AF025304:Homo sapiens protein-tyrosine kinase EPHB2v (EPH
37976_at Cluster Incl. AL034397:Human DNA sequence from clone 159A1 on chromosom
25 33390_at Cluster Incl. AA203487:zx53d03.r1 Homo sapiens cDNA, 5' end /clone=IMAG
36575_at Cluster Incl. S59049:BL34=B cell activation gene [human, mRNA, 1398 nt]
37397_at Cluster Incl. L34657:Homo sapiens platelet/endothelial cell adhesion mo
38404_at Cluster Incl. M55153:Human transglutaminase (TGase) mRNA, complete cds
1780_at M19722 /FEATURE= /DEFINITION=HUMFGR Human fgr proto-oncogene encoded p55

30

METAGENE 50 :

39244_at Cluster Incl. M28211:Homo sapiens GTP-binding protein (RAB4) mRNA, comp
40004_at Cluster Incl. X91868:H.sapiens mRNA for SIX1 protein /cds=(275,1129) /g
35 40685_at Cluster Incl. U10868:Human aldehyde dehydrogenase ALDH7 mRNA, complete
33245_at Cluster Incl. AF004709:Homo sapiens stress-activated protein kinase 4 m

METAGENE 51 :

- 36246_at Cluster Incl. Z35309:H.sapiens mRNA for adenylyl cyclase /cds=(2094,584
 36264_at Cluster Incl. S75168:Matk=megakaryocyte-associated tyrosine kinase [hum
 36044_at Cluster Incl. AF022912:Homo sapiens cGMP phosphodiesterase delta subuni
 36881_at Cluster Incl. X71129:H.sapiens mRNA for electron transfer flavoprotein
5 32796_f_at Cluster Incl. U66061:trypsinogen C /cds=(84,827) /gb=U66061 /gi=15525
 34410_at Cluster Incl. U49260:Human mevalonate pyrophosphate decarboxylase (MPD)
 36169_at Cluster Incl. N47307:yy87a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 36586_at Cluster Incl. U78521:Homo sapiens immunophilin homolog ARA9 mRNA, compl
 1650_g_at U61836 /FEATURE=mRNA /DEFINITION=HSU61836 Human putative cyclin
10 G1 int
 111_at Y08200 /FEATURE= /DEFINITION=HSRABGTRA Homo sapiens mRNA for rab
 geranyl
- METAGENE 52 :
- 15** 32380_at Cluster Incl. Z34974:H.sapiens mRNA for plakophilin (partial) /cds=(252
 34689_at Cluster Incl. AJ243797:Homo sapiens mRNA for deoxyribonuclease III (dm
 35988_i_at Cluster Incl. AI417075:tg78e09.x1 Homo sapiens cDNA, 3 end /clone=IM
 36462_at Cluster Incl. U50383:Human retinoic acid-responsive protein (NN8-4AG) m
20 32751_at Cluster Incl. AF007140:Homo sapiens clone 23711 unknown mRNA, partial c
 160041_at X79568 /FEATURE=cds /DEFINITION=HSBDP1 H.sapiens BDP1 mRNA for
 protein
- METAGENE 53 :
- 25** 36363_at Cluster Incl. U30930:Human UDP-Galactose ceramide galactosyl transferas
 39243_s_at Cluster Incl. U94319:Human autoantigen DFS70 mRNA, partial cds /cds=(
 39967_at Cluster Incl. AB019527:Homo sapiens mRNA for LDOC1 protein, complete cd
 32841_at Cluster Incl. U19765:Human nucleic acid binding protein gene, complete
30
- METAGENE 54 :
- 41100_at Cluster Incl. AB023172:Homo sapiens mRNA for KIAA0955 protein, complete
 36021_at Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from
35 clon
 36103_at Cluster Incl. D90144:Homo sapiens gene for LD78 alpha precursor, comple
 41814_at Cluster Incl. M29877:Human alpha-L-fucosidase, complete cds /cds=UNKNOWN
 1520_s_at X04500 /FEATURE=expanded_cds /DEFINITION=HSIL1B Human gene for
 prointe

METAGENE 55 :

- 39251_at Cluster Incl. M74091:Human cyclin mRNA /cds=UNKNOWN /gb=M74091
5 /gi=1806
 34274_at Cluster Incl. AB029039:Homo sapiens mRNA for KIAA1116 protein, complete
 34723_at Cluster Incl. U79270:Human clone 23707 mRNA, partial cds /cds=(0,460) /
 38277_at Cluster Incl. M29550:Human calcineurin A1 mRNA, complete cds /cds=(107,
 33354_at Cluster Incl. AA630312:ac08f05.s1 Homo sapiens cDNA, 3 end /clone=IMAG

10

METAGENE 56 :

- 35403_at Cluster Incl. AB029017:Homo sapiens mRNA for KIAA1094 protein, complete
 34231_at Cluster Incl. AF074606:Homo sapiens histone acetyltransferase (HBO1) mR
15 38973_at Cluster Incl. AB028943:Homo sapiens mRNA for KIAA1020 protein, partial

METAGENE 57 :

- 35004_at Cluster Incl. U31875:Human Hep27 protein mRNA, complete cds /cds=(433,1
20 38268_at Cluster Incl. U08989:Human glutamate transporter mRNA, complete cds /cd
 39078_at Cluster Incl. U43286:Human selenophosphate synthetase 2 (SPS2) mRNA, co
 40765_at Cluster Incl. D87438:Human mRNA for KIAA0251 gene, partial cds /cds=(0,

METAGENE 58 :

25

- 31668_f_at Cluster Incl. W28193:43d12 Homo sapiens cDNA /gb=W28193 /gi=1308141 /
 31681_at Cluster Incl. X57282:H.sapiens mRNA for soluble erythropoietin receptor
 31997_at Cluster Incl. X15674:Human pTR5 mRNA for repetitive sequence /cds=UNKNO
 32498_at Cluster Incl. L35318:Human rearranged metabotropic glutamate receptor t
30 34078_s_at Cluster Incl. M61854:Human cytochrome P4502C19 (CYP2C19) mRNA, clone
 34089_at Cluster Incl. AB028953:Homo sapiens mRNA for KIAA1030 protein, partial
 34604_at Cluster Incl. L05568:Human Na⁺/Cl⁻ dependent serotonin transporter mRNA
 32335_r_at Cluster Incl. AB009010:Homo sapiens mRNA for polyubiquitin UbC, compl
 33546_at Cluster Incl. AI923984:wn49d12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
35 33985_s_at Cluster Incl. W28616:49b9 Homo sapiens cDNA /gb=W28616 /gi=1308564 /u
 33986_r_at Cluster Incl. W28616:49b9 Homo sapiens cDNA /gb=W28616 /gi=1308564 /u
 34480_at Cluster Incl. AF016272:Homo sapiens Ksp-cadherin (CDH16) mRNA, complete
 34906_g_at Cluster Incl. AA977136:ocq24f02.s1 Homo sapiens cDNA, 3 end /clone=IM
 35434_at Cluster Incl. L16794:Human transcription factor (MEF2) mRNA, complete c

	35956_s_at	Cluster Incl. U18467:Human pregnancy-specific beta 1-glycoprotein 7 (
	36222_at	Cluster Incl. AJ012008:Homo sapiens genes encoding RNCC protein, DDAH p
	36242_at	Cluster Incl. M21539:Human small proline rich protein (sprII) mRNA, clo
	36747_at	Cluster Incl. AF052172:Homo sapiens clone 24617 mRNA sequence /cds=UNKN
5	36762_at	Cluster Incl. X15376:Human mRNA for GABA-A receptor, gamma 2 subunit /c
	37793_r_at	Cluster Incl. AF034956:Homo sapiens RAD51D mRNA, complete cds /cds=(1
	38529_at	Cluster Incl. X68968:H.sapiens mRNA for acetyl-CoA carboxylase /cds=(0,
	38858_at	Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) m
	39305_at	Cluster Incl. AI191826:qd47g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG
10	39657_at	Cluster Incl. X07695:Human mRNA for cytokeratin 4 C-terminal region /cd
	41002_at	Cluster Incl. U59299:Homo sapiens putative monocarboxylate transporter
	41118_at	Cluster Incl. AI921843:wp07a11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41624_r_at	Cluster Incl. AA932443:oo75b11.s1 Homo sapiens cDNA, 3 end /clone=IM
	31829_r_at	Cluster Incl. AF027515:Homo sapiens trans-golgi network glycoprotein
15	33712_at	Cluster Incl. N63574:yy63f05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	33719_at	Cluster Incl. AF010242:AF010242 Homo sapiens cDNA /gb=AF010242 /gi=2612
	34704_r_at	Cluster Incl. AA151971:zo30b03.r1 Homo sapiens cDNA, 5 end /clone=IM
	35208_at	Cluster Incl. AB020681:Homo sapiens mRNA for KIAA0874 protein, partial
	35990_at	Cluster Incl. AB007947:Homo sapiens mRNA for KIAA0478 protein, complete
20	39051_at	Cluster Incl. U31767:Human neuronatin alpha and neuronatin beta genes,
	39383_at	Cluster Incl. AB007882:Homo sapiens KIAA0422 mRNA, partial cds /cds=(0,
	32188_at	Cluster Incl. M96980:Homo sapiens myelin transcription factor 1 (MTF1)
	32228_at	Cluster Incl. AB020706:Homo sapiens mRNA for KIAA0899 protein, partial
	32815_at	Cluster Incl. AI687419:tp95h03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
25	36168_at	Cluster Incl. X66945:H.sapiens N-sam mRNA for fibroblast growth factor
	36573_at	Cluster Incl. U78524:Human Gu binding protein mRNA, partial cds /cds=(0
	37362_at	Cluster Incl. X54871:H.sapiens mRNA for ras-related protein Rab5b /cds=
	37746_r_at	Cluster Incl. U15131:Human p126 (ST5) mRNA, complete cds /cds=(114,35
	38024_at	Cluster Incl. AB020678:Homo sapiens mRNA for KIAA0871 protein, complete
30	39199_at	Cluster Incl. W28661:49h1 Homo sapiens cDNA /gb=W28661 /gi=1308609 /ug=
	40236_at	Cluster Incl. D29990:Human mRNA for cationic amino acid transporter 2,
	40277_at	Cluster Incl. AI799984:wc46f12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	41276_at	Cluster Incl. W27641:37d11 Homo sapiens cDNA /gb=W27641 /gi=1307715 /ug
	1910_s_at	M14745 /FEATURE=cds /DEFINITION=HUMBCL2C Human bcl-2 mRNA
35	1796_s_at	U05681 /FEATURE=expanded_cds /DEFINITION=HSBCL3S2 Human proto-
	oncogene	
	1661_i_at	Antigen, Prostate Specific, Alt. Splice Form 2
	1662_r_at	Antigen, Prostate Specific, Alt. Splice Form 2

1667_s_at J02871 /FEATURE= /DEFINITION=HUMCP45IV Human lung cytochrome P450 (IV

716_at D87002 /FEATURE=cds#5 /DEFINITION=D87002 Homo sapiens immunoglobulin lamb

713_at Helix-Loop-Helix Protein Delta Max, Alt. Splice 1

5 666_at L20965 /FEATURE= /DEFINITION=HUMPDEA Human phosphodiesterase mRNA, comple

160028_s_at X12949 /FEATURE=cds /DEFINITION=HSRETPON Human ret proto-oncogene mR

10 METAGENE 59 :

31502_at Cluster Incl. W27953:39h7 Homo sapiens cDNA /gb=W27953 /gi=1307901 /ug=

37249_at Cluster Incl. AF079529:Homo sapiens cAMP-specific phosphodiesterase 8B

39429_at Cluster Incl. X99050:H.sapiens mRNA; UV Radiation Resistance Associated

15

METAGENE 60 :

37478_at Cluster Incl. Y16752:Homo sapiens mRNA for secretagoin, complete CDS /

32087_at Cluster Incl. M65217:Human heat shock factor 2 (HSF2) mRNA, complete cd

20 33710_at Cluster Incl. U72515:Human C3f mRNA, complete cds /cds=(117,1262) /gb=U

35712_at Cluster Incl. AC004142:Homo sapiens BAC clone RG118D07 from 7q31 /cds=(

37581_at Cluster Incl. X92972:H.sapiens mRNA for protein phosphatase 6 /cds=(21,

38626_at Cluster Incl. AB007859:Homo sapiens KIAA0399 mRNA, partial cds /cds=(0,

39699_at Cluster Incl. D28476:Human mRNA for KIAA0045 gene, complete cds /cds=(1

25 40155_at Cluster Incl. D31883:Human mRNA for KIAA0059 gene, complete cds /cds=(2

40455_at Cluster Incl. AB020637:Homo sapiens mRNA for KIAA0830 protein, partial

40801_at Cluster Incl. AA643063:nr95e11.s1 Homo sapiens cDNA, 3 end /clone=IMAG

32857_at Cluster Incl. L13858:Human guanine nucleotide exchange factor mRNA, com

33420_g_at Cluster Incl. U83857:Human Aac11 (aac11) mRNA, complete cds /cds=(77,

30 35320_at Cluster Incl. AB004857:Homo sapiens mRNA for NRAMP2, complete cds /cds=

36965_at Cluster Incl. U13616:Human ankryrin G (ANK-3) mRNA, complete cds /cds=(1

METAGENE 61 :

35 40314_at Cluster Incl. AJ002309:Homo sapiens mRNA for synaptogyrin 3 /cds=(17,67

40390_at Cluster Incl. J05037:Human serine dehydratase mRNA, complete cds /cds=(

37200_at Cluster Incl. J04162:Human leukocyte IgG receptor (Fc-gamma-R) mRNA, co

37220_at Cluster Incl. M63835:Human IgG Fc receptor I gene /cds=(155,1279) /gb=M

37233_at Cluster Incl. AF079167:untitled /cds=(61,882) /gb=AF079167 /gi=4050003

- 39372_at Cluster Incl. W26480:30b8 Homo sapiens cDNA /gb=W26480 /gi=1307179 /ug=
 41779_at Cluster Incl. U70426:Homo sapiens A28-RGS14p mRNA, complete cds /cds=(9
 33437_at Cluster Incl. AJ005892:Homo sapiens mRNA for JM23 protein, complete cod
 34319_at Cluster Incl. AA131149:zo16d05.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 5 37391_at Cluster Incl. X12451:Human mRNA for pro-cathepsin L (major excreted pro
 33143_s_at Cluster Incl. U81800:Homo sapiens monocarboxylate transporter (MCT3)
 824_at U90313 /FEATURE= /DEFINITION=HSU90313 Human glutathione-S-transferase hom
 189_s_at U09937 /FEATURE=mRNA /DEFINITION=HSUROKR7 Human urokinase-type
 plasmino
- 10
 METAGENE 62 :
- 31719_at Cluster Incl. X02761:Human mRNA for fibronectin (FN precursor) /cds=(0,
 32465_at Cluster Incl. AF009801:Homo sapiens homeodomain protein (BAPX1) mRNA, c
 15 32306_g_at Cluster Incl. J03464:Human collagen alpha-2 type I mRNA, complete cds
 32319_at Cluster Incl. AL022310:dJ395P12.2 (tax-transcriptionally activated glyc
 37459_at Cluster Incl. X57527:Human COL8A1 mRNA for alpha 1(VIII) collagen /cds=
 38181_at Cluster Incl. X57766:Human stromelysin-3 mRNA /cds=(9,1475) /gb=X57766
 38566_at Cluster Incl. X60382:H.sapiens COL10A1 gene for collagen (alpha-1 type
 20 39945_at Cluster Incl. U09278:Human fibroblast activation protein mRNA, complete
 36070_at Cluster Incl. AL049389:Homo sapiens mRNA; cDNA DKFZp586O0118 (from
 clon,
 37578_at Cluster Incl. D25248:Homo sapiens mRNA, clone-RES4-4 /cds=UNKNOWN
 /gb=D
 25 37892_at Cluster Incl. J04177:Human alpha-1 type XI collagen (COL11A1) mRNA, com
 38637_at Cluster Incl. L16895:Human lysyl oxidase (LOX) gene, exon 7 /cds=(0,6)
 39333_at Cluster Incl. M26576:Human alpha-1 collagen type IV gene /cds=(0,5009)
 39695_at Cluster Incl. M31516:Human decay-accelerating factor mRNA, complete cds
 34778_at Cluster Incl. AA418080:zv97h07.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 30 35832_at Cluster Incl. AB029000:Homo sapiens mRNA for KIAA1077 protein, partial
 37310_at Cluster Incl. X02419:H.sapiens uPA gene /cds=(119,1414) /gb=X02419 /gi=
 38127_at Cluster Incl. Z48199:H.sapiens syndecan-1 gene (exons 2-5) /cds=(0,866)
 38420_at Cluster Incl. Y14690:Homo sapiens mRNA for procollagen alpha 2(V) /cds=
 33168_at Cluster Incl. H24861:yl42e11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 35 1372_at M31165 /FEATURE=mRNA /DEFINITION=HUMTSG6A Human tumor necrosis factor-in
 658_at L12350 /FEATURE=mRNA /DEFINITION=HUMTHRSPO Human thrombospondin 2
 (THBS2)
 659_g_at L12350 /FEATURE=mRNA /DEFINITION=HUMTHRSPO Human
 thrombospondin 2 (THBS

553_g_at U02570 /FEATURE= /DEFINITION=HSU02570 Human CDC42 GTPase-activating pro
 120_at X68742 /FEATURE= /DEFINITION=HSINTASA H.sapiens mRNA for integrin, alpha

5 METAGENE 63 :

- 35606_at Cluster Incl. D16583:Human gene for L-histidine decarboxylase, complete
 32363_at Cluster Incl. AF059214:Homo sapiens cholesterol 25-hydroxylase mRNA, co
 31855_at Cluster Incl. U61374:Human novel protein with short consensus repeats o
 10 32666_at Cluster Incl. U19495:Human intercrine-alpha (hIRH) mRNA, complete cds /
 33767_at Cluster Incl. X15306:H.sapiens NF-H gene, exon 1 (and joined CDS) /cds=
 36091_at Cluster Incl. AF051323:Homo sapiens Src-associated adaptor protein (SAP
 36917_at Cluster Incl. Z26653:H.sapiens mRNA for laminin M chain (merosin) /cds=
 38299_at Cluster Incl. X04430:Human IFN-beta 2a mRNA for interferon-beta-2 /cds=
 15 38972_at Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKN
 39038_at Cluster Incl. AF093118:Homo sapiens UP50 mRNA, complete cds /cds=(168,1
 39066_at Cluster Incl. L38486:Human microfibril-associated glycoprotein 4 (MFAP4
 40767_at Cluster Incl. M59499:Human lipoprotein-associated coagulation inhibitor
 41123_s_at Cluster Incl. L35594:Human autotaxin mRNA, complete cds /cds=(49,2796
 20 41124_r_at Cluster Incl. L35594:Human autotaxin mRNA, complete cds /cds=(49,2796
 33834_at Cluster Incl. L36033:Human pre-B cell stimulating factor homologue (SDF
 34388_at Cluster Incl. Y11710:H.sapiens mRNA for extracellular matrix protein co
 34797_at Cluster Incl. AF014402:Homo sapiens type-2 phosphatidic acid phosphatas
 34853_at Cluster Incl. AB007865:Homo sapiens KIAA0405 mRNA, complete cds /cds=(1
 25 36119_at Cluster Incl. AF070648:Homo sapiens clone 24651 mRNA sequence /cds=UNKN
 36156_at Cluster Incl. U41518:Human channel-like integral membrane protein (AQP-
 36617_at Cluster Incl. X77956:H.sapiens Id1 mRNA /cds=(35,499) /gb=X77956 /gi=45
 36618_g_at Cluster Incl. X77956:H.sapiens Id1 mRNA /cds=(35,499) /gb=X77956 /gi=
 36619_r_at Cluster Incl. S78825:Id1 (Id1-b)=transcription regulator helix-loop-h
 30 36627_at Cluster Incl. X86693:H.sapiens mRNA for hevin like protein /cds=(322,23
 37043_at Cluster Incl. AL021154:dJ150O5.2.(Inhibitor of DNA binding 3 (dominant
 38786_at Cluster Incl. AL079279:Homo sapiens mRNA full length insert cDNA clone
 40570_at Cluster Incl. AF032885:Homo sapiens forkhead protein (FKHR) mRNA, compl
 40607_at Cluster Incl. U97105:Homo sapiens N2A3 mRNA, complete cds /cds=(1336,30
 35 41246_at Cluster Incl. AI743134:wg87f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 32551_at Cluster Incl. U03877:Human extracellular protein (S1-5) mRNA, complete
 32612_at Cluster Incl. X04412:Human mRNA for plasma gelsolin /cds=(14,2362) /gb=
 1814_at D50683 /FEATURE= /DEFINITION=D50683 Homo sapiens mRNA for TGF-betaIR al
 1736_at M62402 /FEATURE= /DEFINITION=HUMIGFBP4 Human insulin-like growth factor

- 1596_g_at L06139 /FEATURE= /DEFINITION=HUMTEKRPTK Homo sapiens receptor protein-
- 656_at L08488 /FEATURE= /DEFINITION=HUMINOS Human inositol polyphosphate 1-phosph
- 607_s_at M10321 /FEATURE=mRNA /DEFINITION=HUMVWFM Human von
- 5** Willebrand factor mR

METAGENE 64 :

- 40704_at Cluster Incl. Z29090:H.sapiens mRNA for phosphatidylinositol 3-kinase /
- 10** 41088_at Cluster Incl. X12433:Human pHS1-2 mRNA with ORF homologous to membrane
- 33251_at Cluster Incl. AB018322:Homo sapiens mRNA for KIAA0779 protein, partial
- 34225_at Cluster Incl. AF101434:Homo sapiens Wolf-Hirschhorn syndrome candidate
- 35614_at Cluster Incl. AB012124:Homo sapiens TCFL5 mRNA for transcription factor
- 38341_at Cluster Incl. AL079286:Homo sapiens mRNA full length insert cDNA clone
- 15** 38344_at Cluster Incl. R40666:yf79c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
- 39745_at Cluster Incl. AB011139:Homo sapiens mRNA for KIAA0567 protein, partial
- 40102_at Cluster Incl. AB018315:Homo sapiens mRNA for KIAA0772 protein, complete
- 32148_at Cluster Incl. AI701049:wc78b08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 33917_at Cluster Incl. AB002336:Human mRNA for KIAA0338 gene, partial cds /cds=(
- 20** 34338_at Cluster Incl. D49738:Human cytoskeleton associated protein (CG22) mRNA,
- 34782_at Cluster Incl. AL021938:Homo sapiens DNA sequence from PAC 232K4 on chro
- 36580_at Cluster Incl. AL050139:Homo sapiens mRNA; cDNA DKFZp586M141 (from clone
- 38410_at Cluster Incl. X72964:H.sapiens mRNA for caltractin /cds=(47,565) /gb=X7
- 25** 38771_at Cluster Incl. D50405:Human mRNA for RPD3 protein, complete cds /cds=(63
- 41343_at Cluster Incl. Y16521:Homo sapiens mRNA for CDS2 protein /cds=(258,1595)
- 32561_at Cluster Incl. D63480:Human mRNA for KIAA0146 gene, partial cds /cds=(0,
- 1248_at U37689 /FEATURE= /DEFINITION=HSU37689 Human RNA polymerase II subunit (h

30 METAGENE 65 :

- 41627_at Cluster Incl. D50645:Homo sapiens mRNA for SDF2, complete cds /cds=(39,
- 41659_at Cluster Incl. U46691:Human putative chromatin structure regulator (SUPT
- 37912_at Cluster Incl. X80200:H.sapiens MLN62 mRNA /cds=(85,1497) /gb=X80200 /gi
- 35** 39783_at Cluster Incl. D43947:Human mRNA for KIAA0100 gene, complete cds /cds=(3
- 32181_at Cluster Incl. M60922:Human surface antigen mRNA, complete cds /cds=(126
- 32791_at Cluster Incl. L19183:Human MAC30 mRNA, 3 end /cds=(0,569) /gb=L19183 /
- 34379_at Cluster Incl. AF082657:Homo sapiens Era GTPase A protein (HERA-A) mRNA,
- 36940_at Cluster Incl. D86970:Human mRNA for KIAA0216 gene, complete cds /cds=(4

36988_at Cluster Incl. M80783:Human B12 protein mRNA, complete cds /cds=(153,110
 37700_at Cluster Incl. X92106:H.sapiens mRNA for bleomycin hydrolase /cds=(78,14
 38107_at Cluster Incl. U40998:Human retinal protein (HRG4) mRNA, complete cds /c
 41561_s_at Cluster Incl. AI651368:wb05d07.x1 Homo sapiens cDNA, 3 end /clone=IM

5

METAGENE 66 :

33226_at Cluster Incl. AB020683:Homo sapiens mRNA for KIAA0876 protein, partial
 34240_s_at Cluster Incl. AL049786:Novel human gene mapping to chromosome 13 /cds=
 10 35252_at Cluster Incl. AB011100:Homo sapiens mRNA for KIAA0528 protein, complete
 36915_at Cluster Incl. AI810485:wb89b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 37621_at Cluster Incl. M57230:Human membrane glycoprotein gp130 mRNA, complete c
 38614_s_at Cluster Incl. U77413:Human O-linked GlcNAc transferase mRNA, complete
 39401_at Cluster Incl. W28264:44c9 Homo sapiens cDNA /gb=W28264 /gi=1308212 /ug=
 15 41726_at Cluster Incl. Z35307:H.sapiens mRNA for endothelin-converting-enzyme 1
 39879_s_at Cluster Incl. H16917:ym39e02.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 41533_at Cluster Incl. U79298:Human clone 23803 mRNA, partial cds /cds=(0,1123)
 1719_at U61981 /FEATURE= /DEFINITION=HSU61981 Human putative mismatch repair/bin
 1361_at U40705 /FEATURE= /DEFINITION=HSU40705 Homo sapiens telomeric repeat bind
 20 932_i_atL11672 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finge
 933_f_atL11672 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finge
 783_at U96113 /FEATURE= /DEFINITION=HSU96113 Homo sapiens Nedd-4-like ubiquitin-
 784_g_at U96113 /FEATURE= /DEFINITION=HSU96113 Homo sapiens Nedd-4-like
 ubiquiti
 25 714_at Adenylyl Cyclase-Associated Protein 2

METAGENE 67 :

40045_g_at Cluster Incl. AF009425:Homo sapiens clone 22 mRNA, alternative splici
 30 40046_r_at Cluster Incl. AF009426:Homo sapiens clone 22 mRNA, alternative splice
 34332_at Cluster Incl. D31766:Human mRNA for KIAA0060 gene, complete cds /cds=(4
 36938_at Cluster Incl. U70063:Human acid ceramidase mRNA, complete cds /cds=(17,
 461_at U70063 /FEATURE= /DEFINITION=HSU70063 Human acid ceramidase mRNA, complet

35 METAGENE 68 :

40039_g_at Cluster Incl. W02490:za48b02.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 40090_at Cluster Incl. AI797997:wh80b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 37335_at Cluster Incl. U41668:Human deoxyguanosine kinase mRNA, complete cds /cd

1091_at M65066 /FEATURE= /DEFINITION=HUMRIB Human cAMP-dependent protein kinase

METAGENE 69 :

- 5** 34512_at Cluster Incl. J03853:Human kidney alpha-2-adrenergic receptor mRNA, com
41428_at Cluster Incl. AF104942:Homo sapiens ABC transporter MOAT-C (MOAT-C)
mRN
32680_at Cluster Incl. AB011123:Homo sapiens mRNA for KIAA0551 protein, partial
38735_at Cluster Incl. AB011085:Homo sapiens mRNA for KIAA0513 protein, complete
10 1933_g_at U83661 /FEATURE= /DEFINITION=HSU83661 Homo sapiens multidrug
resistanc

METAGENE 70 :

- 15** 33992_at Cluster Incl. M12523:Human serum albumin (ALB) gene, complete cds /cds=
36036_at Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /cds

METAGENE 71 :

- 20** 38217_at Cluster Incl. U97698:Homo sapiens secretory mucin MUC6 (MUC6) mRNA, par
39567_at Cluster Incl. AB006190:Homo sapiens mRNA for aquaporin adipose, complet
707_s_at Mucin 6, Gastric

METAGENE 72 :

- 25** 41007_at Cluster Incl. AF052497:Homo sapiens clone B18 unknown mRNA
/cds=UNKNOWN
34398_at Cluster Incl. D86956:Human mRNA for KIAA0201 gene, complete cds /cds=(3
37297_at Cluster Incl. AL049422:Homo sapiens mRNA; cDNA DKFZp586A191 (from
30 clone
752_s_at D85429 /FEATURE=expanded_cds /DEFINITION=D85429 Homo sapiens gene
for h

METAGENE 73 :

- 35** 34654_at Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990
34764_at Cluster Incl. D21851:Human mRNA for KIAA0028 gene, partial cds /cds=(18
35642_at Cluster Incl. AF053551:Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene
36544_at Cluster Incl. AF038193:Homo sapiens clone 23608 mRNA sequence /cds=UNKN

- 39796_at Cluster Incl. U11292:Human Ki nuclear autoantigen mRNA, complete cds /c
 36942_at Cluster Incl. D79996:Human mRNA for KIAA0174 gene, complete cds /cds=(6
 37723_at Cluster Incl. U47414:Human cyclin G2 mRNA, complete cds /cds=(135,1169)
 40222_s_at Cluster Incl. AI677689:wd33c06.x1 Homo sapiens cDNA, 3 end /clone=IM
5 33164_at Cluster Incl. AJ132545:Homo sapiens mRNA for protein kinase /cds=(395,2
 33192_g_at Cluster Incl. AW051579:wy87g03.x1 Homo sapiens cDNA, 3 end /clone=IM
 2064_g_at L20046 /FEATURE= /DEFINITION=HUMERCC5A Human ERCC5 excision
 repair pro
 1044_s_at U31556 /FEATURE= /DEFINITION=HSU31556 Human transcription factor E2F-
10 5
 250_at L41067 /FEATURE= /DEFINITION=HUMHFAT4A Homo sapiens NF-AT4c mRNA,
 complet
- METAGENE 74 :
- 15**
- 33678_i_at Cluster Incl. X02344:Homo sapiens beta 2 gene /cds=(0,1337) /gb=X0234
 40683_at Cluster Incl. L76687:Homo sapiens Grb14 mRNA, complete cds /cds=(540,21
 36090_at Cluster Incl. AL080162:Homo sapiens mRNA; cDNA DKFZp434N024 (from
 clone
20 32261_at Cluster Incl. AF072810:Homo sapiens transcription factor WSTF mRNA, com
 1875_f_at D38498 /FEATURE= /DEFINITION=HUMPMS1A Human PMS5 mRNA (yeast
 mismatch
 956_at Tubulin, Beta 2
- 25** METAGENE 75 :
- 39187_at Cluster Incl. AF001450:untitled /cds=(0,1568) /gb=AF001450 /gi=2245523
 1519_at J04102 /FEATURE= /DEFINITION=HUMETS2A Human erythroblastosis virus oncog
- 30** METAGENE 76 :
- 33650_at Cluster Incl. W25911:14h11 Homo sapiens cDNA /gb=W25911 /gi=1306034 /ug
 34171_at Cluster Incl. AI867349:wi24g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 35092_at Cluster Incl. AF032387:Homo sapiens snRNA activating protein complex 19
35 37101_at Cluster Incl. AL050008:Homo sapiens mRNA; cDNA DKFZp564A063 (from
 clone
 41407_at Cluster Incl. L03411:Human RD protein (RD) mRNA, complete cds /cds=(86,
 33706_at Cluster Incl. AB006198:Homo sapiens mRNA for SART-1, complete cds /cds=
 35161_at Cluster Incl. AB020667:Homo sapiens mRNA for KIAA0860 protein, complete

	35628_at	Cluster Incl. AF023676:Homo sapiens lamin B receptor homolog TM7SF2 (TM
	35631_at	Cluster Incl. U37689:Human RNA polymerase II subunit (hsRPB8) mRNA, com
	38260_at	Cluster Incl. AL050306:Human DNA sequence from clone 475B7 on chromosom
	38275_at	Cluster Incl. AF054996:Homo sapiens clone 23783 mRNA sequence /cds=UNKN
5	38640_at	Cluster Incl. AI582831:tn36c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39747_at	Cluster Incl. U52427:Human RNA polymerase II seventh subunit (rpb-7) ge
	39772_at	Cluster Incl. AF007157:Homo sapiens clone 23856 unknown mRNA, partial c
	40076_at	Cluster Incl. AF004430:Homo sapiens hD54+ins2 isoform (hD54) mRNA, comp
	33906_at	Cluster Incl. AB001740:Homo sapiens mRNA for p27, complete cds /cds=(20
10	34325_at	Cluster Incl. AJ005893:Homo sapiens mRNA for JM26 protein, complete CDS
	34828_at	Cluster Incl. AL037557:DKFZp564H2472_r1 Homo sapiens cDNA, 5 end /clon
	34882_at	Cluster Incl. Y12065:Homo sapiens mRNA for nucleolar protein hNop56 /cd
	35765_at	Cluster Incl. X91504:H.sapiens mRNA for ARP1 protein /cds=(11,616) /gb=
	35801_at	Cluster Incl. AF026816:Homo sapiens putative oncogene protein mRNA, par
15	36167_at	Cluster Incl. D89052:Homo sapiens mRNA for proton-ATPase-like protein,
	36602_at	Cluster Incl. D21064:Human mRNA for KIAA0123 gene, partial cds /cds=(0,
	38743_f_at	Cluster Incl. X06409:Human mRNA fragment for activated c-raf-1 (exons
	1470_at	U21090 /FEATURE= /DEFINITION=HSU21090 Human DNA polymerase delta small s
	958_s_at	Rna Polymerase II, 14.5 Kda Subunit
20		
		METAGENE 77 :
	31419_r_at	Cluster Incl. AF023203:Homo sapiens homeobox protein Ogl2 (OGL12) mRN
	31911_at	Cluster Incl. AF000989:Homo sapiens thymosin beta 4 Y isoform (TB4Y) mR
25	32410_at	Cluster Incl. X17651:Human Myf-4 mRNA for myogenic determination factor
	32474_at	Cluster Incl. X96744:H.sapiens PAX7 gene, exon 1 (and joined CDS) /cds=
	34600_s_at	Cluster Incl. U54644:Human tub homolog mRNA, complete cds /cds=(152,1
	35038_at	Cluster Incl. Y10129:H.sapiens mybpc3 gene /cds=(33,3857) /gb=Y10129 /g
	35068_at	Cluster Incl. U88063:Human Agouti related protein (Art) mRNA, complete
30	35115_at	Cluster Incl. AF035300:Homo sapiens clone 23663 mRNA, partial cds /cds=
	32362_r_at	Cluster Incl. D87012:Human (lambda) DNA for immunoglobulin light chain
	33469_r_at	Cluster Incl. X68679:H. sapiens mRNA for DOWN 16 /cds=(23,1018) /gb=X
	35420_r_at	Cluster Incl. AB020720:Homo sapiens mRNA for KIAA0913 protein, partial
	35911_r_at	Cluster Incl. AJ003147:Homo sapiens complete genomic sequence between
35	37831_at	Cluster Incl. AB011117:Homo sapiens mRNA for KIAA0545 protein, partial
	38882_r_at	Cluster Incl. AF096870:Homo sapiens estrogen-responsive B box protein
	40003_at	Cluster Incl. U36221:Human pancreatic zymogen granule membrane protein
	40286_r_at	Cluster Incl. AL050370:Homo sapiens mRNA; cDNA DKFZp566C0546 (from cl
	40298_at	Cluster Incl. AB014603:Homo sapiens mRNA for KIAA0703 protein, complete

- 40342_at Cluster Incl. U66077:Human DAZ mRNA, 3UTR /cds=UNKNOWN /gb=U66077 /gi=1
- 31789_at Cluster Incl. M14564:Human cytochrome P450c17 (steroid 17-alpha-hydroxy
- 32677_at Cluster Incl. AF000979:Homo sapiens testis-specific Basic Protein Y 1 (
- 5 33231_at Cluster Incl. AI761148:wh97h07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 33814_at Cluster Incl. AF005046:Homo sapiens serine/threonine kinase mRNA, compl
- 34221_at Cluster Incl. D83778:Human mRNA for KIAA0194 gene, partial cds /cds=(0,
- 36004_at Cluster Incl. AF074382:Homo sapiens Ikb kinase gamma subunit (IKK-gamma
- 36051_s_at Cluster Incl. X58199:Human mRNA for beta adducin /cds=(322,2502) /gb=
- 10 36464_at Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb
- 37226_at Cluster Incl. U15172:Homo sapiens BCL2/adenovirus E1B 19kD-interacting
- 37898_r_at Cluster Incl. AI985964:wr79d08.x1 Homo sapiens cDNA, 3 end /clone=IM
- 37968_at Cluster Incl. AF031137:Homo sapiens 1C7 precursor, mRNA, alternatively
- 38290_at Cluster Incl. AF037195:Homo sapiens regulator of G protein signaling RG
- 15 40163_r_at Cluster Incl. AC003107:Human DNA from chromosome 19-specific cosmid R
- 33349_at Cluster Incl. AL049378:Homo sapiens mRNA; cDNA DKFZp58611518 (from clon
- 33391_r_at Cluster Incl. S57235:CD68=110kda transmembrane glycoprotein [human, p
- 33841_at Cluster Incl. R48209:yj63d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
- 37687_i_at Cluster Incl. M31932:Human IgG low affinity Fc fragment receptor (FcR
- 20 39167_r_at Cluster Incl. D83174:Human mRNA for collagen binding protein 2, compl
- 39177_r_at Cluster Incl. M54994:Human bile salt-activated lipase (BAL) mRNA, com
- 39821_s_at Cluster Incl. N95168:zb55f11.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 39862_at Cluster Incl. AA528252:nh92c11.s1 Homo sapiens cDNA, 3 end /clone=IMAG
- 39891_at Cluster Incl. AI246730:qk40b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 25 39919_at Cluster Incl. AI423340:tf36c07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 40176_at Cluster Incl. J03407:Human rfp transforming protein mRNA, complete cds
- 40883_at Cluster Incl. W28230:43h12 Homo sapiens cDNA /gb=W28230 /gi=1308178 /ug
- 1988_at X76079 /FEATURE=exons#1-4 /DEFINITION=HSPDGF H.sapiens mRNA for platelet
- 1018_at U81787 /FEATURE= /DEFINITION=HSU81787 Human Wnt10B mRNA, complete cds
- 30 662_at L13848 /FEATURE= /DEFINITION=HUMRNAHELA Human RNA helicase A mRNA, comple
- 225_at M31328 /FEATURE=mRNA /DEFINITION=HUMGNBPB3 Human guanine nucleotide-bindi
- 35 METAGENE 78 :
- 38177_at Cluster Incl. AJ001015:Homo sapiens mRNA encoding RAMP2 /cds=(68,595) /
- 38508_s_at Cluster Incl. U89337:Human HLA class III region containing cAMP respo
- 40399_r_at Cluster Incl. AI743406:wg92g12.x1 Homo sapiens cDNA, 3 end /clone=IM

- 41699_f_at Cluster Incl. AL080149:Homo sapiens mRNA; cDNA DKFZp434B094 (from clo
 31904_at Cluster Incl. U67733:Human cGMP-stimulated 3,5 -cyclic nucleotide phosph
 35137_at Cluster Incl. X69090:H.sapiens mRNA for skeletal muscle 190kD protein /
 35152_at Cluster Incl. AJ001016:Homo sapiens mRNA encoding RAMP3 /cds=(29,475) /
5 36569_at Cluster Incl. X64559:H.sapiens mRNA for tetranectin /cds=(93,701) /gb=X
 36829_at Cluster Incl. AF022991:Homo sapiens Rigui (RIGUI) mRNA, complete cds /c
 38294_at Cluster Incl. X17360:Human HOX 5.1 gene for HOX 5.1 protein /cds=(1243,
 38320_s_at Cluster Incl. L11706:Human hormone-sensitive lipase (LIPE) gene, comp
 32254_at Cluster Incl. AL050223:Homo sapiens mRNA; cDNA DKFZp586L1323 (from
10 clon
 33869_at Cluster Incl. AL080218:Homo sapiens mRNA; cDNA DKFZp586N1323 (from
 clon
 37022_at Cluster Incl. U41344:Human prolargin (PRELP) gene, 5 flanking sequence
 38044_at Cluster Incl. AF035283:Homo sapiens clone 23916 mRNA sequence /cds=UNKN
15 38747_at Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=
 33137_at Cluster Incl. Y13622:Homo sapiens mRNA for latent transforming growth f
 538_at S53911 /FEATURE= /DEFINITION=S53911 CD34=glycoprotein expressed in lympho
 496_s_at U32324 /FEATURE= /DEFINITION=HSU32324 Human interleukin-11 receptor
 alp
20 444_g_at X17360 /FEATURE=mRNA /DEFINITION=HSHOX51 Human HOX 5.1 gene for
 HOX 5.1

METAGENE 79 :

- 25** 33334_at Cluster Incl. X84194:H.sapiens mRNA for acylphosphatase, erythrocyte (C
 41195_at Cluster Incl. U49957:Human LIM protein (LPP) mRNA, partial cds /cds=(24
 33162_at Cluster Incl. X02160:Human mRNA for insulin receptor precursor /cds=(48
 1143_s_at Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 3, K-Sam III
 1136_at L16991 /FEATURE= /DEFINITION=HUMCDC8X Human thymidylate kinase (CDC8)
30 mR

METAGENE 80 :

- 35** 34119_at Cluster Incl. AA704268:zj22a08.s1 Homo sapiens cDNA, 3 end /clone=4509
 37437_at Cluster Incl. AB011162:Homo sapiens mRNA for KIAA0590 protein, complete
 41463_at Cluster Incl. AL042729:DKFZp434B0222_s1 Homo sapiens cDNA, 3 end /clon
 41645_at Cluster Incl. AF064594:Homo sapiens calcium-independent phospholipase A
 37266_at Cluster Incl. U69645:Human zinc finger protein mRNA, complete cds /cds=
 35273_at Cluster Incl. AF007151:Homo sapiens clone 23967 unknown mRNA, partial c

38117_at Cluster Incl. D38555:Human mRNA for KIAA0079 gene, complete cds /cds=(1
 38118_at Cluster Incl. U73377:Human p66shc (SHC) mRNA, complete cds /cds=(194,19

METAGENE 81 :

5

36364_at Cluster Incl. L32961:Human 4-aminobutyrate aminotransferase (GABAT) mRN
 36434_r_at Cluster Incl. AF017724:Homo sapiens glycine receptor alpha 3 subunit
 38187_at Cluster Incl. D90041:Human liver arylamine N-acetyltransferase (EC 2.3.
 39227_at Cluster Incl. AB006621:Homo sapiens mRNA for KIAA0283 gene, partial cds
 10 39304_g_at Cluster Incl. Y14153:Homo sapiens mRNA for beta-transducin repeat con
 40673_at Cluster Incl. U12778:Human acyl-CoA dehydrogenase mRNA, complete cds /c
 32667_at Cluster Incl. M58526:Human alpha-5 collagen type IV (COL4A5) mRNA, 3 e
 32676_at Cluster Incl. M93405:Human methylmalonate semialdehyde dehydrogenase ge
 34759_at Cluster Incl. U68494:Human hbc647 mRNA sequence /cds=UNKNOWN

15

/gb=U68494
 35238_at Cluster Incl. AB000509:Homo sapiens mRNA for TRAF5, complete cds /cds=(
 40522_at Cluster Incl. X59834:Human rearranged mRNA for glutamine synthase /cds=
 33358_at Cluster Incl. W29087:56b8 Homo sapiens cDNA /gb=W29087 /gi=1309053 /ug=
 33446_at Cluster Incl. W26407:29b8 Homo sapiens cDNA /gb=W26407 /gi=1307106 /ug=
 20 34862_at Cluster Incl. AA005018:zh96a09.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 35329_at Cluster Incl. AF091084:Homo sapiens clone 638 unknown mRNA, complete se
 35794_at Cluster Incl. AB023159:Homo sapiens mRNA for KIAA0942 protein, partial
 35822_at Cluster Incl. L15702:Human complement factor B mRNA, complete cds /cds=
 40244_s_at Cluster Incl. AI743654:wg41d01.x1 Homo sapiens cDNA, 3 end /clone=IM

25

METAGENE 82 :

33492_at Cluster Incl. AI624840:ts71g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 35395_at Cluster Incl. X05997:Human mRNA for gastric lipase /cds=UNKNOWN /gb=X05
 30 37817_at Cluster Incl. AF052087:Homo sapiens clone 23604 mRNA sequence /cds=UNKN
 39236_s_at Cluster Incl. AL050372:Homo sapiens mRNA; cDNA DKFZp434A091 (from clo
 40694_at Cluster Incl. X73502:H. Sapiens mRNA for cytokeratin 20 /cds=(0,1019) /
 32831_at Cluster Incl. AA453183:zx46b09.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 33828_at Cluster Incl. AF035262:Homo sapiens BAF57 (BAF57) gene, complete cds /c
 35 39482_at Cluster Incl. W26787:15d8 Homo sapiens cDNA /gb=W26787 /gi=1306078 /ug=
 40636_at Cluster Incl. AI807620:wf49b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40892_s_at Cluster Incl. N91508:za91e09.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 847_at U17969 /FEATURE=exons#1-6 /DEFINITION=HSU17969 Human initiation factor eI

METAGENE 83 :

- 33732_at Cluster Incl. Y08387:H.sapiens mRNA for mu-ARP2 protein /cds=(54,1415)
 37271_at Cluster Incl. L25444:Homo sapiens (TAFII70-alpha) mRNA, complete cds /c
5 38641_at Cluster Incl. AJ133115:Homo sapiens mRNA for TSC-22-like protein /cds=(
 39029_at Cluster Incl. U11861:Human G10 homolog (edg-2) mRNA, complete cds /cds=
 40118_at Cluster Incl. X07290:Human HF.12 gene mRNA /cds=(0,589) /gb=X07290 /gi=
 40134_at Cluster Incl. AF047436:Homo sapiens F1Fo-ATPase synthase f subunit mRNA
 35743_at Cluster Incl. U79569:Human no arches (nar) mRNA, complete cds /cds=(36,
10 38758_at Cluster Incl. R98910:yr31d04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 38831_f_at Cluster Incl. AF053356:Homo sapiens chromosome 7q22 sequence /cds=(25
 1486_at L37127 /FEATURE= /DEFINITION=HUMRPIA Homo sapiens RNA polymerase II
 mRNA
 947_at D55716 /FEATURE= /DEFINITION=HUMP1CDC47 Human mRNA for P1cdc47,
15 complete

METAGENE 84 :

- 35107_at Cluster Incl. AF053712:Homo sapiens osteoprotegerin ligand mRNA, comple
20 35117_at Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromoso
 32331_at Cluster Incl. X60673:Human AK3 mRNA for adenylate kinase 3
 /cds=UNKNOWN
 34461_at Cluster Incl. D67035:Homo sapiens mRNA for SCP-1, complete cds /cds=(17
 35638_at Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(4
25 38291_at Cluster Incl. J00123:Human enkephalin gene /cds=(0,803) /gb=J00123 /gi=
 40415_at Cluster Incl. X14813:Human liver mRNA for 3-oxoacyl-CoA thiolase /cds=(
 40501_s_at Cluster Incl. X73114:H.sapiens mRNA for slow MyBP-C /cds=(81,3452) /g
 37656_at Cluster Incl. D83782:Human mRNA for KIAA0199 gene, partial cds /cds=(0,
 928_at L02785 /FEATURE= /DEFINITION=HUMDRA Homo sapiens colon mucosa-associated
30

METAGENE 85 :

- 36109_at Cluster Incl. J04605:Human prolidase (imidodipectidase) mRNA, complete
 38066_at Cluster Incl. M81600:Human NAD(P)H-quinone oxidoreductase gene /cds=(111,
35 38790_at Cluster Incl. L25879:Homo sapiens p53/HEH epoxide hydrolase (EPHX) mRNA
 40527_at Cluster Incl. AF000571:Homo sapiens kidney and cardiac voltage dependen
 1686_g_at X82554 /FEATURE=mRNA /DEFINITION=HSSPHAR H.sapiens SPHAR gene
 for cycl

251_at L41816 /FEATURE=mRNA /DEFINITION=HUMCKI Homo sapiens cam kinase I mRNA,
c

METAGENE 86 :

5

34586_s_at Cluster Incl. U51003:Human DLX-2 (Dlx2) mRNA, complete cds /cds=UNKNO
33950_g_at Cluster Incl. AF011406:Homo sapiens corticotropin releasing hormone r
38936_at Cluster Incl. M16652:Human pancreatic elastase IIA mRNA, complete cds /
41413_at Cluster Incl. AF037339:Homo sapiens cleft lip and palate transmembrane
10 33801_at Cluster Incl. AF104222:Homo sapiens CD2 cytoplasmic domain binding prot
33806_at Cluster Incl. AF052106:Homo sapiens clone 23781 mRNA sequence /cds=UNKN
38663_at Cluster Incl. AI033692:ow26f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
41356_at Cluster Incl. W27619:35c7 Homo sapiens cDNA /gb=W27619 /gi=1307567 /ug=
1852_at X02910 /FEATURE=expanded_cds /DEFINITION=HSTNFA Human gene for tumor nec
15 1724_at S75174 /FEATURE= /DEFINITION=S75174 E2F-4=transcription factor [human, N
438_at X07767 /FEATURE=cds /DEFINITION=HSPKA Human mRNA for cAMP-dependent
prote

METAGENE 87 :

20

31622_f_at Cluster Incl. M10943:Human metallothionein-I γ gene (hMT-I γ) /cds=(0,1
31623_f_at Cluster Incl. K01383:Human metallothionein-I-A gene, complete coding
37451_at Cluster Incl. AL109695:Homo sapiens mRNA full length insert cDNA clone
38131_at Cluster Incl. AF010316:Homo sapiens Pig12 (PIG12) mRNA, complete cds /c
25 39594_f_at Cluster Incl. R93527:yq35f10.r1 Homo sapiens cDNA, 5 end /clone=IMAG
41446_f_at Cluster Incl. H68340:yr82b10.s1 Homo sapiens cDNA, 3 end /clone=IMAG
39081_at Cluster Incl. AI547258:PN001_AH_H08.r Homo sapiens cDNA, 5 end /clone_
36130_f_at Cluster Incl. R92331:yq03h03.r1 Homo sapiens cDNA, 5 end /clone=IMAG
39120_at Cluster Incl. AA224832:nc33b06.s1 Homo sapiens cDNA /clone=IMAGE-100990
30 926_at J03910 /FEATURE=mRNA /DEFINITION=HUMMT2A Human (clone 14VS)
metallothione
609_f_atM13485 /FEATURE=cds /DEFINITION=HUMMT1B2 Human metallothionein I-B gene

METAGENE 88 :

35

31950_at Cluster Incl. Y00345:Human mRNA for polyA binding protein /cds=(502,240
38924_s_at Cluster Incl. AF001628:Homo sapiens interactor protein Ab1BP4 (Ab1BP4
37263_at Cluster Incl. U55206:Homo sapiens human gamma-glutamyl hydrolase (hGH)

- 38690_at Cluster Incl. AL080097:Homo sapiens mRNA; cDNA DKFZp564P0462 (from
clon
- 39368_at Cluster Incl. AL031668:Human DNA sequence from clone 64K7 on chromosome
- 39738_at Cluster Incl. Z82215:Homo sapiens DNA sequence from PAC 68O2 on chromos
- 5 40813_at Cluster Incl. AI768188:wg82b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG
- 40843_at Cluster Incl. AF012023:Homo sapiens integrin cytoplasmic domain associa
- 40879_at Cluster Incl. AB014599:Homo sapiens mRNA for KIAA0699 protein, partial
- 41187_at Cluster Incl. U26162:Human myosin regulatory light chain mRNA, complete
- 32808_at Cluster Incl. X07979:Human mRNA for integrin beta 1 subunit /cds=(103,2
- 10 33447_at Cluster Incl. X54304:Human mRNA for myosin regulatory light chain /cds=
- 33866_at Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /c
- 34796_at Cluster Incl. X63679:H.sapiens mRNA for TRAMP protein /cds=(121,1245) /
- 35271_at Cluster Incl. AF006083:Homo sapiens actin-related protein Arp3 (ARP3) m
- 36608_at Cluster Incl. D55654:Human mRNA for cytosolic malate dehydrogenase, com
- 15 37333_at Cluster Incl. X63692:H.sapiens mRNA for DNA (cytosin-5)-methyltransfera
- 37747_at Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U0
- 38041_at Cluster Incl. U41514:Human UDP-GalNAc-polypeptide N-acetylgalactosaminy
- 38074_at Cluster Incl. U91932:Homo sapiens AP-3 complex sigma3A subunit mRNA, co
- 32544_s_at Cluster Incl. L12535:Human RSU-1/RSP-1 mRNA, complete cds /cds=(827,1
- 20 709_at J00314 /FEATURE=mRNA#1 /DEFINITION=HUMTBMM40 Human beta-tubulin gene,
clo

METAGENE 89 :

- 25 39942_at Cluster Incl. AF016898:Homo sapiens B-ATF gene, complete cds /cds=(241,
- 32724_at Cluster Incl. AF023462:Homo sapiens peroxisomal phytanoyl-CoA alpha-hyd
- 32506_at Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial
- 208_at M94151 /FEATURE= /DEFINITION=HUMCAPR Homo sapiens cadherin-associated pro

30 METAGENE 90 :

- 35785_at Cluster Incl. W28281:47e7 Homo sapiens cDNA /gb=W28281 /gi=1308436 /ug=
- 39839_at Cluster Incl. M24069:Human DNA-binding protein A (dbpA) gene, 3 end /c
- 32570_at Cluster Incl. L76465:Homo sapiens NAD+-dependent 15 hydroxyprostaglandi
- 35 1058_at S69790 /FEATURE= /DEFINITION=S69790 Brush-1=tumor suppressor {3 region}

METAGENE 91 :

- 33998_at Cluster Incl. U91618:Human proneurotensin/proneuromedin N mRNA, complet

37183_at Cluster Incl. M81883:Human glutamate decarboxylase (GAD67) mRNA, comple
1408_at J02986 /FEATURE=exon#3 /DEFINITION=HUMHST Human transforming protein (hs

METAGENE 92 :

5

41027_at Cluster Incl. AF078096:Homo sapiens forkhead/winged helix-like transcri
39382_at Cluster Incl. AB011089:Homo sapiens mRNA for KIAA0517 protein, partial
40434_at Cluster Incl. U97519:Homo sapiens podocalyxin-like protein mRNA, comple
40488_at Cluster Incl. M18533:Homo sapiens dystrophin (DMD) mRNA, complete cds /
10 41229_at Cluster Incl. AI222594:qg58g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
32780_at Cluster Incl. AB018271:Homo sapiens mRNA for KIAA0728 protein, partial
39544_at Cluster Incl. AB002351:Human mRNA for KIAA0353 gene, partial cds /cds=(
40240_at Cluster Incl. AC004131:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-
40642_at Cluster Incl. AI312646:qp77f01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
15 41266_at Cluster Incl. X53586:Human mRNA for integrin alpha 6 /cds=UNKNOWN /gb=X
41531_at Cluster Incl. AI445461:tj34g07.x1 Homo sapiens cDNA, 3 end /clone=IMAG
1537_at X00588 /FEATURE=cds /DEFINITION=HSEGFPRE Human mRNA for precursor of epi
892_at M90657 /FEATURE= /DEFINITION=HUML6A Human tumor antigen (L6) mRNA,
comple

20

METAGENE 93 :

40329_at Cluster Incl. AL031228:dJ1033B10.10 (membrane protein with histidine ri
33258_g_at Cluster Incl. D26535:Human gene for dihydrolipoamide succinyltransfer
25 37903_at Cluster Incl. L25665:Human GTP-binding protein (HSR1) mRNA, complete cd
37904_s_at Cluster Incl. X66436:H.sapiens hsr1 mRNA (partial) /cds=UNKNOWN /gb=X
41725_at Cluster Incl. U89896:Homo sapiens casein kinase I gamma 2 mRNA, complet
36197_at Cluster Incl. Y08374:H.sapiens gene encoding cartilage GP-39 protein, e
32514_s_at Cluster Incl. AF032906:Homo sapiens cathepsin Z precursor (CTS2) mRNA
30 1162_g_at Guanine Nucleotide-Binding Protein Hsr1

METAGENE 94 :

35412_at Cluster Incl. D13705:Human mRNA for fatty acids omega-hydroxylase (cyto
35 37463_r_at Cluster Incl. L21990:Human spliceosomal protein (SAP 62) gene, comple
40020_at Cluster Incl. AB011536:Homo sapiens mRNA for MEGF2, partial cds /cds=(0
41664_at Cluster Incl. AF026030:Homo sapiens putative mitochondrial inner membra
35151_at Cluster Incl. AF089814:Homo sapiens growth suppressor related (DOC-1R)
36916_at Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2

- 37993_at Cluster Incl. X63422:H.sapiens mRNA for delta-subunit of mitochondrial
 37033_s_at Cluster Incl. X13710:H.sapiens unspliced mRNA for glutathione peroxid
 37691_at Cluster Incl. X63380:Homo sapiens mRNA for serum response factor-relate
 40234_at Cluster Incl. X96484:H.sapiens mRNA for DGCR6 protein /cds=(422,676) /g
 5 41566_at Cluster Incl. AI218364:qh21h01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 1273_r_at L22005 /FEATURE= /DEFINITION=HUMCDC34H Human ubiquitin conjugating
 enz
 335_r_atSpliceosomal Protein Sap 62
- 10 METAGENE 95 :
- 34458_at Cluster Incl. AA586894:nn68c06.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 38925_at Cluster Incl. X95239:H.sapiens mRNA for cysteine-rich secretory protein
- 15 METAGENE 96 :
- 32459_at Cluster Incl. U66088:Human sodium iodide symporter mRNA, complete cds /
 32497_s_at Cluster Incl. S70609:glycine transporter type 1b [human, substantia n
 33002_at Cluster Incl. AF047487:Homo sapiens Nck-2 (NCK2) mRNA, complete cds /cd
 20 35520_at Cluster Incl. AI701514:we35h02.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 34485_r_at Cluster Incl. M21868:Human polymorphic epithelial mucin core protein
 34510_at Cluster Incl. AF070552:Homo sapiens clone 24767 mRNA sequence /cds=UNKN
 35967_at Cluster Incl. M69238:Human aryl hydrocarbon receptor nuclear translocat
 41076_at Cluster Incl. AF099730:Homo sapiens connexin 31 (GJB3) gene, complete c
 25 39375_g_at Cluster Incl. AL022325:Homo sapiens DNA sequence from Fosmid 27C3 on
 689_at L02867 /FEATURE= /DEFINITION=HUMPPA Homo sapiens 62 kDa paraneoplastic an
 242_at M64571 /FEATURE=mRNA /DEFINITION=HUMMAP4 Human microtubule-associated
 pro
- 30 METAGENE 97 :
- 39932_at Cluster Incl. AI655015:wb66a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 41872_at Cluster Incl. AF073308:Homo sapiens nonsyndromic hearing impairment pro
 32026_s_at Cluster Incl. AB002311:Human mRNA for KIAA0313 gene, complete cds /cd
 35 34761_r_at Cluster Incl. U41766:Human metalloprotease/disintegrin/cysteine-rich
 35166_at Cluster Incl. D87343:Homo sapiens mRNA for DCRA, complete cds /cds=(239
 36926_at Cluster Incl. X80692:H.sapiens ERK3 mRNA /cds=(478,2643) /gb=X80692 /gi
 38980_at Cluster Incl. AB018276:Homo sapiens mRNA for KIAA0733 protein, partial
 39032_at Cluster Incl. AJ222700:Homo sapiens mRNA for TSC-22 protein /cds=(191,6

	39759_at	Cluster Incl. AL031781:dJ51J12.1 (human ortholog of zebrafish Quaking p
	39784_at	Cluster Incl. U26032:Human translation initiation factor eIF-2alpha mRNA
	40146_at	Cluster Incl. AL080212:Homo sapiens mRNA; cDNA DKFZp586H0723 (from
	clon	
5	40467_at	Cluster Incl. AB006202:Homo sapiens mRNA for cytochrome b small subunit
	40516_at	Cluster Incl. L19872:Human AH-receptor mRNA, complete cds /cds=(375,292
	41738_at	Cluster Incl. M64110:Human caldesmon mRNA, complete cds /cds=(111,1727)
	33830_at	Cluster Incl. AW026535:vv14f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	33891_at	Cluster Incl. AL080061:Homo sapiens mRNA; cDNA DKFZp564H182 (from
10	clone	
	33905_at	Cluster Incl. AF072242:Homo sapiens methyl-CpG binding protein MBD2 (MB
	34304_s_at	Cluster Incl. AL050290:Homo sapiens mRNA; cDNA DKFZp586G1923 (from cl
	34335_at	Cluster Incl. AI765533:wi81c01.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	34370_at	Cluster Incl. X81198:H.sapiens mRNA (clone p5) for archain /cds=(78,149
15	34840_at	Cluster Incl. AI700633:we38g03.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	34887_at	Cluster Incl. N92548:zb29g04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
	35805_at	Cluster Incl. AA447263:zw93f01.r1 Homo sapiens cDNA, 5 end /clone=IMAG
	36159_s_at	Cluster Incl. U29185:Homo sapiens prion protein (PrP) gene, complete
	36578_at	Cluster Incl. U37547:Human IAP homolog B (MIHB) mRNA, complete cds /cds
20	36688_at	Cluster Incl. U11313:Human sterol carrier protein-X/sterol carrier prot
	36980_at	Cluster Incl. U03105:Human B4-2 protein mRNA, complete cds /cds=(113,10
	37303_at	Cluster Incl. AF057160:Homo sapiens putative poly(ADP-ribosyl) transfer
	37374_at	Cluster Incl. M82809:Human annexin IV (ANX4) mRNA, complete cds /cds=(7
	37381_g_at	Cluster Incl. X59268:Human mRNA for general transcription factor IIB
25	37403_at	Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X0590
	37696_at	Cluster Incl. L06328:Human voltage-dependent anion channel isoform 2 (V
	37731_at	Cluster Incl. Z29064:H.sapiens AF-1p mRNA /cds=(92,2782) /gb=Z29064 /gi
	37762_at	Cluster Incl. Y07909:H.sapiens mRNA for Progression Associated Protein
	38110_at	Cluster Incl. AF000652:Homo sapiens syntenin (sycl) mRNA, complete cds
30	38403_at	Cluster Incl. X77196:H.sapiens mRNA for lysosome-associated membrane pr
	39099_at	Cluster Incl. X97064:H.sapiens mRNA for Sec23A isoform, 2748bp /cds=(15
	39139_at	Cluster Incl. AI357653:qy15c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG
	39150_at	Cluster Incl. U69559:U69559 Homo sapiens cDNA /clone=26077 /gb=U69559 /
	39556_at	Cluster Incl. M96803:Human general beta-spectrin (SPTBN1) mRNA, complet
35	40556_at	Cluster Incl. D42073:Human mRNA for reticulocalbin, complete cds /cds=(
	40953_at	Cluster Incl. S80562:acidic calponin [human, kidney, mRNA, 1607 nt] /cd
	41292_at	Cluster Incl. L22009:Human hnRNP H mRNA, complete cds /cds=(72,1421) /g
	41505_r_at	Cluster Incl. AF055376:Homo sapiens short form transcription factor C
	41601_at	Cluster Incl. AA142964:zl43a07.s1 Homo sapiens cDNA, 3 end /clone=IMAG

- 32585_at Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /c
 32587_at Cluster Incl. U07802:Human Tis11d gene, complete cds /cds=(291,1739) /g
 32597_at Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488
 1815_g_at D50683 /FEATURE= /DEFINITION=D50683 Homo sapiens mRNA for TGF-
5 betaIIr
 1495_at M34057 /FEATURE= /DEFINITION=HUMTGFB1B Human transforming growth factor-

METAGENE 98 :

- 10** 37424_at Cluster Incl. AB029343:Homo sapiens HCR (a-helix coiled-coil rod homolo
 39984_g_at Cluster Incl. U73704:Homo sapiens 48 kDa FKBP-associated protein FAP4
 37888_at Cluster Incl. D87449:Human mRNA for KIAA0260 gene, partial cds /cds=(0,
 38701_at Cluster Incl. AJ000519:Homo sapiens mRNA for ubiquitin-conjugating enzy
 38987_at Cluster Incl. AF052183:Homo sapiens clone 24804 mRNA sequence /cds=UNKN
15 32806_at Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mR
 32820_at Cluster Incl. U71267:Human potential transcriptional repressor NOT4Hp (
 34315_at Cluster Incl. Y18314:Homo sapiens mRNA for paraplegin-like protein /cds
 37001_at Cluster Incl. M23254:Human Ca2-activated neutral protease large subunit
 37378_r_at Cluster Incl. M13452:Human lamin A mRNA, 3end /cds=(0,1547) /gb=M1345
20 38801_at Cluster Incl. AI742846:wg46h09.x1 Homo sapiens cDNA, 3 end /clone=IMAG

METAGENE 99 :

- 36734_at Cluster Incl. M21302:Human small proline rich protein (sprII) mRNA, clo
25 40294_at Cluster Incl. U66676:HSU66676 Homo sapiens cDNA /gb=U66676 /gi=1906561
 31887_at Cluster Incl. J04469:Human mitochondrial creatine kinase (CKMT) gene, c
 37978_at Cluster Incl. D78177:Homo sapiens mRNA for quinolinate phosphoribosyl t
 34826_at Cluster Incl. L21936:Human succinate dehydrogenase flavoprotein subunit
 39122_at Cluster Incl. K03515:Human neuroleukin mRNA, complete cds /cds=(15,1691
30 33197_at Cluster Incl. U39226:Human myosin VIIA (USH1B) mRNA, complete cds /cds=

METAGENE 100 :

- 31353_f_at Cluster Incl. X94553:H.sapiens HFKH4 mRNA for fork head like protein
35 31391_at Cluster Incl. AF040723:Homo sapiens neuroan1 mRNA, complete cds /cds=(1
 31724_at Cluster Incl. L38518:Homo sapiens sonic hedgehog protein (SHH) mRNA, co
 32482_at Cluster Incl. L42563:Homo sapiens (clone ISW34) non-gastric H,K-ATPase
 33594_at Cluster Incl. AB017788:Homo sapiens hdkk-4 mRNA, complete cds /cds=(0,6
 32877_i_at Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-9542

- 32928_at Cluster Incl. AJ012214:Homo sapiens mRNA for PLA-1 protein /cds=(0,1310
 33961_at Cluster Incl. AL109666:Homo sapiens mRNA full length insert cDNA clone
 34905_at Cluster Incl. AA977136:oaq24f02.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 36729_g_at Cluster Incl. M76446:Human alpha-A1-adrenergic receptor mRNA, complet
 5 37058_at Cluster Incl. Y00317:Human mRNA for liver microsomal UDP-glucuronosyltr
 40714_at Cluster Incl. S82198:caldecrin=serum calcium-decreasing factor [human,
 41856_at Cluster Incl. AL049370:Homo sapiens mRNA; cDNA DKFZp586D0918 (from
 clon
 33768_at Cluster Incl. L19267:Homo sapiens 59 protein mRNA, 3 end /cds=(0,1661)
 10 34722_at Cluster Incl. U44385:Human tissue inhibitor of metalloproteinases-2 (TI
 35179_at Cluster Incl. AB009598:Homo sapiens mRNA for glucuronyltransferase I, c
 36075_at Cluster Incl. AL037167:DKFZp564P1564_s1 Homo sapiens cDNA, 3 end /clon
 37648_at Cluster Incl. D63487:Human mRNA for KIAA0153 gene, partial cds /cds=(0,
 33882_at Cluster Incl. AB020664:Homo sapiens mRNA for KIAA0857 protein, partial
 15 36114_r_at Cluster Incl. M19309:Human slow skeletal muscle troponin T mRNA, clon
 39448_r_at Cluster Incl. W27095:20c10 Homo sapiens cDNA /gb=W27095 /gi=1306467 /
 39816_g_at Cluster Incl. AA883101:am24d05.s1 Homo sapiens cDNA, 3 end /clone=IM
 40268_at Cluster Incl. X16706:Human fra-2 mRNA /cds=(3,983) /gb=X16706 /gi=31464
 41321_s_at Cluster Incl. AA528077:nh90a11.s1 Homo sapiens cDNA, 3 end /clone=IM
 20 33178_at Cluster Incl. AF003837:Homo sapiens Jagged1 (JAG1) mRNA, complete cds /
 33215_g_at Cluster Incl. Y11681:Homo sapiens mRNA for mitochondrial ribosomal pr
 2091_at H23429 /FEATURE= /DEFINITION=H23429 ym52d12.s1 Soares infant brain 1NIB
 2079_s_at M13970 /FEATURE=mRNA /DEFINITION=HUMGFI21 Human insulin-like
 growth fa
 25 1908_at L16464 /FEATURE= /DEFINITION=HUMETSONC Human ETS oncogene (PEP1)
 mRNA, c
 1153_f_at J00117 /FEATURE=mRNA /DEFINITION=HUMCGB Human chorionic
 gonadotropin (
 1041_at U26403 /FEATURE= /DEFINITION=HSU26403 Human receptor tyrosine kinase lig
 30 336_at D38081 /FEATURE= /DEFINITION=HUMHTAR Human mRNA for thromboxane A2
 recept
 188_at U09303 /FEATURE= /DEFINITION=HSU09303 Human T cell leukemia LERK-2 (EPLG2
 METAGENE 101 :
 35 34912_at Cluster Incl. AF052941:Homo sapiens DAP-kinase related protein 1 mRNA,
 37844_at Cluster Incl. AI263885:qi08d08.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 36846_s_at Cluster Incl. AA121509:zk88c10.s1 Homo sapiens cDNA, 3 end /clone=IM
 37187_at Cluster Incl. M36820:Human cytokine (GRO-beta) mRNA, complete cds /cds=

37629_at Cluster Incl. M55268:Human casein kinase II alpha subunit mRNA, complet
 41742_s_at Cluster Incl. AF061034:Homo sapiens FIP2 alternatively translated mRN
 32538_at Cluster Incl. S95936:transferrin [human, liver, mRNA, 2347 nt] /cds=(79

5 METAGENE 102 :

33581_at Cluster Incl. AF023259:Homo sapiens RNA-binding protein (RBMS3) mRNA, c
 36810_at Cluster Incl. AB007954:Homo sapiens mRNA, chromosome 1 specific transcr
 41845_at Cluster Incl. W29036:55d12 Homo sapiens cDNA /gb=W29036 /gi=1308993 /ug
 10 1937_at Retinoblastoma 1

METAGENE 103 :

33052_at Cluster Incl. U95301:Human calcium-dependent group X phospholipase A2 m
 15 32336_at Cluster Incl. X05236:Human fibroblast mRNA for aldolase A /cds=(146,124
 39631_at Cluster Incl. U52100:Human XMP mRNA, complete cds /cds=(63,566) /gb=U52
 33326_at Cluster Incl. D42087:Human mRNA for KIAA0118 gene, partial cds /cds=(0,
 35207_at Cluster Incl. X76180:H.sapiens mRNA for lung amiloride sensitive Na⁺ ch
 35646_at Cluster Incl. Z35093:H.sapiens mRNA for SURF-1 /cds=(14,916) /gb=Z35093
 20 39712_at Cluster Incl. AI541308:pec1.2-4.F11.r Homo sapiens cDNA, 5 end /clone_
 33399_at Cluster Incl. AA142942:zl43c04.s1 Homo sapiens cDNA, 3 end /clone=IMAG
 35841_at Cluster Incl. N24355:yx14b01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 36113_s_at Cluster Incl. AJ011712:Homo sapiens TNNT1 gene, exons 1-11 (and joine

25 METAGENE 104 :

36459_at Cluster Incl. AB020686:Homo sapiens mRNA for KIAA0879 protein, complete
 39779_at Cluster Incl. U38847:Human TAR RNA loop binding protein (TRP-185) mRNA,
 40456_at Cluster Incl. AL049963:Homo sapiens mRNA; cDNA DKFZp564A132 (from
 30 clone
 33436_at Cluster Incl. Z46629:Homo sapiens SOX9 mRNA /cds=(359,1888) /gb=Z46629
 33933_at Cluster Incl. X63187:H.sapiens HE4 mRNA for extracellular proteinase in

METAGENE 105 :

35 37157_at Cluster Incl. X56667:Human mRNA for calretinin /cds=(43,858) /gb=X56667
 40297_at Cluster Incl. AC005053:Homo sapiens BAC clone RG041D11 from 7q21 /cds=(
 31902_at Cluster Incl. AF093774:Homo sapiens type 2 iodothyronine deiodinase mRN
 32072_at Cluster Incl. U40434:Human mesothelin or CAK1 antigen precursor mRNA, c

39698_at Cluster Incl. U51712:HSU51712 Homo sapiens cDNA /gb=U51712 /gi=1255282
 36686_at Cluster Incl. U07919:Human aldehyde dehydrogenase 6 mRNA, complete cds
 37319_at Cluster Incl. M35878:Human insulin-like growth factor-binding protein-3
 1586_at M35878 /FEATURE=expanded_cds /DEFINITION=HUMIBP3 Human insulin-like grow

5

METAGENE 106 :

31738_at Cluster Incl. W28912:53f11 Homo sapiens cDNA /gb=W28912 /gi=1308860 /ug
 32021_at Cluster Incl. AI560890:tq41d05.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 10 32988_at Cluster Incl. Z30643:H.sapiens mRNA for chloride channel (putative) 213
 34549_g_at Cluster Incl. X55764:Human mRNA for cytochrome P-450 (11 Beta) /cds=(
 35041_at Cluster Incl. X53655:H.sapiens mRNA for NGF-2 /cds=(43,816) /gb=X53655
 32881_at Cluster Incl. U88834:Human clone 295, 5cM region surrounding hepatocyte
 35005_at Cluster Incl. AF051941:Homo sapiens type 6 nucleoside diphosphate kinas
 15 35374_at Cluster Incl. AB007914:Homo sapiens mRNA for KIAA0445 protein, complete
 35913_at Cluster Incl. U88047:Homo sapiens DNA binding protein homolog (DRIL1) m
 36281_at Cluster Incl. M96739:Human NSCL-1 mRNA sequence /cds=UNKNOWN
 /gb=M96739
 37885_at Cluster Incl. AF038169:Homo sapiens clone 23790 unknown protein mRNA, c
 20 38880_at Cluster Incl. AB011168:Homo sapiens mRNA for KIAA0596 protein, partial
 40359_at Cluster Incl. M91083:Human DNA-binding protein (HRC1) mRNA, complete cd
 41079_at Cluster Incl. AB010575:Homo sapiens mRNA for sodium channel, complete c
 32048_at Cluster Incl. AL049675:Human gene from PAC 886K2, chromosome 1 /cds=UNK
 34241_at Cluster Incl. L34357:Homo sapiens GATA-4 mRNA, complete cds /cds=(240,1
 25 35197_at Cluster Incl. AF038188:Homo sapiens clone 23940 mRNA sequence /cds=UNKN
 35666_at Cluster Incl. U38276:Human semaphorin III family homolog mRNA, complete
 36479_at Cluster Incl. AF050078:untitled /cds=(122,1558) /gb=AF050078 /gi=381846
 38629_at Cluster Incl. AF047863:untitled /cds=(17,1075) /gb=AF047863 /gi=2909668
 39044_s_at Cluster Incl. D73409:Homo sapiens mRNA for diacylglycerol kinase delt
 30 39720_g_at Cluster Incl. X56777:H.sapiens mRNA for ZP3 gene /cds=(30,1148) /gb=X
 32752_at Cluster Incl. W72440:zd65e10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-
 33450_at Cluster Incl. AB015906:Homo sapiens mRNA for actin-related protein, com
 33908_at Cluster Incl. X04366:Human mRNA for calcium activated neutral protease
 34318_at Cluster Incl. AJ005896:Homo sapiens mRNA for JM4 protein, complete CDS
 35 34784_at Cluster Incl. Z83844:Human DNA sequence from clone 37E16 on chromosome
 39915_at Cluster Incl. AB001535:Homo sapiens mRNA, complete cds /cds=(445,4956)
 41279_f_at Cluster Incl. AF007134:Homo sapiens clone 23565 unknown mRNA, partial
 2038_g_at M13995 /FEATURE=mRNA /DEFINITION=HUMBCL2B Human B-cell
 leukemia/lympho

- 1742_at S61953 /FEATURE= /DEFINITION=S61953 c-erbB3=receptor tyrosine kinase {al
 1353_g_at U11870 /FEATURE=mRNA /DEFINITION=HSU11870 Human interleukin-8
 receptor
 1000_at X60188 /FEATURE=mRNA /DEFINITION=HSERK1 Human ERK1 mRNA for protein
5 seri
 678_at J04948 /FEATURE=mRNA /DEFINITION=HUMALP1GC Human alkaline phosphatase
 (AL
 679_at J04990 /FEATURE=cds /DEFINITION=HUMCAPG Human cathepsin G gene, complete
 416_s_at X61755 /FEATURE=mRNA /DEFINITION=HSHOX3D Human HOX3D gene for
10 homeoprot

METAGENE 107 :

- 31907_at Cluster Incl. D87735:Homo sapiens mRNA for ribosomal protein L14, compl
15 35054_at Cluster Incl. AF035278:Homo sapiens clone 23676 mRNA sequence /cds=UNKN
 36449_s_at Cluster Incl. D13897:Human DNA for peptide YY, complete cds /cds=(91,
 37098_at Cluster Incl. D38537:Human mRNA for protoporphyrinogen oxidase, complet
 41406_at Cluster Incl. AL080172:Homo sapiens mRNA; cDNA DKFZp434G231 (from
 clone
20 37924_g_at Cluster Incl. AA846749:aj99c10.s1 Homo sapiens cDNA, 3 end /clone=IM
 40770_f_at Cluster Incl. AB017019:Homo sapiens mRNA for JKTBP2, complete cds /cd
 32169_at Cluster Incl. AB020682:Homo sapiens mRNA for KIAA0875 protein, partial
 32244_at Cluster Incl. AB018280:Homo sapiens mRNA for KIAA0737 protein, complete
 40188_f_at Cluster Incl. W28846:52g2 Homo sapiens cDNA /gb=W28846 /gi=1308812 /u
25 646_s_at L29218 /FEATURE=mRNA /DEFINITION=HUMCLK2B Homo sapiens clk2
 mRNA, compl

METAGENE 108 :

- 30** 31521_f_at Cluster Incl. X60484:H.sapiens H4/e gene for H4 histone /cds=(0,311)
 34027_f_at Cluster Incl. AA010078:ze16d01.s1 Homo sapiens cDNA, 3 end /clone=IM
 37557_at Cluster Incl. U62531:Human AE2 anion exchanger (SLC4A2) mRNA, complete
 32822_at Cluster Incl. J02966:Human mitochondrial ADP/ADT translocator mRNA, com
 40955_at Cluster Incl. U79287:Human clone 23867 mRNA sequence /cds=UNKNOWN
35 /gb=U
 41822_at Cluster Incl. AF060503:Homo sapiens zinc finger protein (ZF5128) mRNA,
 792_s_at X52611 /FEATURE=cds /DEFINITION=HSAP2 Human mRNA for transcription
 fact

181_g_at S82470 /FEATURE= /DEFINITION=S82470 BB1=malignant cell expression-enhancer

METAGENE 109 :

- 5**
- 35853_at Cluster Incl. AL049654:Novel human mRNA similar to mouse gene PICK1 (TR
- 37129_at Cluster Incl. AI936758:wp69b11.x1 Homo sapiens cDNA, 3' end /clone=IMAG
- 37153_at Cluster Incl. AB014573:Homo sapiens mRNA for KIAA0673 protein, partial
- 40033_at Cluster Incl. AL022328:Human DNA sequence from clone 402G11 on chromoso
- 10** 40705_at Cluster Incl. AF103905:Homo sapiens Rap1 guanine-nucleotide exchange fa
- 41036_at Cluster Incl. AL022314:dJ1170K4.1 (novel protein similar to KIAA0176 an
- 31837_at Cluster Incl. U62317:Chromosome 22q13 BAC Clone CIT987SK-384D8 complete
- 33707_at Cluster Incl. AF058921:Homo sapiens cytosolic phospholipase A2-gamma mR
- 33708_at Cluster Incl. AF045584:Homo sapiens PB39 mRNA, complete cds /cds=(76,17
- 15** 34206_at Cluster Incl. AB018325:Homo sapiens mRNA for KIAA0782 protein, partial
- 34224_at Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (B
- 35156_at Cluster Incl. AL050297:Homo sapiens mRNA; cDNA DKFZp564N123 (from clone
- 35170_at Cluster Incl. AF044414:Homo sapiens alpha mannosidase 6A8B (6a8b) mRNA,
- 20** 36452_at Cluster Incl. AB028952:Homo sapiens mRNA for KIAA1029 protein, complete
- 37201_at Cluster Incl. D38535:Human mRNA for PK-120 /cds=(129,2921) /gb=D38535 /
- 37268_at Cluster Incl. U43368:Human VEGF related factor isoform VRF186 precursor
- 37992_s_at Cluster Incl. AI436567:ti03b09.x1 Homo sapiens cDNA, 3' end /clone=IM
- 38671_at Cluster Incl. AB014520:Homo sapiens mRNA for KIAA0620 protein, partial
- 25** 39424_at Cluster Incl. U70321:Human herpesvirus entry mediator mRNA, complete cd
- 41160_at Cluster Incl. AC005943:Homo sapiens chromosome 19, cosmid R30538 /cds=(
- 33409_at Cluster Incl. AA158243:zo76c01.s1 Homo sapiens cDNA, 3' end /clone=IMAG
- 35823_at Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mR
- 37042_at Cluster Incl. U09577:Homo sapiens lysosomal hyaluronidase (LUCA2/HYAL2)
- 30** 39893_at Cluster Incl. AB010414:Homo sapiens mRNA for G-protein gamma 7, complet
- 40266_at Cluster Incl. AB028959:Homo sapiens mRNA for KIAA1036 protein, complete
- 41532_at Cluster Incl. Y09723:H.sapiens mRNA for Miz-1 protein /cds=(126,2537) /
- 1795_g_at M92287 /FEATURE= /DEFINITION=HUMCYCD3A Homo sapiens cyclin D3 (CCND3)
- 35** 1116_at M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD
- 541_g_at S67070 /FEATURE= /DEFINITION=S67070 heat shock protein HSP72 homolog [h
- 210_at M95678 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-
- 214_at M97676 /FEATURE= /DEFINITION=HUMHOX7 Homo sapiens (region 7) homeobox pro

METAGENE 110 :

- 39943_at Cluster Incl. U27459:Human origin recognition complex protein 2 homolog
5 32725_at Cluster Incl. AF042083:Homo sapiens BH3 interacting domain death agonis
 38369_at Cluster Incl. U70451:Human myleoid differentiation primary response pro
 33149_at Cluster Incl. U73524:Human putative ATP/GTP-binding protein (HEAB) mRNA

METAGENE 111 :

10

- 31600_s_at Cluster Incl. D38435:Homo sapiens hPMS3 mRNA, partial cds /cds=(0,772
 35119_at Cluster Incl. X56932:H.sapiens mRNA for 23 kD highly basic protein /cds
 34532_at Cluster Incl. AF035318:Homo sapiens clone 23705 mRNA sequence /cds=UNKN
 34928_at Cluster Incl. AF060865:Homo sapiens chromosome 16 zinc finger protein Z
15 35007_at Cluster Incl. AC004940:Homo sapiens PAC clone DJ0978E18 from 7p21 /cds=
 31866_at Cluster Incl. AC005239:Homo sapiens chromosome 19, cosmid F23149 /cds=(
 31873_at Cluster Incl. U52112:ARD1 N-acetyl transferase related protein /cds=(97
 32689_s_at Cluster Incl. D86096:Human DNA for prostaglandin E receptor EP3 subty
 33760_at Cluster Incl. AB017546:Homo sapiens Pex14 mRNA for peroxisomal membrane
20 35139_at Cluster Incl. AL049341:Homo sapiens mRNA; cDNA DKFZp566A163 (from
 clone
 35688_g_at Cluster Incl. Z24459:H.sapiens MTCP1 gene, exons 2A to 7 (and joined
 36005_at Cluster Incl. AF042800:Homo sapiens suppressor of white apricot homolog
 36538_at Cluster Incl. AB018314:Homo sapiens mRNA for KIAA0771 protein, partial
25 36545_s_at Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, comple
 37254_at Cluster Incl. U09366:Human zinc finger protein ZNF133 /cds=(445,2409) /
 37955_at Cluster Incl. AB015631:Homo sapiens mRNA for type II membrane protein,
 38648_at Cluster Incl. U80760:Homo sapiens CAGH1 alternate open reading frame mR
 39367_at Cluster Incl. AA522537:ni38e08.s1 Homo sapiens cDNA, 3 end /clone=IMAG
30 39423_f_at Cluster Incl. AJ000644:Homo sapiens mRNA for SPOP /cds=(157,1281) /gb
 40436_g_at Cluster Incl. J03592:Human ADP/ATP translocase mRNA, 3 end, clone pH
 41765_at Cluster Incl. AI541285:pec1.2-4.D10.r Homo sapiens cDNA, 5 end /clone_
 32246_g_at Cluster Incl. AF014837:Homo sapiens m6A methyltransferase (MT-A70) ge
 33406_at Cluster Incl. AL050345:Novel human gene mapping to chomosome 22 /cds=(1
35 35270_at Cluster Incl. W16505:zb05e12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-
 36132_at Cluster Incl. S74728:antiquitin=26g turgor protein homolog [human, kidn
 38751_i_at Cluster Incl. AA426364:zv61b06.s1 Homo sapiens cDNA, 3 end /clone=IM
 39184_at Cluster Incl. AI857469:w157f04.x1 Homo sapiens cDNA, 3 end /clone=IMAG
 40956_at Cluster Incl. X90857:H.sapiens mRNA for -14 gene, containing globin reg

1308_g_at D14533 /FEATURE= /DEFINITION=HUMXPAC Human mRNA for XPAC protein

METAGENE 112 :

5

31705_at Cluster Incl. X99977:H.sapiens ARS gene, component B /cds=(26,337) /gb=
 33637_g_at Cluster Incl. U87459:Human autoimmunogenic cancer/testis antigen NY-E
 38903_at Cluster Incl. AF099731:Homo sapiens connexin 31.1 (GJB5) gene, complete
 40402_at Cluster Incl. X91117:H.sapiens HG NET gene exon 1 /cds=(49,1902) /gb=X9
 10 40740_at Cluster Incl. M93650:Human paired box gene (PAX6) homologue, complete c
 41435_at Cluster Incl. AB014554:Homo sapiens mRNA for KIAA0654 protein, partial
 41469_at Cluster Incl. L10343:Huma elafin gene, complete cds /cds=(516,869) /gb=
 35978_at Cluster Incl. AF009242:Homo sapiens proline-rich Gla protein 1 (PRGP1)
 37576_at Cluster Incl. U52969:Human PEP19 (PCP4) mRNA, complete cds /cds=(81,269)
 15 39394_at Cluster Incl. AF007149:Homo sapiens clone 23568, 23621, 23795, 23873 an
 40150_at Cluster Incl. AA205857:zq50e04.r1 Homo sapiens cDNA, 5 end /clone=IMAG
 36178_at Cluster Incl. U23143:Human mitochondrial serine hydroxymethyltransferas

METAGENE 113 :

20

37873_g_at Cluster Incl. AF072468:Homo sapiens (JH8) mRNA, partial cds /cds=(0,1
 32047_at Cluster Incl. U91985:Human DNA fragmentation factor-45 mRNA, complete c
 40139_at Cluster Incl. U88966:Human protein rapamycin associated protein (FRAP2)
 33425_at Cluster Incl. X97548:H.sapiens mRNA for TIF1beta zinc finger protein /c
 25 37330_at Cluster Incl. U24266:Human pyrroline-5-carboxylate dehydrogenase (P5CDh
 37331_g_at Cluster Incl. U24266:Human pyrroline-5-carboxylate dehydrogenase (P5C
 39158_at Cluster Incl. AB021663:Homo sapiens mRNA for leucine-zipper protein, co
 41249_at Cluster Incl. AL031282:dJ283E3.6.1 (PUTATIVE novel protein similar to m
 382_at X70218 /FEATURE= /DEFINITION=HSPPX Homo sapiens mRNA for protein phosphat
 30 163_at U46461 /FEATURE= /DEFINITION=HSU46461 Human dishevelled homolog (DVL)
 mRN

METAGENE 114 :

35 31432_g_at Cluster Incl. U12255:Human IgG Fc receptor hFcRn mRNA, complete cds /
 38280_s_at Cluster Incl. W28432:47f2 Homo sapiens cDNA /gb=W28432 /gi=1308443 /u
 39408_at Cluster Incl. Z80345:H.sapiens SCAD gene, 5 UTR exon 1 and 2 (and joine
 41230_at Cluster Incl. U71087:Human MAP kinase kinase MEK5b mRNA, complete cds /
 35358_at Cluster Incl. AB028998:Homo sapiens mRNA for KIAA1075 protein, partial

- 39561_at Cluster Incl. AL008583:dJ327J16.3 (novel CHROMObox family protein) /cds
 40165_at Cluster Incl. AB015345:Homo sapiens HRIHFB2216 mRNA, partial cds /cds=(
 41596_s_at Cluster Incl. U43572:Human alpha-N-acetylglucosaminidase (NAGLU) gene
 33182_at Cluster Incl. AJ018523:ou47d07.x1 Homo sapiens cDNA, 3' end /clone=IMAG
5 1897_at L07594 /FEATURE= /DEFINITION=HUMTGFB3C Human transforming growth factor-
 1099_s_at L38503 /FEATURE= /DEFINITION=HUMGSTT2A Homo sapiens glutathione S-
 tran
 484_at U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-
- 10** METAGENE 115 :
- 35511_at Cluster Incl. AB014559:Homo sapiens mRNA for KIAA0659 protein, partial
 36422_s_at Cluster Incl. AF038198:Homo sapiens clone 23928 mRNA sequence /cds=UN
 34503_at Cluster Incl. AF007146:Homo sapiens clone 23686 and 23885 mRNA sequence
15 35428_g_at Cluster Incl. W28256:44b9 Homo sapiens cDNA /gb=W28256 /gi=1308204 /u
 37838_at Cluster Incl. M31315:Human coagulation factor XII (Hageman) mRNA, 3' en
 39276_g_at Cluster Incl. M76558:Human neuronal DHP-sensitive, voltage-dependent,
 40379_at Cluster Incl. J02625:Human cytochrome P-450j mRNA, complete cds /cds=(1
 32135_at Cluster Incl. U00968:Human SREBP-1 mRNA, complete cds /cds=(166,3609) /
20 40766_at Cluster Incl. U24578:Human RP1 and complement C4B precursor (C4B) genes
 38425_at Cluster Incl. U49719:Human hydroxymethylglutaryl-CoA lyase (HMGCL) gene
 38783_at Cluster Incl. J05581:Human polymorphic epithelial mucin (PEM) mRNA, com
 38784_g_at Cluster Incl. J05581:Human polymorphic epithelial mucin (PEM) mRNA, c
 38785_at Cluster Incl. X52228:Human mRNA for secreted epithelial tumour mucin an
25 40552_s_at Cluster Incl. AL049987:Homo sapiens mRNA; cDNA DKFZp564F112 (from clo
 41271_at Cluster Incl. Y18483:Homo sapiens mRNA for SLC7A8 protein /cds=(730,233
 1083_s_at M35093 /FEATURE=cds /DEFINITION=HUMETMAGA Human secreted
 epithelial tu
 1020_s_at U85611 /FEATURE= /DEFINITION=HSU85611 Human DNA-PK interaction
30 protein
 927_s_at J05582 /FEATURE=mRNA /DEFINITION=HUMPANMU Human pancreatic
 mucin mRNA,
 700_s_at Mucin 1, Epithelial, Alt. Splice 9
 247_s_at M26856 /FEATURE=cds /DEFINITION=HUMCP21OH Human 21-hydroxylase
35 B gene,

METAGENE 116 :

- 33634_at Cluster Incl. AF038007:Homo sapiens FIC1 mRNA, complete cds /cds=(0,375

- 34506_at Cluster Incl. M13928:Human delta-aminolevulinate dehydratase mRNA, comp
 32633_at Cluster Incl. U26591:Human clone IS10 diabetes mellitus type I autoanti
 32634_s_at Cluster Incl. U38260:Human islet cell autoantigen ICAp69 mRNA, comple
 36830_at Cluster Incl. U80034:Human mitochondrial intermediate peptidase precurs
 5 33375_at Cluster Incl. AB002387:Human mRNA for KIAA0389 gene, complete cds /cds=
 35313_at Cluster Incl. AB002308:Human mRNA for KIAA0310 gene, complete cds /cds=
 36959_at Cluster Incl. U49278:Homo sapiens UEV-1 (UBE2V) mRNA, partial cds /cds=
 40602_at Cluster Incl. AF052178:Homo sapiens clone 24523 mRNA sequence /cds=UNKN
 41841_at Cluster Incl. AF052138:Homo sapiens clone 23718 mRNA sequence /cds=UNKN
 10 1458_at M64572 /FEATURE= /DEFINITION=HUMCAP Human protein tyrosine phosphatase m

METAGENE 117 :

- 34084_at Cluster Incl. Z28339:H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-red
 15 35585_at Cluster Incl. X15675:Human pTR7 mRNA for repetitive sequence /cds=UNKNO
 36417_s_at Cluster Incl. AF035295:Homo sapiens clone 23623 mRNA, partial cds /cd
 33487_at Cluster Incl. D31628:Human gene for 4-hydroxyphenylpyruvic acid dioxyge
 37166_at Cluster Incl. Z29481:H.sapiens mRNA for 3-hydroxyanthranilic acid dioxy
 37430_at Cluster Incl. U78294:Homo sapiens 15S-lipoxygenase mRNA, complete cds /
 20 38178_at Cluster Incl. L40802:Homo sapiens 17-beta-hydroxysteroid dehydrogenase
 31841_at Cluster Incl. M94151:Human cadherin-associated protein-related (cap-r)
 33308_at Cluster Incl. M15182:Human beta-glucuronidase mRNA, complete cds /cds=(
 33699_at Cluster Incl. M18667:Human pepsinogen C gene /cds=(73,1230) /gb=M18667
 37203_at Cluster Incl. L07765:Human carboxylesterase mRNA, complete cds /cds=(67
 25 37540_at Cluster Incl. X69089:H.sapiens mRNA for skeletal muscle 165kD protein /
 38642_at Cluster Incl. Y10183:H.sapiens mRNA for MEMD protein /cds=(0,1748) /gb=
 39054_at Cluster Incl. X08020:Human mRNA for glutathione S-transferase subunit 4
 34892_at Cluster Incl. AF016266:Homo sapiens TRAIL receptor 2 mRNA, complete cds
 37322_s_at Cluster Incl. X82460:H.sapiens mRNA for 15-hydroxy prostaglandin dehy
 30 40201_at Cluster Incl. M76180:Human aromatic amino acid decarboxylase (ddc) mRNA
 692_s_at J02947 /FEATURE=mRNA /DEFINITION=HUMSODEC Human extracellular-
 superoxid
 556_s_at M96233 /FEATURE=expanded_cds /DEFINITION=HUMGSTM4A Human
 glutathione tr
 35 217_at S39329 /FEATURE= /DEFINITION=S39329 glandular kallikrein-1 {alternatively

METAGENE 118 :

- 34637_f_at Cluster Incl. M12963:Human class I alcohol dehydrogenase (ADH1) alpha